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Essential Biodiversity Variables for measuring change in global freshwater biodiversity

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ABSTRACT

A critical requirement in assessing progress towards global biodiversity targets is improving our capacity to measure changes in biodiversity. Global biodiversity declined between 2000 and 2010, and there are indications that the decline was greater in freshwater than in terrestrial or marine systems. However, the data, tools and methods available during that decade were inadequate to reliably quantify this decline. Recent advances in freshwater monitoring make a global assessment now close to becoming feasible. Here we identify priorities for freshwater biodiversity assessment for 2020 and 2030, based on the Essential Biodiversity Variables (EBV) framework. We identify 22 priority activities for 2020 under three of the EBV classes (species populations, community composition, and ecosystem structure), which include: a globally systematic approach to collecting and assessing species data, collating existing and new data within global platforms, coordinated effort towards mapping wetland extent at high spatial resolution, linking in-situ data to modelling across regions, and mobilising citizen science for the collection and verification of data. Accomplishing these will allow the state of global biodiversity to be assessed according to a Red List Index with expanded geographic and taxonomic cover, an improved freshwater Living Planet Index with a greater number and phylogenetic range of species, measures of alpha and beta diversity, and globally-consistent estimates of wetland extent. To assess variables in the other EBV classes (genetic composition, species traits, and ecosystem function) we identify 15 priorities, which include development of environmental DNA methods, species-traits databases, eco-informatics and modelling over the next 15 years.

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1. Introduction

Global freshwater biodiversity continues to decline at an alarming rate (Collen et al., 2014) despite efforts to prevent such loss. These efforts include actions towards decadal targets set by the Convention on

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Biological Diversity (CBD) to address major causes of biodiversity decline (CBD, 2010). A mid-term assessment showed that most of the Aichi targets are unlikely to be met (Leadley et al., 2014). Effective action in meeting these targets is impeded by our limited capacity to determine how and where biodiversity is changing across the world. Improving this capacity now can help achieve the Aichi targets as well as the Sustainable Development Goals (SDGs) proposed for 2030 (Osborn et al., 2015). The SDGs are important for freshwater biodiversity because they include explicit commitments to the conservation, restoration and sustainable use of fresh water linking for the first time ecosystem health to human well-being into an agenda agreed by all United Nations members (Griggs et al., 2013). SDGs 6 (Clean water and sanitation) and 15 (Life on land) are particularly relevant to freshwater biodiversity because they include explicit commitments to the conservation, restoration and sustainable use of fresh water ecosystems (Griggs et al., 2013). SDG 12 also calls for achieving the sustainable management and efficient use of natural resources by 2030 including significantly reducing release of pollutants to air, water and soil.

A decade ago, Revenga et al. (2005) determined that the prospects for assessing the state of global freshwater biodiversity were poor in relation to the 2010 CBD targets. They also identified aspects where the greatest progress could be made and recommended focussing on those. Ten years on, some of these remain as major challenges e.g. improving taxonomic information for invertebrate fauna for much of the tropics, a comprehensive network of gauging stations, water quality monitoring and mapping, and in-situ observations of groundwater. On the other hand, there have been significant advances towards meeting some of the recommendations of Revenga et al. (2005). These include the completion of a global database of stream and river networks (Lehner and Grill, 2013), a more comprehensive database on the location of large dams and reservoirs (GRanD - <http://sedac.ciesin.columbia.edu/data/set/grand-v1-dams-rev01>), as well as new regional assessments of freshwater biodiversity (e.g. Darwall et al., 2011).

The past decade has also seen the rise of global networks aiming to develop earth observation systems, most notably the Group on Earth Observations (GEO: <https://www.earthobservations.org/index.php>), whose vision is “a future wherein decisions and actions for the benefit of humankind are informed by coordinated, comprehensive and sustained Earth observations and information”. GEO’s biodiversity observation network (GEO BON) was formed in 2008 to support the development of an Earth observation system for biodiversity (Scholes et al., 2008). GEO BON aims to build on the experience and evolution of remote sensing systems (Rose et al., 2015, Lausch et al., 2016) and developments in the fields of macro-ecology (Heino, 2013), metagenomics (Gibson et al., 2015) and ecoinformatics (Michener and Jones, 2012). Outputs of an earth observation system for biodiversity would include global maps of biodiversity condition. These could be generated by combining in-situ biodiversity observation with abiotic remote-sensing data (e.g. climate, terrain and substrate) by means of ecological modelling (e.g. Ferrier, 2011), to infer the state of biodiversity. GEO BON has provided a mechanism for collaboration and integration in the field of biodiversity observation and this has led to innovation: the Essential Biodiversity Variables (EBVs) framework (Pereira et al., 2013). Six broad classes of EBVs have been proposed, each representing a major component of biodiversity:

- genetic composition;
- species populations;
- species traits;
- community composition;
- ecosystem structure; and
- ecosystem function.

A list of globally agreed EBV is not yet available although an unofficial list of 22 candidate EBVs was proposed in the report of the 17th

meeting of the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA; UNEP/CBD/SBSTTA/17/INF/7). To help with the application of the EBV framework in the freshwater realm, here we evaluate existing knowledge on freshwater biodiversity under the six EBV classes and identify short and medium-term priorities towards global assessments of status and trends in freshwater biodiversity.

