How Earth Observation can support genetic diversity monitoring from Space

Running title: EO to monitor genetic diversity

List of authors: ISSI International Team "Genes from Space": Meredith C. Schuman[1,2,*,†], Claudia Roeoesli[1,*,†] Alicia Mastretta-Yanes[3,4,a], Isabelle S. Helfenstein[1], Oliver Selmoni[1,5,6], Cristiano Vernesi[7], Katie L. Millette[8], Wolke Tobón-Niedfeldt[9], Clement Albergel[10], Deborah M. Leigh[11,12], Sophie Hebden[10,13], Sean M. Hoban[14], Santiago G. Lago[15-18], Michael E. Schaepman[19], Linda Laikre[20], Ghassem R. Asrar[21]

Institutional affiliations:

[1]Remote Sensing Laboratories, Department of Geography, University of Zurich, Zurich, Switzerland

[2]Department of Chemistry, University of Zurich, Zurich, Switzerland

[3]Consejo Nacional de Humanidades, Ciencias y Tecnologías, Mexico City, Mexico

[4]Institute of Ecology, National Autonomous University of Mexico (UNAM), Mexico City, Mexico

[5]Department of Embryology, Carnegie Institution for Science, Baltimore, MD 21218, USA

[6]Department of Plant Biology, Carnegie Institution for Science, Stanford, CA 94305, USA

[7]Fondazione Edmund Mach, San Michele All'adige, Trento, Italy

[8]Group on Earth Observations Biodiversity Observation Network (GEO BON), McGill University, Montreal, Quebec, Canada

[9]Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO), Mexico City, Mexico

[10]European Space Agency (ESA) Climate Office, ECSAT, Harwell Campus, Didcot, Oxfordshire, United Kingdom

[11]Senckenberg - Leibniz Institution for Biodiversity and Earth System Research, Senckenberg Research Institute and Natural History Museum Frankfurt, 60325 Frankfurt, Germany

[12]Institute of Ecology, Evolution and Diversity, Faculty of Biosciences, Goethe University Frankfurt, Max-von-Laue-Str. 9, 60438 Frankfurt, Germany

[13]Future Earth Secretariat, Stockholm, Sweden

[14]The Center for Tree Science, The Morton Arboretum, Lisle, IL 60187, USA

[15]European Molecular Biology Laboratory, Genome Biology Unit, Heidelberg, Germany

[16]European Molecular Biology Laboratory, Molecular Systems Biology Unit, Heidelberg, Germany

[17]Division of Computational Genomics and Systems Genetics, German Cancer Research Center (DKFZ), Heidelberg, Germany

[18]Chair of Data Science in Earth Observation, Department of Aerospace and Geodesy, Technical University of Munich, Munich, Germany
[19]University of Zurich, Zurich, Switzerland
[20]Department of Zoology, Stockholm University, Stockholm, Sweden
[21]iCREST Foundation, 3001 Bridgeway, Suite 312, Sausalito, CA 94965, USA
[a]Current address: Royal Botanic Gardens, Kew, Richmond, UK

***Contact information**: claudia.roeoesli@geo.uzh.ch, +41 44 63 56522; meredithchristine.schuman@uzh.ch, +41 44 63 55162
† Meredith C. Schuman and Claudia Roeoesli should be considered joint first authors.

Abstract

Genetic diversity within and among populations is essential for species persistence. Yet, genetic diversity is challenging to measure at scales relevant for many biodiversity patterns and processes, such as the range of a species or the extent of an ecosystem; or for biodiversity management, such as the territory of a country. Conservationists, ecosystem managers, and Parties to the Convention on Biological Diversity (CBD) all require reliable and efficient assessments of genetic diversity at scales relevant for policy- and decision-making. Researchers require measures of genetic diversity at scales relevant for predicting and understanding biodiversity change. Here, we describe how space-based Earth observation (EO) can make essential contributions to the assessment and monitoring of genetic diversity indicators at relevant scales. We introduce a stepwise workflow for integrating EO accessibly into existing genetic diversity monitoring approaches as part of biodiversity mapping and inventorying activities. We show how this approach can empower progress towards the aims of the Global Biodiversity Framework (GBF) and aligned efforts. As an outlook, we discuss examples using EO data for research into the genetic diversity of populations, for suitable species.

Keywords

remote sensing (RS) — Kunming-Montreal Global Biodiversity Framework (GBF) — effective population size (N_e) > 500 Headline Indicator A.4 — populations maintained (PM) Complementary Indicator A.CY.22 — essential biodiversity variables (EBVs)

Introduction

Genetic diversity and biodiversity

Genetic diversity is a foundational level of biodiversity underlying species diversity: It is an essential component of the variation within and between individuals. Genetic diversity thus underlies adaptive potential, which is material to the fitness of individuals and allows populations of species to persist in the face of change (*i.e.*, resilience and resistance). Therefore, genetic diversity needs to be monitored as part of biodiversity assessments, conservation and restoration actions, and for safeguarding nature's contributions to people and ecosystem services (Hoban et al., 2020, 2021; Stange et al., 2021).

