Genes from space: Leveraging Earth Observation satellites to monitor genetic diversity

Running title: EO to monitor genetic diversity

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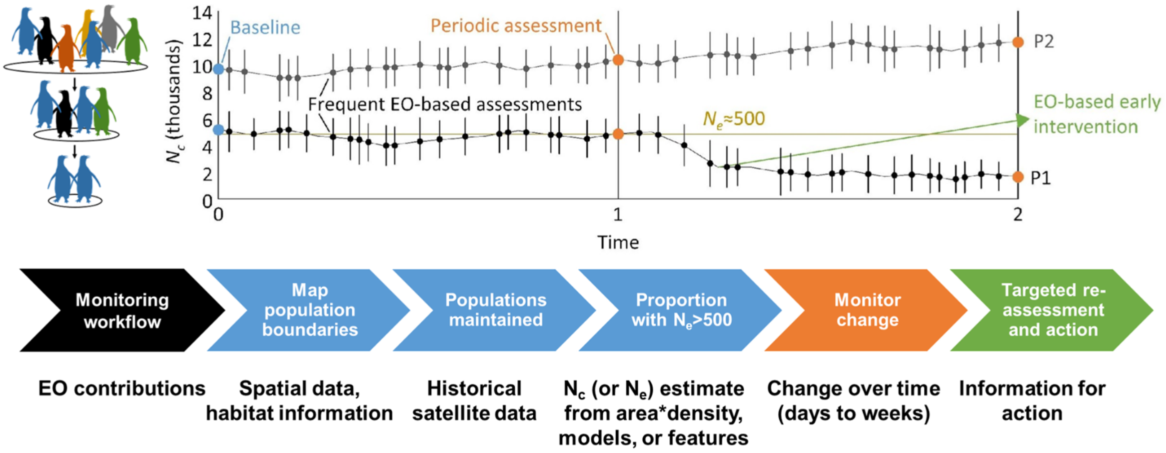
Abstract

Genetic diversity within and among populations is essential for species persistence. While targets and indicators for genetic diversity are captured in the Kunming-Montreal Global Biodiversity Framework, assessing genetic diversity across many species at national and regional scales remains challenging. Parties to the Convention on Biological Diversity (CBD) need accessible tools for reliable and efficient monitoring at relevant scales. Here, we describe how Earth Observation satellites (EO) make essential contributions to enable, accelerate, and improve genetic diversity monitoring and preservation. Specifically, we introduce a workflow integrating EO into existing genetic diversity monitoring strategies and present a set of examples where EO data is or can be integrated to improve assessment, monitoring, and conservation. We describe how available EO data can be integrated in innovative ways to support calculation of the genetic diversity indicators of the GBF monitoring framework and to inform management and monitoring decisions, especially in areas with limited research infrastructure or access. We also describe novel, integrative approaches to improve the indicators that can be implemented with the coming generation of EO data, and new capabilities that will provide unprecedented detail to characterize the changes to Earth's surface and their implications for biodiversity, on a global scale.

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



*Earth observation satellites (EO) support and improve the establishment of baseline data, effective regular monitoring, and targeted re-assessment and interventions to conserve the genetic diversity of natural populations. Top: Example trajectories are shown for two imaginary populations, P1 and P2: P1 drifts below the threshold for the effective population size (N_e) > 500 headline indicator for genetic diversity monitoring, and P2 is maintained above this threshold close to an N_e of ca. 1 000 (N_e ~ 0.1 * N_c, where N_c is the census number of reproductively mature adults and N_e is the genetically effective population size). Bottom: Overview of general workflow and contributions of EO.*

Introduction

Genetic diversity is an essential aspect of biodiversity protection

International treaties and national programs for the protection of biodiversity have required assessments of the state of nature since the 1970s, for example the 1971 Ramsar Convention on Wetlands (Director, Office of International Standards and Legal Affairs & United Nations Educational, Scientific and Cultural Organization (UNESCO), 1994), the 1992 Convention on Biological Diversity (Secretariat of the Convention on Biological Diversity, 2011), the 2010 Aichi Biodiversity Targets (Conference of the Parties to the Convention on Biological Diversity, 2010), the 2015 Sustainable Development Goals[1], and the 2022 Kunming-Montreal Global Biodiversity Framework, which for the first time includes specific indicators to measure progress (Conference of the Parties to the Convention on Biological Diversity, 2022a). Genetic diversity is a foundational level of biodiversity that occurs below the species level, within and between populations (Allendorf, 2017). Genetic diversity underpins the adaptive potential which allows species to persist in the face of change (i.e., resilience and resistance) and is central to fitness of individuals. Genetic diversity loss eventually leads to inbreeding, maladaptation, population decline, and eventually extinction. Therefore, genetic diversity needs to be monitored as part of biodiversity assessments, conservation and restoration actions, and for safeguarding nature's contributions to people (Hoban, Bruford, et al., 2021; Hoban et al., 2020). Studies of multi-species genetic diversity trends have only recently become possible, and indicate loss over time as a result of human activities (Exposito-Alonso et al., 2022; Leigh et al., 2019; Millette et al., 2020).

Measuring genetic diversity usually involves DNA-based data collected from a comprehensive sample of a species, as when assessing genetic Essential Biodiversity Variables (EBVs) (**Box 1**) (Hoban et al., 2022; Junker et al., 2023; Navarro et al., 2017; Pereira et al., 2013). Despite technological advances, sequencing DNA from individuals remains laborious, expensive – in the range of 10-1000 USD / sample depending on technique, genome size, and coverage, *not* including the cost to obtain the DNA samples in the first place, e.g. (Lou et al., 2021) – and thus difficult to repeat across many species at national and global scales. To overcome this challenge, indicators for genetic diversity have been developed for country- and global-scale genetic diversity assessments and monitoring, which can be assessed with or without DNA-based data (Hoban et al., 2020; Laikre et al., 2020; Mastretta-Yanes et al., 2023) (**Box 2**).

The first indicator focuses on genetic diversity within populations and comprises the proportion of populations within a species having an effective population size (N_e) > 500, which is an approximate, yet efficient, threshold to avoid the loss of quantitative genetic variation and adaptive potential over time (Crow & Kimura, 2009; Frankham, 1995, 2022; Franklin, 1980; Hoban et al., 2020, 2023, 2024; Jamieson & Allendorf, 2012; Laikre et al., 2020) but see (Frankham et al., 2014); hereafter the "N_e > 500 indicator". Importantly, the N_e can be estimated based on DNA data, or it can be approximated as 10% of the number of mature individuals

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

(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). A second indicator focuses on conserving genetic diversity between populations, and it is estimated as the proportion of populations within species that are maintained over time, hereafter the “PM indicator” (Hoban et al., 2020, 2023, 2024; Laikre et al., 2020; Mastretta-Yanes et al., 2023). This 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 the gold standard for quantifying genetic diversity locally, these indicators offer a globally affordable and accessible metrics to facilitate immediate monitoring (Hunter et al., 2024).

Box 1: 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 2**).
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 2**).
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: degree of genetic differentiation among populations or units. Related to the PM indicator.

