Monitor indicators of genetic diversity from space using Earth Observation data

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Use Earth Observation (EO) for monitoring and reporting on the Kunming-Montreal Global Biodiversity Framework (GBF) indicators of genetic diversity. EO has high potential and practical importance for advancing biodiversity monitoring within the GBF [32]. We propose that these advances are artificially limited by the consensus that genetic variation cannot be observed from space [32, 31]. Here, we explain how EO can also advance genetic diversity monitoring within the GBF, especially by helping to develop the headline and complimentary indicators of genetic diversity recently adopted at the 15th Conference of the Parties to the CBD (COP15). Ahead of the 2024 COP and the preceding meeting of its Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA), we propose that EO should be rapidly integrated into genetic diversity monitoring workflows, to accelerate the ongoing development of these indicators while helping Parties to fulfill their reporting commitments.

The genetic variation distributed across the individuals and populations of Earth's species is essential for their adaptation and persistence in changing environments, and for the maintenance of biodiversity [6, 23]. Its importance is recognized within the monitoring framework of the GBF adopted at COP15 [3], which includes a headline indicator on the maintenance of genetic diversity in species populations. Yet despite rapid advances in sequencing technology, it remains laborious and expensive to monitor changes in genetic diversity by repeatedly sampling populations and sequencing their DNA. Fortunately, the COP15 headline indicator and other key indicators of genetic diversity can be assessed based on information about species populations inferred from local knowledge, field surveys, and other sources, and do not necessarily require genetic sequence data [23, 16, 17]. This represents a useful but indirect means of genetic diversity assessment, and additional biodiversity observation data is needed to improve indicator quality [22]. Here, we present a framework and show examples for how existing, public data from EO satellites can provide complementary biodiversity observations that could immediately be used to improve monitoring and reporting on indicators of genetic diversity (Figure 1).

EO is generally not considered for genetic diversity assessment because genetic information cannot be retrieved easily or directly from satellite observations [31]. However, EO products can directly help countries to locate and delineate species populations, and monitor their change over time. We not only show how EO can facilitate genetic diversity monitoring as implemented within the GBF, but also look ahead to potential EO contributions in the assessment of genetic Essential Biodiversity Variables (EBVs). We call for the advising of Parties on how to use existing EO products for genetic diversity monitoring and for the co-development and dissemination of accessible tools.

Key indicators of genetic diversity can be effectively monitored without genetic sequence information. Effective conservation and management of biodiversity rely on maintaining sufficient genetic diversity within species to safeguard adaptive potential, especially under rapid environmental change [23]. This diversity is harbored within and between populations of each species. A key concept from population genetics, the *effective population size* (N_e) indicates a population's probability to lose its genetic variation, often due to random chance ("drift") or inbreeding. Concretely, N_e represents the size of an imaginary population that meets certain simplifying assumptions and which is predicted to lose genetic diversity at the same rate as a given real population [18, 35]. N_e can be estimated from population genetic data and is approximately one order of magnitude smaller than the *census number* of reproductively mature individuals (N_c) in the real population [8, 23, 15, 16]. The proportion of populations with an $N_e > 500$, which is generally considered safe to avoid genetic erosion (although it is not a guarantee [9]), is a headline indicator provided by the monitoring framework for the GBF [3] and can be assessed in the absence of DNA sequence data by estimating whether the N_c of populations is above or below 5000 [19, 23, 17]. A complementary indicator requires assessing the proportion of

Source Information	Population Definition	Population Assessment	Intervention Design
Earth Observation	Systematic delineation of habitats and (yet-unknown) populations	Frequent, systematic monitoring of habitat and presence (and size)	Up-to-date information on relevant conditions, systematic re-assessment
Local Knowledge	Locations, status, life history	Local events influencing populations	Specifics, contingencies, boundary conditions
Field Surveys	Boundaries, census numbers, genetic samples	Changing population boundaries, size, composition	Targeted assessment, planning, preliminary tests
Citizen Science	Opportunistic location reports	Opportunistic event and location reports	Raising awareness, opportunistic re-assessment