Loss of genetic diversity leads to maladaptation, population decline, inbreeding and, eventually, species extinction. Studies of multi-species genetic diversity trends indicate a net loss over time as a result of human activities (Exposito-Alonso, 2025; Exposito-Alonso et al., 2022; Leigh et al., 2019; Millette et al., 2020; Shaw et al., 2025). These studies have only recently become possible due to a slowly accumulated critical mass of DNA-based data, aggregating past information across species and regions. However, conserving genetic diversity requires monitoring at large scales (dozens to hundreds of species) to estimate ongoing, local trends in a timely manner that supports mitigation of adverse impacts. This remains a grand and unmet challenge, and is among the main objectives of the Kunming-Montreal Global Biodiversity Framework (GBF; CBD/COP/DEC/15/4).

The GBF is implemented in National Biodiversity Strategy and Action Plans by 196 Parties to the Convention on Biological Diversity (CBD), with progress measured *via* National Reports and global stocktaking. Indicators based on the persistence and size of distinct local populations were adopted to monitor genetic diversity across these scales (CBD/COP/DEC/15/5, **Box 1**). The indicators can be calculated with or without DNA data (Joint Nature Conservation Committee, 2025; Mastretta-Yanes, Da Silva et al., 2024; Mastretta-Yanes et al., 2024; Mouton et al., 2026), making them measurable in regions with little molecular research infrastructure, or generally wherever genetic studies are too slow to capture change. A feasibility study showed that these indicators, based on population persistence or size, could be quantified in 83% of species across nine countries and 919 taxa where more traditional DNA-based metrics would often fail because many of these taxa lacked DNA data (Mastretta-Yanes, da Silva et al., 2024).

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 within individual 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 Complementary Indicator A.CY.22 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 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 flexibility of the GBF genetic diversity indicator framework allows it to accommodate the wide range of taxa, monitoring systems, and available data across countries. Continued efforts toward standardisation and harmonisation across taxa, regions, and countries will further improve consistency and comparability. However, monitoring hundreds of taxa across large geographic regions, often spanning national boundaries, requires coordination, shared expertise, and accessible data. As expected for a global monitoring framework at this early stage, reporting capacity and implementation vary greatly among countries. Earth observation-based approaches, such as those proposed here, can complement these ongoing efforts by supporting harmonised large-scale assessments while building on the important progress already made toward global genetic diversity monitoring. Many countries would benefit from a standardized, rapid, affordable approach that does not require high technical expertise.

The contribution of satellite Earth observation (EO)

EO has become indispensable for understanding and monitoring global change and 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 methods based on airborne and field-mobile platforms are also used, here we focus on Space-based EO from satellites such as the Copernicus Sentinels the USGS Landsat program and NASA Earth Observing System (EOS), which provide global data every few days to weeks, are publicly available and in many instances free of charge (Malenovský et al., 2012). See **Appendix Table A.1** for a detailed list of several platforms supporting access to public EO data, and **Appendix Box A.1** for a list of general information and applications of EO.

Biodiversity-relevant information from EO is obtained at the pixel level and often interpreted at the ecosystem and landscape level. Examples are land use and land cover (LULC) change which can be derived from optical as well as radar and LiDAR remote sensing; vegetation biochemical properties, conditions, or traits (see **Glossary**) that are assessed using indices such as the Normalized Difference Vegetation Index (NDVI); structural information such as green leaf area index (LAI), vegetation height and vertical structure; and land surface phenology. This information can be used in models to infer species composition, functional diversity, and other properties of ecosystems (Mayor et al., 2024, 2025; Pasetto et al., 2018). Uniquely and importantly, EO provides non-intrusive, repeated, standardised and systematic measurements of the same area on a time scale of days to weeks, globally. In addition, a large archive of EO data exists dating back to the 1970s, allowing us to examine biodiversity-relevant data retrospectively, with the caveat that the technical capabilities of these early EO systems differ from modern systems. Nevertheless, these observations can be used to fill gaps that may exist in long-term records. More recently, the availability of foundation model embeddings, derived from historical archives of multiple sensor modalities, provides a powerful mechanism for data-driven prioritization and stratification of ecosystem changes over time (Brown et al., 2025).

Genetic diversity has traditionally been considered beyond the scope of EO-based biodiversity monitoring because molecular variation is perceived not to be directly measurable from Space (Skidmore *et al.*, 2021). The challenge lies in systematically connecting properties accessible from Space to variation within species (*e.g.*, detection of distinct populations). From Space, we can detect indications of population-level variation and health, and relevant processes impacting the conditions that allow populations to persist, or threaten their survival. For example, when viewing a forest from Space, we may not be able to dissect the signal of the understory from the signal from the canopy. However, if the canopy has been cleared, we can assume suitable habitat for the understory occupants has been removed or severely degraded. Indeed, some recent initiatives connect landscape and other environmental features, or signatures of population activity, to the detection or conditions of populations (Barber-Meyer et al., 2007; Cousins et al.,

2022; Fernández, 2013; Fretwell & Trathan, 2009). Such information about the condition of populations and their environment, if made easily accessible, can greatly streamline genetic diversity assessment for biodiversity monitoring and conservation. For example, this information could contribute to setting conservation or restoration priorities on populations whose local habitat is under threat, in comparison to those whose habitat appears stable, or – at the other extreme – has already been lost.