The indicators were adopted by the United Nations Parties to the Convention on Biological Diversity (CBD) at the fifteenth meeting of the Conference of the Parties (COP15) in 2022, by the monitoring framework of the Kunming-Montreal Global Biodiversity Framework (GBF, CBD/COP/DEC/15/5) (Conference of the Parties to the Convention on Biological Diversity, 2022b), and are expected to be reported by CBD Parties. Concretely, this means that signing Parties must monitor genetic diversity to prevent its loss, and provide reports every five years. The first reports are expected in 2026, and thus it is urgent to implement existing genetic monitoring approaches for indicator assessments (Andersson et al., 2022; *Genetic Diversity Indicator Guidelines*, 2024/2024; Hoban et al., 2023; Mastretta-Yanes et al., 2023; Thurfjell et al., 2022) and to further develop scalable, globally accessible and affordable methods for genetic diversity indicator calculation.

To facilitate the implementation of reporting for the genetic diversity indicators, researchers and practitioners recently assessed these indicators in nine countries utilizing existing DNA studies, census population sizes, and georeferenced occurrence data (Mastretta-Yanes et al., 2023). Challenges identified in this assessment were the lack of 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.

Box 2: CBD genetic diversity indicators

The $N_e > 500$ indicator. This is headline indicator A.4 in the KMGBF monitoring framework. Effective population size (N_e) is a key parameter in population genetics that is used to quantify the rate at which quantitative 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 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 relationship between N_e and N_c 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 are needed. Therefore the census size can be used in the absence of other N_e assessments. Identifying populations and determining whether or not they comprise at least 5000 reproductively mature individuals is a simplified way to assess and monitor the maintenance of genetic diversity within populations (Laikre et al. 2020, Hoban et al. 2020, 2023, 2024).

The populations maintained (PM) indicator. This is a complimentary indicator to $N_e > 500$ in the KMGBF monitoring framework. In order to calculate the proportion of populations above the N_e threshold, it is first necessary to know how many populations there are. However, the number of biogeographically distinct populations that are maintained within a species is already an important indicator of its genetic diversity. This is 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). Thus, populations can harbor unique genetic diversity that can be detected with DNA-based methods (Andersson et al. 2022). If a population is lost, the genetic diversity within this population is also lost, and this can include unique genotypes. Thus, it is 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).

Earth Observation satellites as a method for biodiversity assessment

Earth Observation satellites (EO), equipped with passive instruments (that measure reflected and emitted radiation from Earth's atmosphere and surface) or active instruments (with their own source of energy to illuminate the atmosphere or Earth's surface), 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 and assess changes in biodiversity (Mairota et al., 2015). While Earth observation is also conducted with airborne and field-mobile platforms, here we focus on space-based EO such as the Copernicus Sentinel satellites and the NASA Earth Observing System (EOS) (**Table 1**), which make (global) data publicly available and free of charge (Malenovský et al., 2012).

***Table 1**. EO platforms that lower or eliminate technical and financial barriers to using EO for genetic diversity monitoring and other applications by non-EO experts.*

	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
	Google Earth Pro Desktop	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)
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 repository on satellite data	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

EO data have unique attributes such as covering large geographical 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 various information for environmental analyses and biodiversity monitoring often at the ecosystem level. Examples are land use and land cover (LULC) change, vegetation biochemical properties and conditions, structural information such as green leaf area index (LAI), vegetation height, land surface phenology, and photosynthetically active radiation (PAR) that determine vegetation health and productivity (Verrelst et al., 2015). This information is then often used in models to determine species composition and other properties of ecosystems at the landscape level (Mayor et al., 2024; Pasetto et al., 2018). However, EO data is not widely considered to be useful for genetic diversity monitoring and assessment (Skidmore et al., 2021; Timmermans & Kissling, 2023), although there are some demonstrations of its potential for this purpose (Fernández, 2013; Schuman et al., 2023). 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 2**) to facilitate the monitoring, assessment and conservation of genetic diversity in support of the GBF.

EO contributions to genetic diversity monitoring: an overview

Whether a population still exists, and whether it has grown, shrunk, or maintained its size, is often linked to changes in its habitat (Mace et al., 2010). EO can support monitoring of changes in habitat area and conditions and the composition and size of populations, including the likelihood of their continued existence, thus supporting estimations of the PM indicator. This relies on the assumptions that a habitat patch of a particular size can support a species population; that habitat quality can be sufficiently well assessed by EO; and that the considered threats to populations are visible at the habitat scale (e.g., land-use change, but not poaching). Thus, some evidence of species occupation or activity (Example 1: Emperor Penguins), habitat changes such as land cover or land use change (Example 2: Crop Wild Relatives), or landscape modification and fragmentation can be detected and quantified using EO for the assessment of PM (**Figure 1**).

Similarly, the size of particular habitat patches can be monitored using EO. By estimating a relationship between habitat size and the number of mature individuals of a species living in this habitat, EO can be used to estimate changes in N_c and, in some cases (for large and immobile individuals such as trees), N_c may be more directly estimated from EO (Example 3: Common Beech forests). 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 (**Figure 1**).