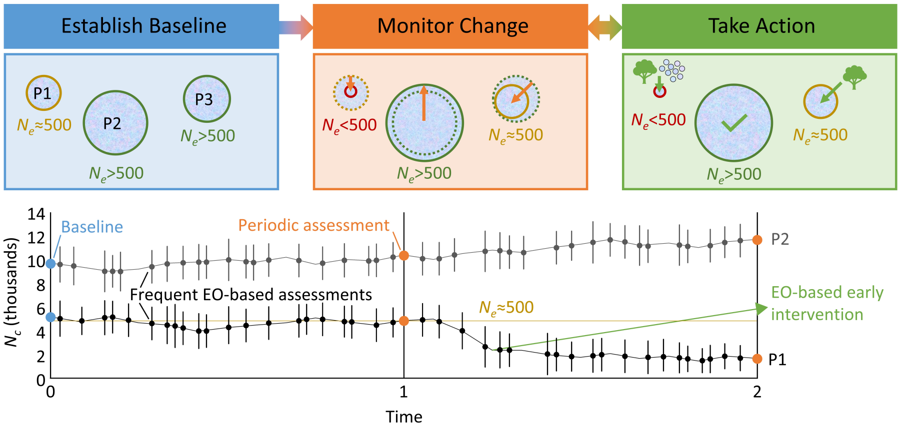

Fig. 1. Earth Observation (EO) facilitates key steps in genetic diversity monitoring and conservation of species populations. EO provides public, global data at high temporal resolution and spatial coverage, in the form of standardized observations that can complement and fill gaps in monitoring information provided by local knowledge, field surveys, citizen science, and other complementary information sources. Together, these support the headline indicator for monitoring and reporting on genetic diversity: the proportion of populations within a species having an effective population size $(N_e) > 500$ (corresponding approximately to a census number of reproductively mature individuals $(N_c) > 5000$). Knowledge of baseline conditions and periodic ground-based assessments can be combined with EO-derived information to establish baseline data. In between ground-based assessments, parameters indicative of population presence, extent, and size can be monitored frequently from space, allowing systematic checks of critical events that may require intervention or adjustment of other monitoring actions. In the conceptual example shown here, EO indicates a problematic drop in population size (P1) occurring in between ground-based monitoring activities, which could facilitate timely interventions, such as targeted breeding programs or habitat protection and restoration.

populations maintained within a species (extant populations divided by the original number at a baseline date). These indicators are valuable, particularly in the absence of DNA sequence data – which may be limiting especially when monitoring species populations in megadiverse countries – as recently demonstrated in pilot studies conducted across nine countries, calculating indicators for around 100 species per country [17].

Monitoring genetic diversity from space

Once sufficient local knowledge on the baseline state of focal populations is established, EO data can be used to monitor changes in their status and that of their habitat and its extent, to estimate the probability that any known population has disappeared or dropped below the threshold of $N_e > 500$ $(N_c > 5000)$, and to set priorities for field surveys and interventions.

"Sufficient local knowledge" implies both georeferenced population areas as well as at least approximate census size (N_c) and estimated population density.

Publicly available EO resources can, and should, already support genetic diversity monitoring. Dozens of orbiting satellites currently provide global, free, and open data on features of the Earth's surface, at spatial resolutions ranging from about 10 m to several km, and at temporal resolutions ranging from days to weeks over multiple decades [36]. The resulting EO products can directly help countries to locate and delineate species populations, and monitor their change over time. Components of habitat suitability derived from these EO products, including temperature, precipitation, and topography, information on land surface phenology, and characteristics including vegetation indices and forest cover, can provide input for species distribution models and otherwise support the assessment of suitable habitats and inform field surveys [33, 4, 17]. In cases where georeferenced areas of species populations are already known, time-stamped images from satellite sensors can facilitate estimations of population maintenance, loss, and change by showing the status of Earth surface features associated with populations: habitat characteristics and their change over time; or even by revealing individual species and their activity. These can guide the prioritization of sites for *in-situ* population surveys and conservation efforts, and help to quantify change and to set baseline values.

EO data can further support assessing changes in N_c above or below the threshold value of 5000, and N_c estimates will be more accurate where *in-situ* counts are available for comparison. For example, it is already possible to monitor the proportion of populations above or below $N_c \approx 5000$ for emperor penguins from space using publicly available EO products. The Sentinel Playground interface (https://www.sentinel-hub.com/explore/) facilitated the rapid review of known emperor penguin habitats in Antarctica, leading to the discovery of seven previously unknown colonies by coloration typical of penguin guano against the snow and ice [11]. The resulting shapefile of all known extant colonies could be used to monitor change over time in the proportion of populations maintained, using EO data. An existing metapopulation model of emperor penguins under climate change [20] further supports predictions of colony persistence and growth or shrinkage of N_c that can be checked against public EO data, ideally combined with public access to selected scenes with higher spatial resolution from commercial EO products. In addition to the relatively advantageous case of emperor penguins (high contrast between dark guano and white surface), Landsat Enhanced Thematic Mapper (ETM) imagery was used to identify guano from other seabirds against background geology and vegetation [10]. In these examples, atmospheric corrections introduce some uncertainty, and there is a bias towards identifying large guano concentrations; satellite-based counts of individuals are also associated with high uncertainty in these cases, and best supported by field surveys [10, 11].