Here, we describe a workflow using EO to support the standardized and efficient monitoring of genetic diversity across taxa and regions (**Fig. 1**). This workflow combines changes to the Earth's surface detectable with EO (*e.g.*, changes in habitat and vegetation) with other types of knowledge (*e.g.*, local knowledge, historical information, occurrence data, DNA data), and delivers estimates of population size changes over time, which can be used to calculate the GBF genetic diversity indicators. We then discuss how this workflow could evolve in the future toward a more direct assessment of population sizes and genetic differentiations from Space.

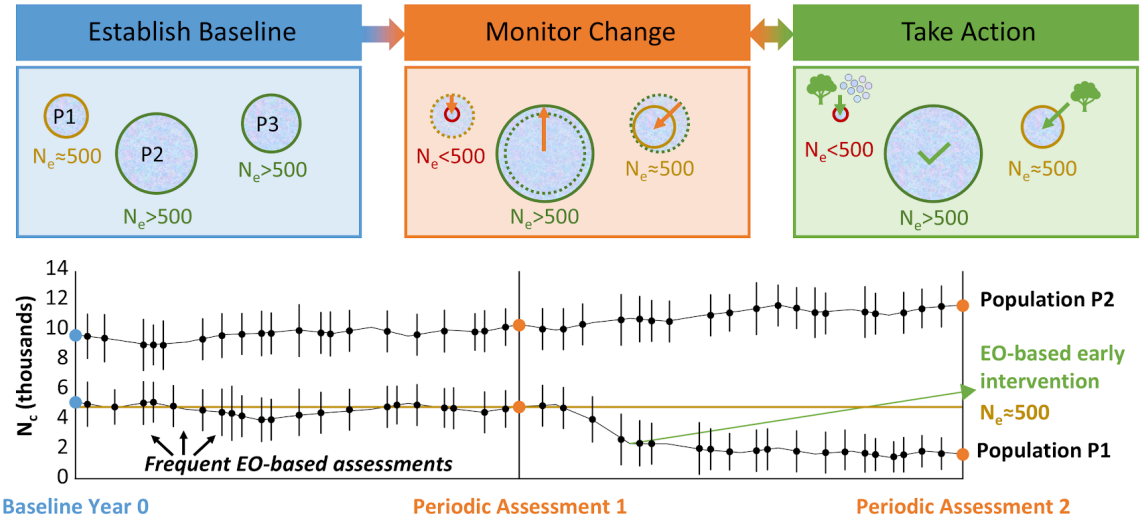

Figure 1: Publicly available Earth Observation (EO) data improve the establishment of baselines, regular monitoring complemented with periodic assessments from other data sources (e.g., DNA observations), and targeted re-assessment and intervention to conserve the genetic diversity of natural populations. Examples are shown for three imaginary populations of the same species, P1, P2, and P3. Their census sizes (N_c) are shown on the y-axis and these values are used to assess N_e using the common ratio $N_e/N_c \approx 0.1$ P1 drifts below the threshold value (N_e ~ 200) for the genetically effective population size (N_e), as defined within the N_e>500 Global Biodiversity Framework's Headline Indicator A.4 for genetic diversity monitoring. P2 is maintained to be above this threshold (N_e ~ 1000) while P3 (not shown in the second panel) drops close to the threshold (N_e ~ 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.

A proposed workflow using EO to support genetic diversity monitoring

We propose a workflow that combines EO data with ground-based observations, historical information and expert knowledge to infer genetic diversity trends for assessment and monitoring of biodiversity in support of the GBF (see definition of indicators in **Box 1**).

- Informing the N_e>500 indicator by estimating habitat size: If the location of a population is known, experts can evaluate whether the EO-measured habitat size is sufficiently large to support a population with N_e>500. This evaluation can be based on previous knowledge on population density, or on comparisons with other populations where N_e>500 is known.
- Informing the PM indicator: If estimated habitat size or quality descends below a certain threshold, a population is assumed to be lost.
- Supporting prioritization of *in situ* monitoring, conservation or restoration actions, or an early alert system: This information can help to direct resources to the regions where more change is occurring and ground-based observations are most needed.

In practice, the workflow can be summarized in the following three steps:

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 habitats harbor different populations) or eco-biogeographic differences (*e.g.*, different environmental zones harbor different populations) (Hoban et al., 2023; Tobón-Niedfeldt et al., 2022).
2) The second step is to assess whether populations' habitats have been maintained since their first observation. EO data can be used in such situations to detect habitat change using either visual inspection of satellite images or by analyzing satellite-derived time series of LULC change, such as tree-cover loss or gain, which are publicly available free-of-charge from repositories such as the Copernicus Browser or Global Forest Watch (**Appendix Table A.1**). Here we consider loss of habitat quantity, but quality could (and should) also be assessed.
3) The third step is to estimate genetic diversity indicators from habitat information from steps 1 and 2. For the PM indicator (**Box 1**), the proposed procedure is straightforward: Populations that have lost most or all of their habitat over time are expected to be lost, and the fraction of populations with remaining habitat above some minimal threshold may be taken to correspond to the PM indicator. For the N_e>500 indicator (**Box 1**), we must then estimate the population's census size N_c from habitat size and a species-appropriate density per area of reproductively mature individuals, and calculate N_e from a

species-appropriate N_e:N_c ratio. 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. Habitat quality information could also be integrated to tune estimates.