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

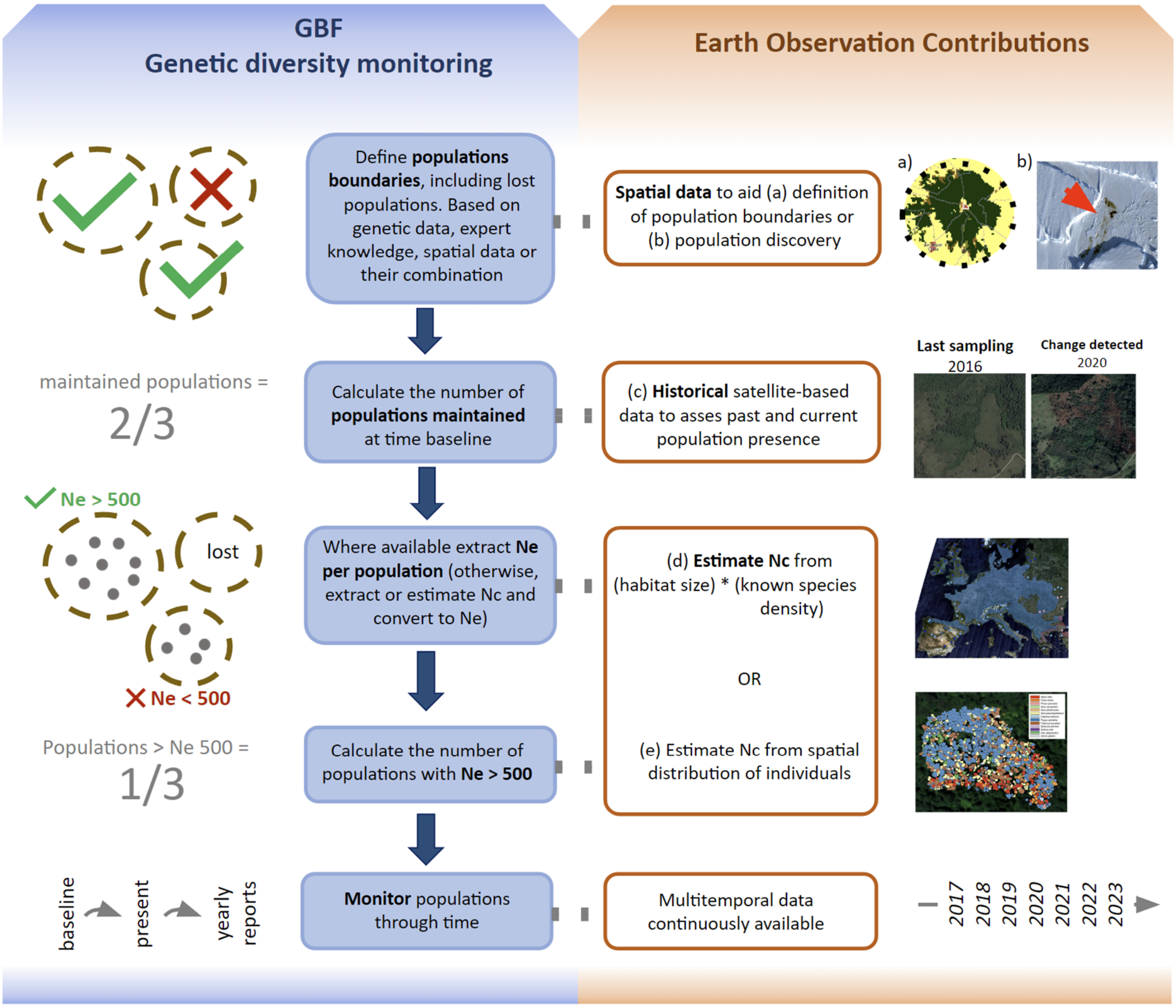

Figure 1. *Overview of the proposed workflow for integrating EO data into genetic diversity monitoring in the GBF (see also **Box 3**).*

Uniquely and importantly, EO typically provide repeat measurements on a time scale of days to weeks, globally. For example, the Copernicus Sentinel-2 mission monitors the entire globe in five days with multi-spectral images, with more frequent observations for some locations on Earth depending on the satellite orbit[3,4]. The Sentinel family of satellites have observed the Earth surface with different instruments continuously starting in 2014, detecting radiation in the visible, infrared, microwave, and other ranges with maximum 10 spatial resolution, depending on the satellite, continuously (Malenovský et al., 2012). Sentinel-2 as one out of the currently five different sensor types in orbit images the reflected sunlight from the Earth in differentl spectral bands. It can be used to assess, for example, vegetation properties such as LAI from

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

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

visible and near-infrared measurements (Sebastiani et al., 2023) or vegetation conditions such as water content from short-wave infrared measurements (Helfenstein et al., 2024). The open-access Copernicus Sentinel data 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 in this way 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, freely available data from the Copernicus 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 without the time-consuming, inefficient, and sometimes infeasible process of downloading a very large amount of data to a local computer for analysis, and supports simple analysis of large numbers of observations. This facilitates much-needed access to the resulting information by researchers and other stakeholders, especially for areas with limited observations or that are difficult to access.

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.

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 4**) (Pahlevan et al., 2021; Silva et al., 2008). The integration of EO data as an additional source of information in genetic indicator assessments and monitoring requires the co-development and production of such information through collaboration among experts in population and conservation genetics and genomics, remote sensing, geography and

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

geospatial information, ecology, conservation, and practitioners who will ultimately use this information routinely.

Box 4: What to know when using EO
Key references are given in the main text referring to Box 4.

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. 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.
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.
6. 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 may not be possible for datasets leveraging AI or interpolation to improve spatial resolution or image aesthetics.

EO contributions to genetic diversity monitoring: three examples

Here, we describe how EO can be used to facilitate genetic diversity monitoring according to the GBF and support the further implementation of genetic diversity indicators. Three examples: emperor penguins in Antarctica, crop wild relatives in Mexico, and common beech forests in Europe (**Table 2**), demonstrate what is possible today, and where additional development is needed. The third example also illustrates how advances in EO capabilities (e.g., spectral and spatial resolution) can provide additional information towards more precise assessments of the indicators or even assessing genetic EBVs, beyond what is available and possible to do today.

***Table 2**. Overview of examples.*

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 ● Difficult to estimate colony size from space 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
Common beech in European forests	Infer PM and N_e Infer genetic EBVs	Inference based on forest coverage and biochemical and structural differences mapped across tree canopies	● Geographic isolation ≠ genetic isolation due to wind pollination ● Only dominant trees are 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)

Example 1: Finding penguins by their poo

Key points

The identification and monitoring of emperor penguin (*Aptenodytes forsteri*) colonies in Antarctica by EO is only a step away from using EO to estimate the $N_e > 500$ and PM indicators. Emperor penguins are considered a biomonitor of ecosystem change in the Southern Ocean, as they occur throughout the seasonal pack-ice areas, tend to stably occupy specific sites, and are long-lived upper-trophic-level predators (Bargagli, 2005; Kato et al., 2004; Kooyman & Mullins, 1990). Not only do these birds live in one of the most inaccessible and inhospitable areas on Earth, but their habitat is under increasing threat from global and regional climate change, in particular changes in sea-ice distribution, marine food webs, and storm frequency and intensity. EO have become useful for monitoring penguin colonies, taking advantage of the sharp contrast between penguins, their dark guano, and the background ice.

Detailed description

Barber-Meyer and colleagues (Barber-Meyer et al., 2007) characterized two new penguin colonies using a combination of multispectral and panchromatic images retrieved from the QuickBird satellite from September–November 2005 and 2006 (**Figure 2**). Data from five other known colonies, with abundance data obtained from ground counts or aerial photography, was then used to develop a regression equation to estimate relative abundances (< 3 000 or > 5 000 adult birds) from panchromatic satellite image classifications for the two inaccessible colonies. This study demonstrated how to leverage EO with other observations to obtain unique data on colony occurrence and size while offering a feasible approach to monitor changes in colonies. This was possible even given limitations such as the need to collect images during a short time window months with minimal shadows in Antarctica (e.g., November with highest solar angle) and to combine multispectral (superior differentiation of penguins, guano, and ice but low spatial resolution) with panchromatic (higher resolution) images (**Figure 2**). Genetic data show that colonies interact and are genetically mixed (Younger et al., 2017). There are at least four geographically distinct emperor penguin metapopulations, each comprising several colonies. Thus, for the PM and $N_e > 500$ indicators to be assessed and tracked, these Earth Observation-detected colonies must be assigned to the four genetically detected metapopulations.