As a second example, it is already possible to estimate and monitor changes in N_c from space for many temperate forest trees. Public EO products support local and global tree inventories as well as forest cover change detection, as exemplified by the Global Forest Watch initiative (https://www.globalforestwatch.org/) [34, 13, 29]. Public tools are increasingly available to classify tree species from EO data, especially for mono-dominant species in temperate forests, although high-spatial-resolution data (i.e., meter to sub-meter spatial data) are generally still required [1]. However, such classification results can be used to obtain a baseline estimate of N_c, and detection of changes from this baseline can be achieved with EO products having lower spatial resolution e.g. via changes in land cover, forest extent, and biophysical or biochemical traits typical of particular species and groups. Discrimination of tropical forest tree species from EO data is more challenging and likewise benefits from greater spatial resolution than is available from public EO platforms [7], but is feasible for some dominant and large-crowned species, and when incorporating the more detailed spectral information becoming available with the advent of spaceborne imaging spectroscopy [27].

Advances in assessing biophysical and biochemical properties of forest canopies with EO, which provides detailed information on characteristics of tree populations and their functioning in different environments – as well as aspects of their habitat provisioning – support moving beyond the GBF genetic indicators toward assessing genetic EBVs [2, 14, 28, 26, 37]. Upcoming imaging spectroscopy missions including the European Space Agency's Copernicus Hyperspectral Imaging Mission for the Environment (CHIME), the US National Aeronautics and Space Administration Surface Biology and Geology (SBG) mission, and the French-Indian Trishna mission may provide additional opportunities to develop space-based proxies for genetic diversity [33, 37], as indicated by studies using aerial imaging spectroscopy in combination with 3D structural information from LiDAR observations to assess genetic and phylogenetic differentiation among temperate and tropical forest trees [12, 5, 30]. However, we note that the environmental dependence and temporal dynamics of plant canopy spectra must be accounted for when using these data to distinguish species and assess their genetic variation [25, 24, 5].

Make EO more accessible to reporting Parties. Important EO products should be made more accessible to countries and independent organizations for biodiversity monitoring and reporting. The examples above use EO products that are freely available to the public (e.g. via https://dataspace.copernicus.eu/browser/), but specialized knowledge is required for their use and interpretation, and reporting organizations may not be aware of the availability of these products or know how to effectively use them to monitor genetic diversity. Capacity-building efforts should focus first on supporting Parties to access and utilize public EO tools through training and dissemination. These efforts and the increased use of EO platforms by Parties should then inform and stimulate the co-creation of new tools and applications to improve the accessibility and usefulness of EO data for biodiversity monitoring and reporting, for example through the "BON-in-a-Box" platform from GEO BON (https://boninabox.geobon.org/frontend/index). Promoting the use of EO data for genetic diversity monitoring may also encourage co-development of new monitoring products from EO platforms to meet practicioners' needs. A framework for integrated user-requirement analysis incorporating policy, EO, and and ecology was recently proposed [32].

Co-creation driven by the needs of countries, national and international organizations, combined with a deep interdisciplinary understanding and guided by local knowledge, can support standardized and effective biodiversity monitoring complemented by citizen science (Figure 1) and, furthermore, provide data for regions that may not be well covered by field surveys [21]. In addition to increasing access to EO data beyond basic map products for use in monitoring, the scientific value of adding EO data to genetic diversity monitoring must be tested and further developed through cases in which the frequency and quality of information from EO products improve genetic diversity indicators and eventually contribute to the assessment of genetic EBVs. For example, the biochemical information encoded in imaging spectroscopy data over landscapes has revealed cases in which the dissimilarity of detected spectra corresponds to differences in genotype-by-environment interactions that can be attributed to genetic distance or to differences in groups of species and their traits. These studies suggest an approach that intersects with classical genetics and conducts phenotyping remotely by airborne and/or spaceborne platforms; one major challenge is to genetically interpret the composites of organisms in a single pixel [5, 14, 38].

We hope to foster the use of EO data as existing, public information for biodiversity monitoring by providing a framework and concrete examples, and thus to help Parties achieve their 2030 GBF commitments [17]. The rapid integration of existing, publicly available EO products into genetic diversity monitoring and reporting will facilitate the location, delineation, and monitoring of species populations as well as their conservation, and will help the Parties to make informed decisions about the effective use of their monitoring resources.

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