Our proposed workflow thus relies on the following assumptions:

- That a suitable habitat supports a species population;
- That habitat extent (and quality) is correlated to population size;
- That habitat extent (and quality) can be assessed sufficiently well by EO;
- That relevant threats to the focal populations are visible at the habitat scale (*e.g.*, land-use change, but not poaching);
- That it is possible to distinguish populations by their biogeographical distribution (*e.g.*, spatial distribution of species observations; barriers to dispersal and gene flow);
- That sufficient supporting information is available (*e.g.* locations where populations are known or expected to occur or where individuals have been observed, knowledge of species-typical habitats, dispersal distances, and population densities);
- That detailed ground information at a given reference time point will improve the interpretability of the additional information provided by EO.

Based on these assumptions, the proposed workflow is best suited for species where habitat changes can be detected and quantified using EO, such as *via* LULC change, or landscape modification and fragmentation.

***Table 1**. Proposed applications of EO data for monitoring genetic diversity.*

Uses of EO data	**Implementation for genetic diversity monitoring**	**Current limitations of this use**
Population and habitat mapping *Accuracy increases with prior knowledge, supporting observations, and in terrestrial habitats*	*Inferred population locations can be combined with other data (*e.g.*, biogeographical, traditional knowledge) to* **infer population boundaries** *or support the design of DNA studies for confirmation* **Census size N_c can be inferred** *from dispersal distance data, occupation density data, or occasionally counts of dominant individuals; supports* **assessment of N_e>500**	Cannot independently identify genetic relatedness or genetically distinct populations Cannot directly measure effective or census population sizes (N_e or N_c)
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 threats to individuals that do not cause habitat change detectable from Space (*e.g.*, poaching). Currently challenging in marine systems

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**	Use to directly estimate genetic diversity is not established

The proposed workflow requires co-development and validation based on local knowledge – such as information on suitable habitat, population boundaries and density, and appropriate ground data including direct observation of where individuals or populations occur, and, where available, census counts (*i.e.*, N_c), or DNA sequence information at relevant times. EO can then fill the gaps to enable monitoring, especially for locations where information about change over time is limiting, or for estimating regional- or country-scale population changes where ground data are available for some, but not all target populations. Where ground-based data are already sufficient, EO still offers complementary measurements that are repeated in space and time. These may help to interpolate in-between ground-based observations, and may be used for early warning signals and for assessing risks of population decline. While the EO data considered here are openly available to anyone on the internet, co-development with EO experts is crucial to facilitate simple but correct generation and access to the required information, with due consideration of advantages and limitations of the different technologies and data sources.

Although some supporting information is required, the cost-effectiveness of an approach based on public EO data – particularly if automated – is noteworthy, as many biodiversity hotspots are located in economic resource-limited regions, and public EO data allow upscaling to more timepoints, more species, and larger areas without incurring local costs for additional observations. Because public EO data are regularly updated, the workflow can help managers prioritize interventions and target them in space and time to areas where changes are taking place, hence mitigating damage, maintaining or enhancing resilience, and protecting biodiversity (Langhammer et al., 2024).

In summary, the proposed workflow will be most useful for cases in which ground-based data are not yet sufficient to calculate the GBF genetic diversity indicators, but information is available regarding 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). We furthermore expect that this approach can facilitate and accelerate indicator calculation in cases where N_c estimates are available, but not frequent, by making regular remote observation and assessment possible. In a few cases, N_c estimates may even be possible directly from EO data (**Outlook**). Critically, we expect this approach to enable more frequent change monitoring in all cases (**Fig.**

1). The major challenge is to ensure the usability and accessibility of EO data for biodiversity monitoring, as it requires expert knowledge to extract the needed information (**Appendix Box A.1)** (Pahlevan et al., 2021; Silva et al., 2008).

Example: Monitoring habitat change to estimate genetic diversity indicators in wild relatives of domesticated crops

The wild relatives of modern-day crops (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 and several species (spp.) are endangered, some critically (Goettsch et al., 2021). Wild avocados (*Persea* spp.) and teosintes (*Zea* spp., related to maize) inhabit remote locations that are challenging to visit.

The first example species is *Persea* (*P.*) *cinerascens*, a wild avocado growing among the trees 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[1]. The species' presence was confirmed during the last visit to the known field localities in 2017, but no population size measurement was conducted. The second example species is the teosinte *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). Based on DNA data, the N_e of both documented *Z. perennis* populations is below 500 (Rivera-Rodríguez et al., 2023)

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 direct assessment of this suspected habitat change and thereby support monitoring genetic diversity for these two species. Direct inspection of true-color satellite images (from Google Earth and Sentinel-2; **Fig. 2A** and **2C**) allows a rapid assessment of vegetation and LULC change by comparing images taken before the last ground sampling (2016 for *P. cinerascens* and 2006 for *Z. perennis*) with more recent images. This method showed that for *P. cinerascens,* a controlled forest fire likely 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. Although other

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

threats may affect this population, this already allows key insights in the absence of further ground data.