Fretwell & Trathan used Landsat ETM (Enhanced Thematic Mapper) images from the Landsat Image Mosaic of Antarctica (LIMA[6]) to detect fecal staining of ice to indicate colony locations (P. T. Fretwell & Trathan, 2009). Thanks to an estimated 85-95 % coverage of the entire coastline due to the Landsat multi-decadal archive, this study identified 10 new sites of colony occupation, relocated or corrected positions for six other breeding sites, and confirmed the positions of 17 previously identified sites. This pan-Antarctic delineation of emperor penguin distribution set the benchmark for colony trajectory assessments. A subsequent satellite-based study confirmed 37 out of the 38 colonies found (P. T. Fretwell et al., 2012). The 2012 study was based on satellite imagery from QuickBird, WorldView-2 and Ikonos satellites with 10 m spatial resolution to complement the Landsat ETM 30 m images (or 15 m panchromatic images). The relationship between the colony area (m^2) and the number of adult birds present at a colony was estimated using linear regression with data from seven colonies where both estimates from satellites and direct counts were available. This allowed an estimation of total population size in 2009 notwithstanding uncertainties, in particular due to methodological errors and natural variability. This study demonstrated the use of EO to monitor emperor penguin population size and population persistence in consecutive breeding seasons and on regional to global scales.

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[6] https://lima.usgs.gov/

With the launch of Copernicus Sentinel-2 satellites, Fretwell and Trathan used optical imagery from 2016, 2018 and 2019 to locate emperor penguin colonies across the entire continent of Antarctica (P. T. Fretwell & Trathan, 2021). Eleven additional new colonies were identified, and a first-order assessment of colony size was attempted using the comparative sizes of previously known colonies. These preliminary assessments allowed the authors to conclude that the new colonies may increase the total global population size estimated by Jenouvrier and colleagues by 5–10% (Jenouvrier et al., 2020).

Taking a combined Earth Observation approach that leveraged the broader coverage of Copernicus Sentinel-2 imagery with the Very High-Resolution WorldView-3 imagery (spatial resolution down to 0.3 m) enabled the investigation of seasonal effects of breeding. The first recorded incident of widespread breeding failure linked to large-scale sea ice loss was reported by Fretwell and colleagues, with four out of five colonies experiencing total or near-total breeding failure in 2022 (P. T. Fretwell et al., 2023). The study was prompted by a climate-related event: in early December 2022, the sea ice extent across Antarctica reached an all-time low, with the greatest regional negative anomaly recorded in the Bellingshausen Sea region, west of the Antarctic Peninsula where, during November, some regions lost 100% of sea ice extent. Emperor penguins breed on landfast sea ice: compact sea ice held in place by ice shelves and grounded icebergs. For successful breeding, this ice must remain stable from April to January. Four sites with visible colonies in late October 2022 or early November 2022 did not present any visible sign of a colony (i.e., brown indicative pixels on sea ice) by the start of the fledgling season in early December 2022.

Collectively, these studies indicate how EO can provide complementary and cost-effective data for genetic indicator assessments for a biomonitor species in an inaccessible location. Colony size estimation via EO opens the way for continuous estimation of the $N_e > 500$ indicator as well as the PM indicator, although these calculations must be evaluated in terms of the four genetically detected metapopulations (Younger et al., 2017). This may be achieved by leveraging additional EO information on habitat. Labrousse and colleagues investigated how different habitats are associated with the presence of emperor penguins around Antarctica based on landfast sea ice extent and variability data, intra- and interspecific trophic competition factors, and geography (Labrousse et al., 2023). They calculated landfast sea ice extent from March 2000 to March 2018 at 1 km and 15-day resolution from NASA MODIS data. The team combined a principal component analysis of the environmental variables and a model-based Bayesian clustering approach, identifying five geographically distinct habitat clusters, with the fifth cluster in a restricted geographic extent where three colonies live. Interestingly, four of these clusters corresponded to the four metapopulations identified by DNA-based analyses (Younger et al., 2017). This suggests that the identified genetic structure may be associated with adaptation to specific habitat conditions, and thus each metapopulation likely houses unique genetic variation. Accordingly, the identified breeding populations and habitats should be considered separate units for genetic monitoring, management, and population projections. These habitat clusters show differences in extent and projected future persistence of landfast sea ice, and thus may have very different future success rates. As extreme climate-related events are expected to occur more frequently and with greater severity, the temporal resolution provided by EO data is vital to signal harmful biodiversity loss and guide conservation intervention. Such information can be used to project expected trends in genetic indicators and help guide species management. Similar models of habitat suitability can be built for other species and will be particularly relevant for the PM indicator. This example with emperor penguins can pave the way for developing new methods and analytical procedures applicable to other organisms and habitats, as already demonstrated for some other seabirds (P. T. Fretwell et al., 2015).

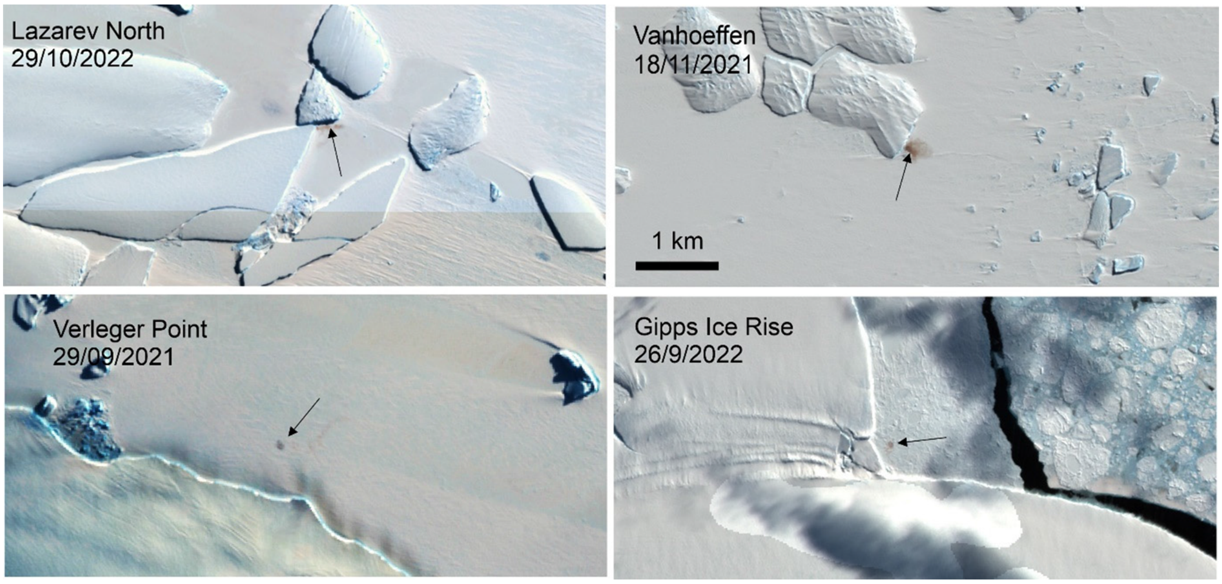


***Figure 2**. Sentinel-2 images of the four new sites taken at consistent scale. Arrows show locations of emperor penguin colonies. Image and caption from Figure 2 of (P. Fretwell, 2024), CC BY.*

Example 2: Monitoring habitat and population maintenance in wild relatives of domesticated crops

Key points

EO are not yet used to monitor crop wild relatives (wild plant species closely related to modern-day crops), but this could be achieved using publicly available EO data in a few straightforward steps. The wild relatives of modern-day crops harbor an important proportion of crops' genetic diversity (Maxted et al., 2006). In Mexico, crop wild relatives 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 or individuals of these species cannot be directly observed from EO due to limited size or number, 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 and assessed using EO to infer which populations may be experiencing greater decline.