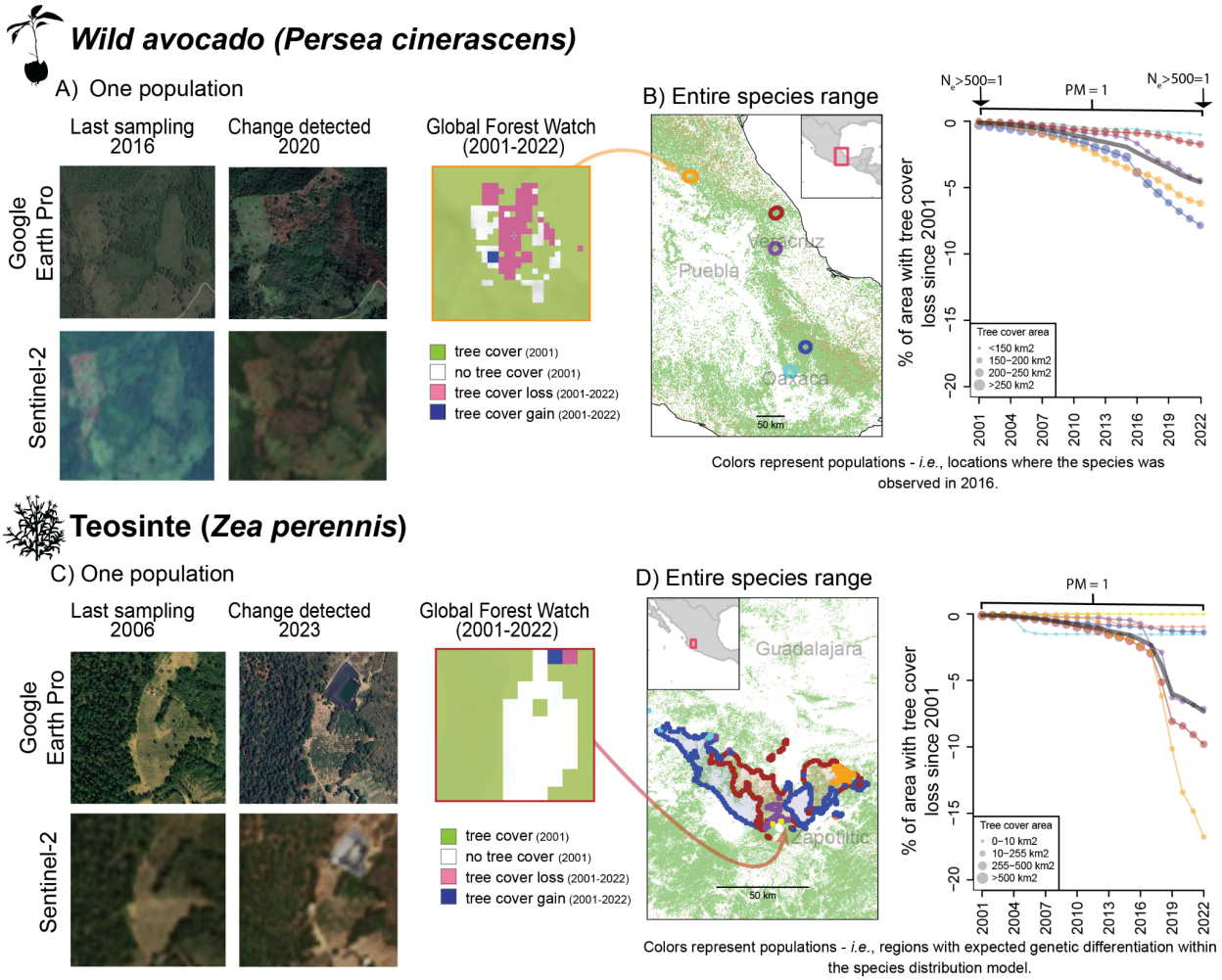

***Figure 2**. Examples of habitat monitoring and estimation of genetic diversity indicators using EO for A-B) a wild avocado* (P. cinerascens) *and C-D) a teosinte* (Z. perennis)*. A) Comparisons of imagery available from Google Earth Pro (better than 5 m spatial resolution) or Copernicus Sentinel-2 (10-20 m spatial resolution) showing habitat change for a wild avocado population, and the evaluation of tree cover change from Global Forest Watch. 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. Data are shown for individual populations (colored circles) as well as a mean trend (thick grey line). C) Data from Google Earth Pro and Sentinel-2 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. 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. 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). Data are shown for individual populations (colored circles) as well as a mean trend (thick grey line).

The proposed workflow could be used to standardize and extend genetic diversity monitoring throughout the known range of these two species. In practice, the definition of the population boundaries depends on the available data. For species with few occurrences – such as *P. cinerascens* – buffer zones around 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) can be used to define 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 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 into populations, they can be regarded as different populations for monitoring purposes.