Biogeographical information and species distribution models can be employed to assess the risks to PM and N_e posed by spatial patterns of habitat loss. Initial data on population locations and size are needed as a baseline, and EO can effectively be used to monitor habitat change and prioritize field visits, management and conservation actions.

Detailed description

Habitat loss due to logging and conversion to agriculture or urban development is a global threat to biodiversity (Tilman et al., 2017). For instance, most Mesoamerican crop wild relatives are affected by agriculture and urban development (65% and 25% of assessed species, respectively) (Goettsch et al., 2021). In terms of its impact on genetic diversity, habitat loss could mean population extinction (habitat annihilation in a given region, PM decline) or shrinkage of the effective population size (smaller habitat space, fewer individuals, N_e decline and thus elevated loss of genetic diversity through genetic drift). The first step in assessing whether habitat loss affects populations of species is to define population boundaries (**Figure 1**) based on occurrence points 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 in terms of time and cost. Importantly, access to the locations may also be restricted or unsafe due to geopolitical conflicts and security issues (Malthaner, 2014). EO data can be used in such situations to detect habitat loss using either visual inspection of satellite images or a variety of spatial and temporal data analysis methods based on time series of land use or land cover change, such as tree-cover loss, derived from EO data. In the following examples, we describe how freely available and accessible data and online platforms could be used for monitoring habitat and population maintenance to support the assessment of the PM and $N_e > 500$ indicators. We focus on Sentinel Hub, Google Earth, and Global Forest Watch (**Table 1**) as examples of easily accessible and widely used data archive and analysis hubs.

Wild avocados (*Persea* spp.) grow among the tree species composing cloud forests, Mexico's most biodiverse terrestrial ecosystem type per unit area (Conabio, 2023; Rojas-Soto et al., 2012). *Persea* (*P.*) *cinerascens*, as an example, occupies less than 500 km^2 in a total of five populations separated by ca. 50-200 km in three geographic locations (*Persea cinerascens*, n.d.). The species' presence was confirmed during the last visit to the known field localities in 2017, although no population size measurement was conducted. Similarly, the location of a teosinte species (*Zea* [*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 that data, the N_e of both teosinte populations is below

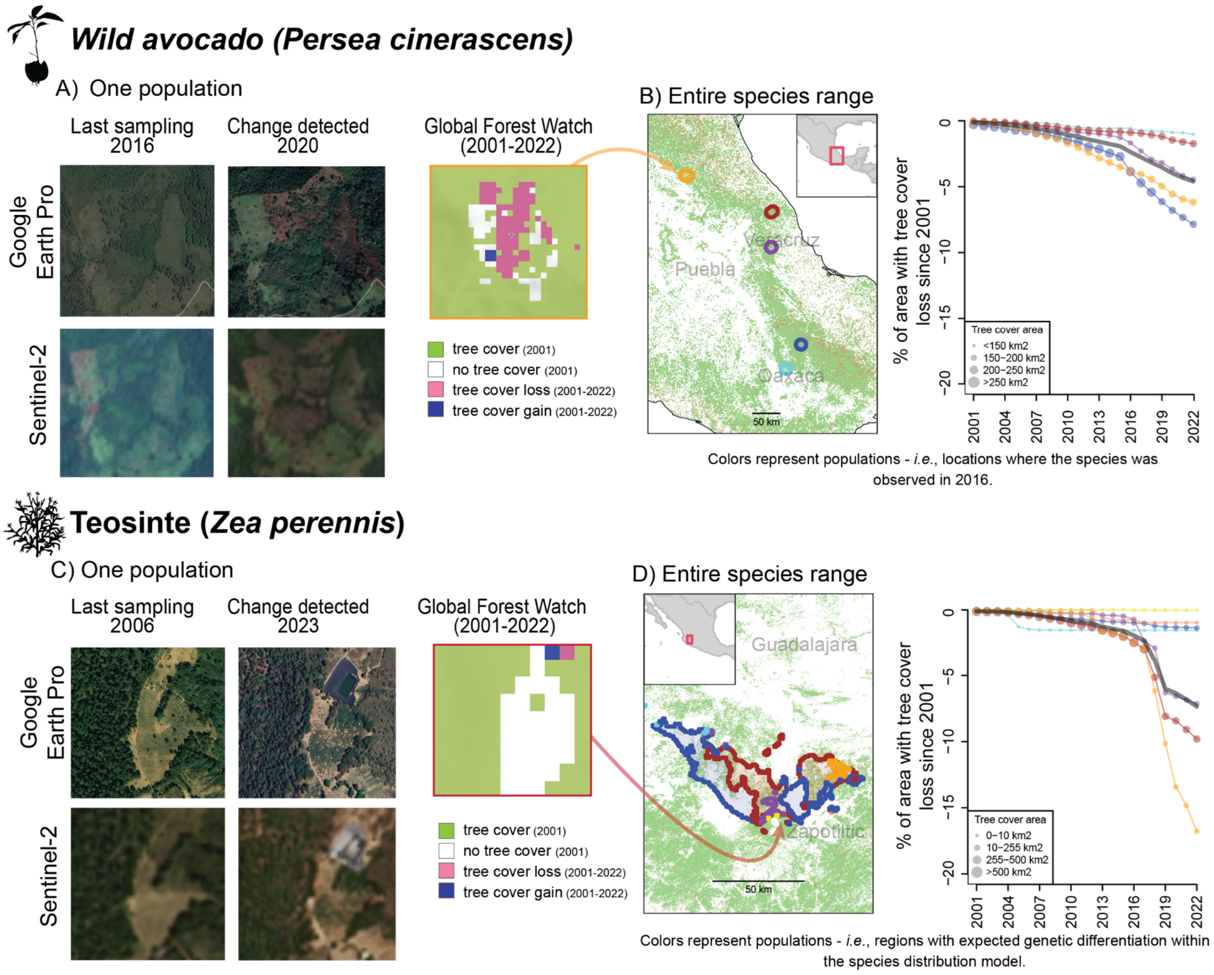
500, so the $N_e > 500$ indicator value for the species is zero according to the first multinational assessment of genetic diversity indicators (Mastretta-Yanes et al., 2023).

Unfortunately, although populations of both species were observed in the field relatively recently (2017 and 2008, respectively), their habitat is expected to have decreased or even disappeared entirely due to rapid land use change. Cloud forests (wild avocado habitat) face particularly alarming deforestation rates, with half of them already lost in the last few decades, and 55% of the remaining habitat degraded (Conabio, 2023; Rojas-Soto et al., 2012). Visiting the wild avocado locations is not cost-effective because they are in remote mountain areas. In the teosinte case, it was hypothesized that the teosinte populations might have disappeared as a result of land use change – ironically, due to domesticated avocado farming. Avocado farms have been expanding in the region at very high rates (Ramírez-Mejía et al., 2022), and are expected to further increase 117% by 2050 relative to 2011 (Denvir, 2023). Visiting the teosinte habitat has also become prohibitively dangerous since 2008, due to organized crime and associated personnel safety risks.