To measure habitat change over time, we used the Global Forest Watch dataset, 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 from optical as well as LiDAR remote sensing (Hansen et al., 2013; Potapov et al., 2021). In the case of *P. cinerascens* (**Fig. 2B**), 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. 2D**), the “red” population exhibited the most significant decline and is the second smallest, while the “yellow” population appears not to have lost habitat. Note that the individual population trends differ from the species mean (thick grey line), highlighting the importance of separately evaluating populations within a given species.

In both species used for this example, 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 km² 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. Note that the assumed density is a critical parameter that can significantly affect the value of the indicator. For example, the N_e>500 indicator value would 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. Estimating the densities and sizes of individual populations is infeasible for this very rare species. However, it is notable that habitat size declined by an average of 7%, with two populations (as defined in the SDM) experiencing even steeper declines of up to 15%.

These examples show how leveraging EO for habitat monitoring can inform the approximate assessment of GBF indicators and the prioritization of *in situ* observations and interventions. Importantly, the example furthermore indicates that EO-based assessments enable the identification, characterization, and ranking of threats to populations prior to GBF indicator decline. We envision such a habitat monitoring approach to be the most common case for using EO to support population-level genetic diversity assessments, including for monitoring under the GBF. We acknowledge that specific, appropriate parameters will need to be provided for different species.

Outlook: beyond habitat monitoring

Cases in which populations can be counted from Space

In some cases, it is possible to directly observe populations from Space, for example, estimates of forest cover change provided by Global Forest Watch. Although these are provided as forest cover and not tree population change, it is the observability of localized forest canopies from Space that enables them. We expect such cases to include primarily canopy-forming plants such as trees, and some sufficiently large and stationary animals occurring against strongly contrasting backgrounds. We acknowledge that such species are highly specific, however many are keystone species or ecosystem drivers, making them of sentinel importance for monitoring.

Attempts to directly observe populations of such species from space often use private data with higher spatial resolution to supplement public datastreams, *e.g.* (Cubaynes et al., 2024; Kaplan et al., 2025; LaRue et al., 2024). Even so, the geometry of square, two-dimensional pixels is different from the geometries of individuals and groups: even if the spatial scale of a pixel is on the scale of an individual, or a group of individuals, the pixel may encompass edges and gaps.

These geometric considerations change when introducing three-dimensional information about surfaces from radar technologies or from LiDAR.

As an example (see **Table 1**), we consider how EO data can support the assessment of GBF genetic diversity indicators (**Box 1**) for a dominant forest-forming tree: the European beech *Fagus* (*F.*) *sylvatica*. *F. sylvatica* has substantial ecological, cultural, and economic importance across Europe, and is now threatened by increasingly severe droughts across much of its natural range; the future of Europe's widespread beech forests is thus 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). *Fagus* species 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) – which is common for widespread forest-forming trees. The moderate isolation of *F. sylvatica* populations by distance (Lazic et al., 2024; Milesi et al., 2024) reveals the species' post-glacial migration history but also depends on management and planting decisions in forestry. The baseline N_e:N_c ratio of 0.1 is appropriate for this species: Genetic analysis of a stand in France having 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).

It is possible to infer the number of dominant (canopy-forming) *F. sylvatica* trees and to distinguish them from a limited number of co-occurring tree species in high-resolution (<10 m) EO images (Kaplan et al., 2025; Yao et al., 2021), and this could be used to estimate N_c. Generally, binary classification of trees, *e.g.* as either beech or not-beech, is more accurate than multiple classification of pixels to several co-occurring species (Kaplan et al., 2025; van Moorsel et al., 2026). It remains a challenge to scale such EO-based classification approaches to the spatial resolution of public EO data (≥10 m, see **Fig. 3**). As an example, a recent study combined active and passive EO data, from Sentinel-1 and Sentinel-2 annual time series, with forest inventory data to obtain species mapping in forest stands across Switzerland (Blickensdörfer *et al*., 2024). Forest cover and inventory data are generally helpful to select specific regions, *e.g.* those with beech-dominated stands. Derived N_c estimates could then be used to approximate the N_e>500 indicator. This approach would likely yield an underestimation because N_c from EO would count dominant (canopy-forming) trees that are the easiest to detect from Space, 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 for an area of interest.

EO-based functional diversity can support genetic diversity assessments

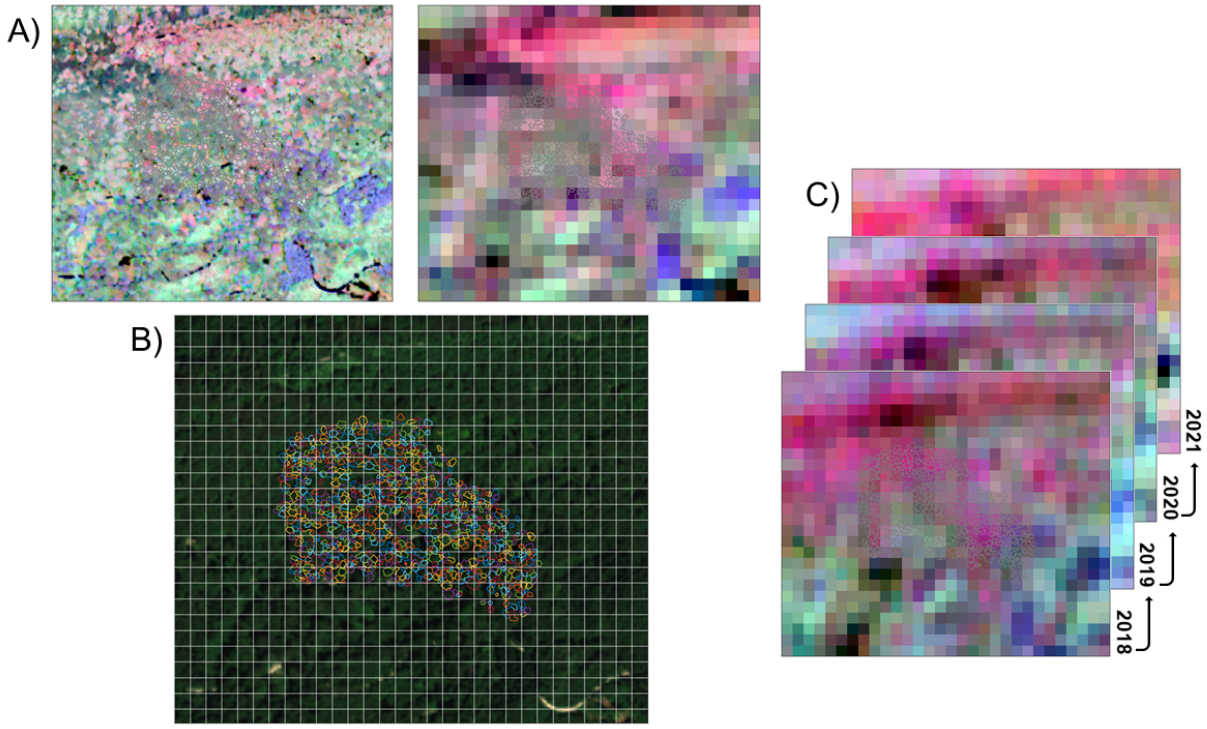

***Figure 3**. Mapping the diversity of forest canopy characteristics using EO. A) Impact of spatial resolution on the derived canopy traits, such as chlorophyll, estimated using spectral indices from Sentinel-2 bands. Chlorophyll content, estimated using the red-edge chlorophyll index CIre (green); 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 the Laegern forest in Switzerland. For 20 m pixels, multiple individuals contribute to the signal per pixel. C) EO data for monitoring: Canopy traits mapped for the area of interest for four consecutive years using Sentinel-2 data.*

Traits of directly observed individuals and groups (*e.g.*, canopies, colonies) can also be informative when assessing habitat. For example, the state of forest trees can be used to differentiate intact from degraded, but still present, forest habitats. EO-based techniques can be used to assess change in canopy vitality prior to tree loss, via changes in trait values (Asner & Martin, 2016; Helfenstein et al., 2022). EO-derived trait assessments could thus improve assessments of habitat by considering areas of healthy vegetation compared with degraded areas. Such remotely observed canopy traits and their local diversity, obtained from EO data at 20 m spatial resolution (**Fig. 3**), can be related to the forest canopies and their response to environmental conditions such as drought (Helfenstein et al., 2022, 2024; Sturm et al., 2022). Such

trait maps can also be used when assessing genetic variation of forests, especially in cases where relevant populations can be directly detected from Space.

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[2]) and NASA (Eagle: Explorer for Artemis Geology Lunar and Earth[3]) 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 of trees and forest canopies to better distinguish different species and populations and estimate other components of their genetic variation beyond indicators described so far, as demonstrated by some published studies using imaging spectroscopy (Cavender-Bares et al., 2020; Czyż et al., 2023; Seeley, Stacy, et al., 2023; Seeley, Vaughn, et al., 2023).

Summary and conclusion

The incorporation of EO data 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 approach (**Fig. 1**) focuses on assessing habitat availability for populations (**Fig. 2**) and is currently under development for its general usability and independent evaluation. The workflow described here and its use is enabled by GEO BON's "BON-in-a-Box" platform (Griffith et al., 2026) to make it widely available and facilitate its use for biodiversity monitoring. BON in a Box supports users to run open-source pipelines on its servers or on their own local platform, and to input required data without having to share it – an important consideration for sensitive observation data.

We furthermore provide an outlook on ways to integrate additional information on population size and habitat conditions derived from EO, in cases where direct observation of individuals or groups is feasible from Space (*e.g.* **Fig. 3**). We acknowledge limitations that are illustrated and discussed in the presented examples and summarized in **Table 1** and in the **Appendix Table A.2**.