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

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., drought season) and examining such an annual time series.

Additionally, derived products 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 gain derived through automated interpretation of 30 x 30 m EO data (Hansen et al., 2013; Potapov et al., 2022). Although each dataset comes with its own caveats, such as the potential misidentification of oil palm plantations as “tree cover”, their accuracy is generally high and documented. 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) (**Figure 3B and D**). Given sufficient expert knowledge, automated and statistical analysis of EO data can also be tailored to specific needs using freely available datasets and platforms like Google Earth Engine[7]. A combination of these EO data enabled us to identify land use and cover changes, such as the gradual encroachment of agricultural activities into previously undisturbed habitats, thus providing valuable insights into the dynamics of habitat degradation and its implications for population monitoring, particularly for populations of *P. cinerascens* and *Z. perennis* in Mexico.



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

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*

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[7] https://earthengine.google.com/

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.

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, e.g., (Tobón-Niedfeldt et al., 2022). For species with few occurrences – which is often the case for crop wild relatives – 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, 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 or cover change can be quantified and assessed in terms of habitat loss trends. For instance, in the case of wild avocado (**Figure 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 (**Figure 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. This example shows how habitat monitoring by EO can inform the assessment of the GBF indicators and the prioritization of *in situ* observations.

Example 3: A window into the future – assessing genetic diversity and resilience of beech forests using EO

Key points

EO can be used to assess important aspects of forest canopy structure, phenology and functions such as their height and density, greening and browning, pigment concentration and water content, or to characterize tree species and even within-species variation. These attributes of forests are the subject of active research and, with evolving EO technology and knowledge, have the potential to help improve indicators of genetic diversity for monitoring. Especially for dominant tree species that tend to form large portions of temperate forest canopies, it is possible to build on these developments to estimate and monitor change in the PM and N_e > 500 indicators from repeated EO data over forests. To illustrate the current state of research and development, we use the common beech, *Fagus sylvatica*, a keystone tree species forming forests across Europe into Eurasia, where it is also economically important.

This wind-pollinated species has relatively low genetic differentiation among different forest stands (Stefanini et al., 2023), making divisions into populations challenging. N_e estimates are likewise challenging: for example, genetic analysis of a stand in France with 167 individuals yielded in N_e estimates ranging from 2-25 depending on the calculation method used (Gargiulo et al., 2024). We describe how the current and new developments in EO technologies can support the assessment of beech genetic diversity, and illustrate the potential for upscaling these approaches to EO to develop and calculate genetic diversity indicators.

Detailed description

Common beech is normally considered to form two subspecies: the European beech *F. sylvatica sylvatica* and the Oriental beech *F. sylvatica orientalis* (Hrivnák et al., 2022). We have overlaid detailed 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) (**Figure 4**). The weak, yet discernible genetic structure of beech reveals its post-glacial migration history but also depends on management and planting decisions in forestry. Decades of population genetics studies 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. Due to the difficulties in comparing results from these different methods, only subsets of these data can be combined to estimate patterns of genetic diversity across the species range (Stefanini et al., 2023) and to support the definition of populations or meta-populations as input to our proposed monitoring workflow (**Figure 1**). For common beech, as for many forest trees, it is more straightforward to monitor the condition of forest stands than to monitor populations, similar to monitoring the condition of penguin colonies that form meta-populations (Example 1).

To estimate the potential occurrence and coverage of *F. sylvatica*, distribution data over the species range (e.g., **Figure 4**) can be divided into forested and non-forested areas (e.g., with LULC) and, within these, into 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. As a further option, 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 (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 developing such Earth Observation-based species classification (Fassnacht et al., 2016).

Such data are available from the Laegern forest in Switzerland, a temperate mixed forest with a high proportion of *F. sylvatica sylvatica*. Laegern is the subject of over a decade of remote sensing data collection by 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 sylvatica* versus all other trees in a beech-dominated stand at Laegern (**Figures 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 both subspecies of beech are co-planted, D'Odorico and colleagues distinguished the subspecies with somewhat lower accuracy (kappa accuracy of 67-72%) using in-field spectroscopy for leaves from the top of tree canopies, with a similar spectral range and resolution as imaging spectroscopy (D'Odorico et al., 2023). They used either leaf traits (nitrogen, lignin, cellulose, leaf mass per area, water, wax, and pigmentation) estimated from the spectroscopy data), or else a set of specific (short-wave infrared) wavelengths. Both of these approaches used signal characteristics overlapping with the detection ranges of current EO instruments, indicating that current EO could already be used to distinguish and quantify the relative abundance of beech subspecies.

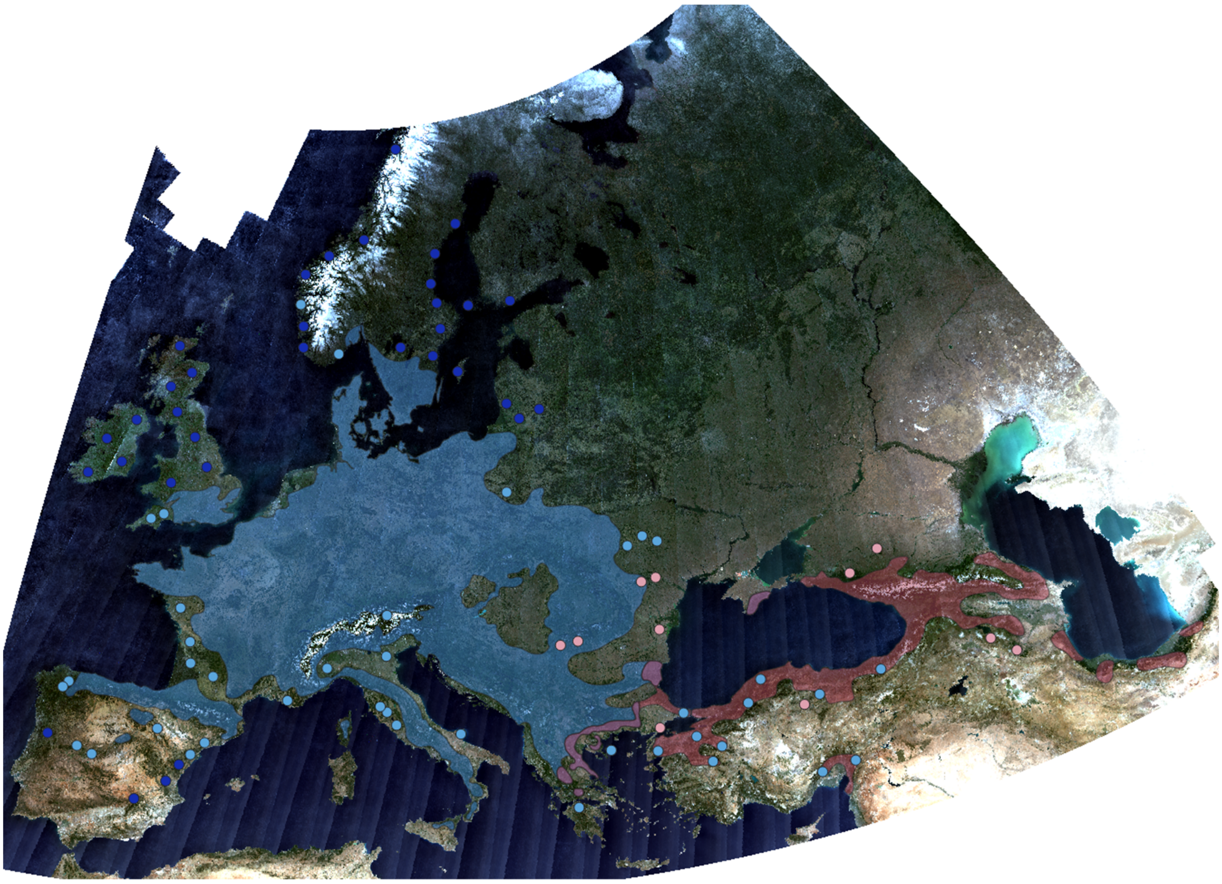

Figure 4*. Layers of geospatial information on the distribution of* Fagus sylvatica*: Sentinel-2 mosaic from Google Earth Engine (Gorelick et al., 2017) for visualization purposes, overlaid with species distribution and isolated localities (dots) (Caudullo et al., 2017):* F. sylvatica sylvatica *(blue)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

Thus, a census number (N_c) of reproductively mature beech trees could be locally estimated directly from beech canopy pixels discernible from EO data, e.g. using images with 1-10 m spatial resolution as introduced in Example 1, via species (and subspecies) classification. This could then be used to approximate the $N_e > 500$ indicator. This would likely yield an underestimate because N_c from EO would count reproductively mature, dominant 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, can 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* can also be assessed by forest cover loss, similarly to Example 2, and predicted by assessing changes in canopy vitality via changes in trait values (Helfenstein et al., 2024; Sturm et al., 2022) (**Figure 5**).

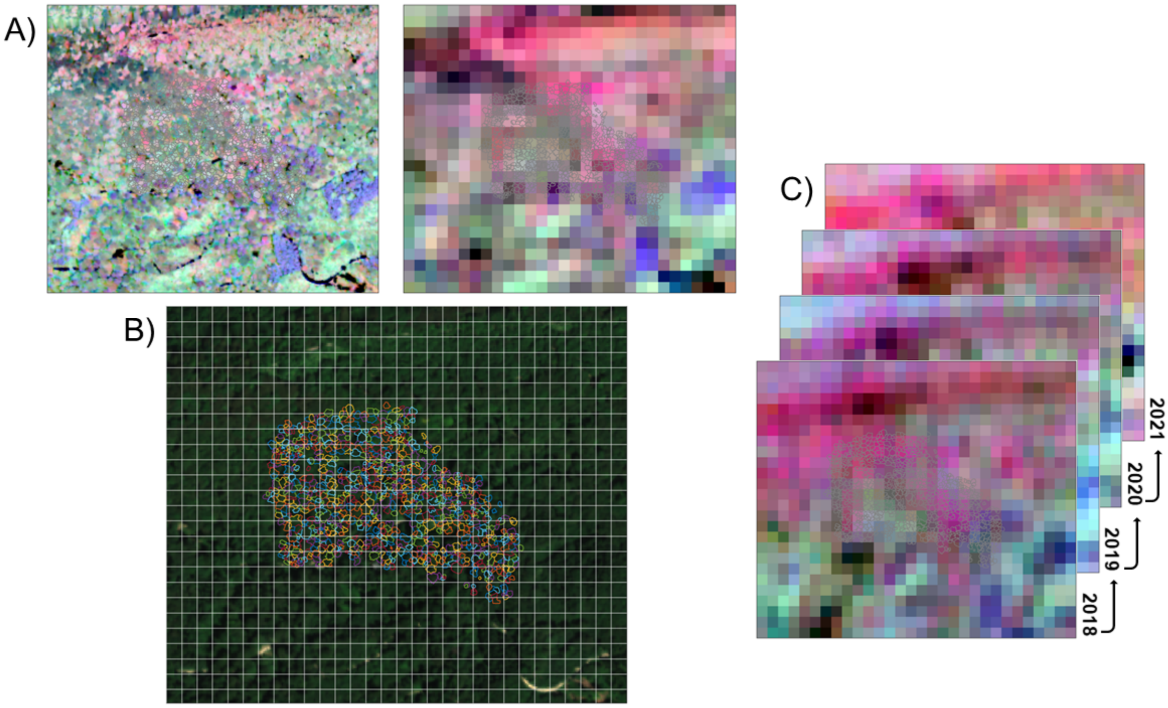

***Figure 5**. Components of change monitoring over forest canopies using EO. A) Spatial scaling of the canopy traits chlorophyll (green), carotenoids (red) and water content (blue) assessed using 2-m aerial imaging spectroscopy data (left), or 20-m EO data (right). B) 20-m Sentinel-2 pixels compared 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.*

Czyż and colleagues used time series data from imaging spectroscopy 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 **Figure 6A**), and correlated these differences 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) (**Figure 6B**). This illustrates that features that can be used to predict genetic variation based on EO are also affected by environmental factors. Interestingly, while European beech forests are increasingly threatened by drought, individual trees vary in their susceptibility, in part due to genetic differences (Bolte et al., 2016; Braun et al., 2021; Pfenninger et al., 2021). Such studies help to investigate how predictable these 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 (**Figures 5 and 6**). Combined with a large and growing database of single-time-point genetic data for beech across its range, it is also 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 1**). 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 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 spatial and spectral resolution and thus relatively high certainty in assigning spectral data to individual trees (Czyż et al., 2023; D’Odorico et al., 2023; Petibon et al., 2021). Scaling approaches are currently being established, starting with trait estimates such as canopy pigmentation and water content that are already possible with space-based EO multispectral sensors (Helfenstein et al., 2022) (**Figure 5**).

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 (Czyż et al., 2023; D’Odorico et al., 2023; Fassnacht et al., 2016; Helfenstein et al., 2022; Li et al., 2023; Petibon et al., 2021; Torabzadeh et al., 2019).