As EO data become increasingly available and accessible for non-experts, especially for new applications such as described here, their use and interpretation still require technical expertise (**Appendix Box A.1**). This need for greater technical expertise becomes even more acute with the anticipated advances in EO such as the upcoming hyperspectral imaging spectroscopy missions this decade (see **Glossary**; *e.g.*, CHIME, and EAGLE). In combination with the needs of practitioners and the

[2] https://www.esa.int/ESA_Multimedia/Images/2020/11/CHIME
[3] https://science.nasa.gov/earth-science/decadal-surveys/decadal-sbg/

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 directly accessible and implementable. The situation is similar for new platforms making public genetic diversity data more accessible, such as GenDivRange (Csilléry et al., 2025), that accompany rapid advances in, and falling costs of generating genetic data in high throughput. These exciting technical and data advances will require co-development to realize their potential, 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 (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 real-world needs. In return, biodiversity practitioners and decision-makers can benefit from advances in EO, especially for data limited regions of the world. We hope that such collaborative and co-creative initiatives as ours will not only help democratize access to EO data, but also enable shared use of detailed and well-documented information resulting from a combination of EO with other types of data for new and innovative applications. Together such efforts will enable effective and timely implementation of Kunming-Montreal Global Biodiversity Framework (GBF).

Glossary

Population genetics and related terms

- **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 heritable variation, usually measured by DNA sequence diversity, 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, genetic drift can decrease genetic diversity rapidly.
- **Habitat** is the geographical, environmental, and biotic space that a species can inhabit.
- $\mathbf{N_c}$ (census size) is the number of reproductively mature individuals in a population.
- $\mathbf{N_e}$ (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).
- **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 (Allendorf, 2017; Waples & Gaggiotti, 2006), genetically distinct from other similar groups. Populations occupy a geographical space, *i.e.*, a subsection of the species distribution range.
- **Species range** is the geographical area that encompasses all the remaining extant (*i.e.*, non-extinct) populations of a species.
- **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 without direct contact. 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 often used (*e.g.*, in the US) to refer to satellite observation; however, like EO, RS can be used for any measurement techniques without direct contact to the object.
- **Hyperspectral** is a term often used to describe sensors covering a range of the electromagnetic spectrum in discrete, adjacent, narrow-wavelength bands (*e.g.*, 10 nm for CHIME), which is finer than current multispectral sensors onboard the Copernicus Sentinel-2 satellites. The use of such sensors to generate pixel-based images is also referred to as **imaging spectroscopy**.
- **Imaging spectroscopy** is used to mean the imaging of light reflected from the Earth surface with discrete, adjacent, narrow-wavelength spectral bands.
- **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 (band). Each band represents a contiguous part of the spectrum, but the bands may not be adjacent along the

spectrum, and may be differently sized (targeting more or fewer wavelengths per band).

- **Spatial resolution** of an image is defined as the distance on the ground represented by one side of one square pixel (ground sampling distance, GSD). Copernicus 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.
- **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.
- **Time series** are multitemporal 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 supporting change detection, time series are used to study the type, speed, and duration of observed changes. In contrast, **multitemporal data** consists of at least two images acquired at two different times, typically used for change detection only.

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-example

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Author contributions

Conceptualization: AM-Y, CA, CR, CV, GRA, ISH, KLM, LL, MCS, WT-N; Data curation: AM-Y, CR, ISH, OS; Formal analysis: AM-Y, CR, ISH, OS, WT-N; Funding acquisition: CR, MCS, MES; Methodology: AM-Y, CR, CV, DML, GRA, ISH, KLM, LL, MCS, OS, WT-N; Project administration: CR, MCS; Resources: AM-Y, CA, CR, ISH, MCS, SH, WT-N; Supervision: CR, MCS; Validation: AM-Y; Visualization: AM-Y, CR, DML, ISH, MCS, OS, WT-N; Writing - original draft: AM-Y, CR, CV, GRA, KLM, LL, MCS, OS; Writing - review & editing: All

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Appendix

***Table A.1**. Selection of EO platforms that lower or eliminate technical and financial barriers to application 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

Many EO platforms are available for change detection. 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[4,5], but less frequent usable observations depending on cloud cover (**Box A.1**). 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., 2025; 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 A.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 (**Table A.1**). 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.

[4] https://sentiwiki.copernicus.eu/web/s2-applications
[5] https://esamultimedia.esa.int/docs/S2-Data_Sheet.pdf

Box A.1: Key concepts and considerations when using EO data

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 pixel-level information 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.

***Table A.2**. A reflection on applications of EO to monitor and study genetic diversity based on published examples and examples mentioned in this article.*

Case	Aims	EO contributions	Challenges	Information for action
Emperor penguins in the Antarctic (Fretwell et al., 2012; Fretwell & Trathan, 2009)	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 change from Space-based images of guano deposits instead of penguin counts when using public EO data	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 (Goettsch et al., 2021; Rivera-Rodríguez et al., 2023; Tobón-Niedfeldt et al., 2022)	Infer PM and sometimes N_e Establish a warning trend	Inference based on habitat maintenance or change Provides data for locations that are too dangerous to visit *in situ* due *e.g.* to social conflicts or remoteness	Habitat may persist although populations are lost How does habitat change relate to changes in N_e? Density estimates are 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 (Gargiulo et al., 2024; Helfenstein et al., 2025; Kaplan et al., 2025; Lazic et al., 2024)	Infer PM and N_e Infer genetic composition EBVs	Inference based on forest coverage and biochemical and structural differences mapped across tree canopies for a dominant temperate forest tree	Weak geographic separation of genotypes Only dominant trees are visible from above 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 interventions, such as assisted gene flow