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

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

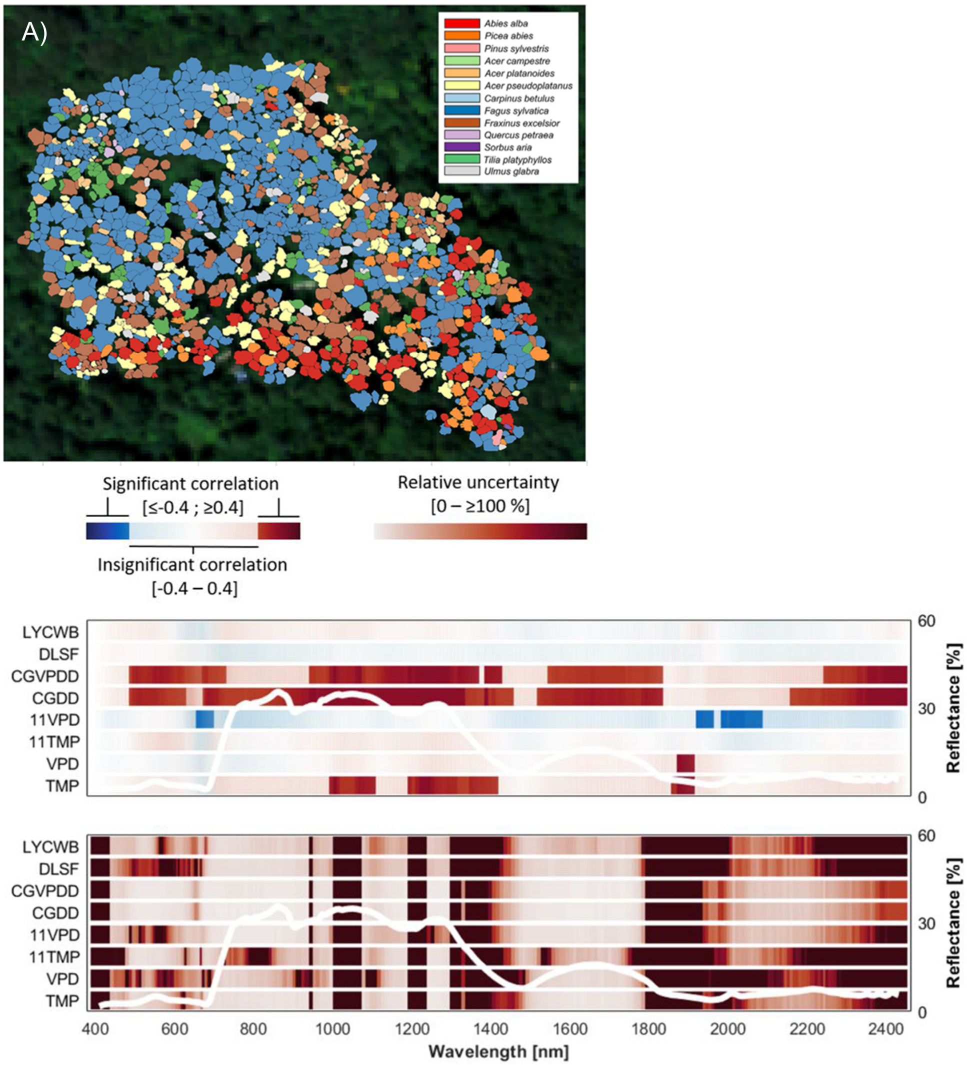

Figure 6. *Spectroscopy can help to distinguish species and assess genetic variation. A) Dominant tree crowns assigned to species by aligning forest inventory data with a 3D model of tree crowns and trunks made using LiDAR and photogrammetry; reproduced with permission from (Guillén-Escribà et al., 2021), CC BY. B) Spectral similarity is correlated with a relatedness measure for beech canopies in (A), with correlation strength related to 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). Lower panel: estimated relative uncertainties of correlations. White lines: mean canopy reflectance measured for focal trees (0-60% of incident sunlight). Reproduced with permission from (Czyż et al., 2023), CC BY.*

Ways forward for using EO in genetic diversity assessments

EO offer repeated measurements in space and time and in wavelengths beyond what we humans can see with our eyes. These observations, and the landscape-level information they capture and provide, along with the multidimensional information about Earth's surface that can be derived from their spectral properties, 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 genetic diversity, as illustrated in the examples above and summarized in **Table 3**. This information can furthermore help managers prioritize interventions and target them to the areas where rapid changes are taking place, towards mitigating damage, maintaining or enhancing their resilience and biodiversity.

Available EO data and information, combined with traditional 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: (1) informing the PM indicator if habitat loss or species vitality surpasses a certain threshold, below which a species can be assumed to be locally lost; (2) informing the N_e > 500 indicator directly if species density per unit area is known or if groups of mature individuals can be directly observed, or indirectly by indicating if populations expected to be declining in size: where a baseline N_e value is known for a given population, the expected decline could be estimated as a function of habitat loss; (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 3. 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 distinctiveness** *or support the design of comprehensive DNA studies to confirm this*	Cannot independently identify genetically distinct populations
Detect habitat and ecosystem change	*Develop EO-based alert systems to support genetic diversity* **protection**	Cannot detect all on-the-ground threats to individuals

Requires a baseline and continued monitoring	**in real time** *and to* **monitor inferred PM or N_e>500 over time**	(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*	Cannot directly estimate genetic diversity

This information should ideally be complemented with ground data, 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. EO will nevertheless continue to provide independently valuable information.

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. This need for greater technical expertise becomes even more acute with the anticipated advances in EO such as the CHIME and SBG 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. On one hand, this implies co-developing the tools to incorporate the needs, workflows and on-the-ground context of practitioners and ensuring the tools and resulting information are fit for purpose, hence contributing to development of capacity for non-traditional users of EO (Jacobi et al., 2022; Speaker et al., 2022; Tabor & Holland, 2021). On the other, this also 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 archival and distribution of detailed and well-documented information resulting from a combination of EO with other types of data for new and innovative applications.

In summary, we demonstrate in three distinct and complementary examples 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 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 its 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 EBVs. This represents a surprisingly simple, yet fundamental change in our ability to monitor, assess, preserve and protect biodiversity at the national, regional, and global scales, especially in areas with limited accessibility. The proposed workflow, combining EO with other biodiversity data, could be developed on current and future platforms such as GEO BON's "BON-in-a-Box" to make it widely available and facilitate its use for biodiversity monitoring.

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.
- **Genetics** is the study of heritable differences. This can be achieved using a variety of approaches. Molecular genetics is a collective term for the study of DNA-based genetic variation, typically referring to lower-resolution methods (e.g. analysis of single genes, microsatellite markers, etc.) where only small portions of genomes are characterized.
- **Genomics** (related to high-throughput sequencing, next-generation sequencing) refers to methods that study the diversity of DNA sequences and associated molecular features across the majority, ideally entirety, 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 sexually mature individuals in a population. Note: adult and reproductively mature individuals usually cannot be distinguished.
- **N_e** (effective population size) is the size of an idealized population that has the same rate of genetic diversity loss 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.
- **Nuclear microsatellites**: 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.
- **Population**: a group of spatially aggregated, interbreeding individuals, genetically distinct from other similar groups. Note: population is rather flexibly used within population genetics and often incorrectly refers to distinct sampling localities.
- **Population genetics** is a field of research referring to theoretical and molecular study of genetic diversity within and among populations.

- **Species range** is the geographical space 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**: refers to sensors covering continuously, in high-resolution the electromagnetic spectrum (often referred to imaging spectroscopy).
- **Imaging spectroscopy**: imaging light reflected from the Earth surface with continuous, narrow high-resolution spectral bands (often also referred to as hyperspectral imaging).
- **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.
- **Spatial resolution** of an image is defined as the area on the ground represented in one pixel. Sentinel-2 imagery is, for instance, available in 10x10 m pixel 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 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 as revisit time for a satellite to observe the same area on Earth’s surface. Depending on the satellite configuration, revisit time varies from hours to days.
- **Time series**: a sequence of observations obtained over a certain period of time (aka, multitemporal datasets). 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).

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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