2. Measuring change in genetic composition

The most widely used variable in this EBV class is allelic diversity, which can help estimate genetic diversity at the individual, population, or species level (Pereira et al., 2013). Analysis of genetic composition is rarely included as an objective in biodiversity monitoring programs, especially in freshwater environments. One of the main reasons for this is the previously high cost of obtaining genetic information. However, recent advances in DNA sequencing technology (next-generation sequencing) are providing us with rapid and affordable access to vast amounts of genetic information (Thomsen and Willerslev, 2015). Improvements in lab methods based on microbiology and ancient DNA research have enabled the detection of small quantities of DNA through analysis of water samples, as all animals deposit their DNA in the environment around them as a result of regular biological processes such as sloughing of skin cells or urination. This data source is termed “environmental DNA” (eDNA) and has recently emerged as an effective method for assessing species presence/absence in a wide range of aquatic habitats, including threatened species of conservation significance (Fukumoto et al., 2015; Boothroyd et al., 2016).

Currently, the application of these techniques to biodiversity assessments in freshwater ecosystems focuses primarily on their value in detecting species’ presence/absence. Environmental DNA techniques can help overcome difficulties with identifying cryptic species or juvenile life stages and with bias associated with non-standardized sampling (Thomsen and Willerslev, 2015). They can also help detect threatened species without intrusive sampling (Laramie et al., 2015), and alien species at invasion fronts (Nathan et al., 2015). By combining eDNA sampling with next-generation sequencing, and “universal” markers that target many species within a group, “metabarcoding” enables the concurrent detection of several taxa without prior knowledge of community composition (Valentini et al., 2016). The advancement and application of ecogenomics can provide an understanding of the relationships between genetic composition and ecosystem function (Gibson et al., 2015). These opportunities have resulted in a rapid increase in the genetic data available for freshwater species and systems. Databases included in the International Nucleotide Sequence Database Collaboration (INSDC; <http://www.insdc.org>) already contain a large amount of reference data for freshwater species. The best documented freshwater groups include fishes, amphibians and mammals. These groups are also the main targets of the International Barcode of Life Project (iBOL; <http://www.barcodeoflife.org/>).

Despite the rapidly increasing accessibility of genetic data, reference sequences are not available for many species and databases are somewhat limited in their current potential to measure genetic diversity within a species or population. The molecular marker most widely used in DNA barcoding is the mitochondrial CO1 gene (Hebert et al., 2003). Although this marker has been useful for identifying genetic variants in commercial fish species (Ardura et al., 2011), it was specifically chosen for detecting species rather than detecting intra-specific differences, and it shows only limited inter-population polymorphism (Hebert et al., 2003). Also, the CO1 region often does not have enough variation within fragments that are short enough to be useful for environmental DNA applications, because the DNA from environmental samples is typically highly degraded. Successful measurement of genetic composition variables, such as population-level allelic diversity (Pereira et al., 2013), will partly depend on achieving two things: increasing the coverage of freshwater species in DNA reference sequence

libraries; and developing inexpensive methods and molecular markers that reveal population-level allelic diversity.

3. Measuring change in freshwater species populations

Information on the diversity, distribution, and conservation status of freshwater species has improved dramatically since 2005. The first overview of taxa reliant on freshwater ecosystems (The Freshwater Animal Diversity Assessment) was completed in 2008, covering 126,000 species in eight large zoogeographic regions (Balian et al., 2008). In the same year, a higher-resolution global bio-regionalisation defined 426 freshwater ecoregions, largely based on freshwater fishes (Abell et al., 2008), showing global patterns of species richness and endemism for fish, amphibians, turtles, crocodiles, birds and mammals as well as some data on the extent of threat (FEOW, 2013).

The most important source of regularly updated information on species' distributions and conservation status is the IUCN Red List of Threatened Species (IUCN, 2016). Species assessed are mapped to individual river or lake sub-catchments, delineated according to the HydroBASINS global database (Lehner and Grill, 2013). Although major progress in assessing freshwater species has been made in the last decade, significant taxonomic and geographic gaps remain, particularly among invertebrates in the tropics (Carrizo et al., 2013). To monitor changes in conservation status over time, Red List assessments should be repeated every five to ten years, with the resulting data used to calculate a global Red List Index for some taxonomic groups (RLI: Butchart et al., 2007). To increase taxonomic coverage more quickly and affordably, the Sampled Red List Index (SRLI) assesses a randomly selected and globally representative sub-sample of species within each taxonomic group (Collen et al., 2009).

A recent compilation of global patterns of species diversity, endemism and conservation status, for freshwater-dependent mammals, reptiles, amphibians, fishes, crabs and crayfishes revealed high levels of regionally-specific threats to freshwater species (Collen et al., 2014). At the level of population trends, the Living Planet Index (LPI) also indicated much higher levels of decline in freshwater species relative to their terrestrial and marine counterparts (McLellan et al., 2014). Only vertebrate species are included in the freshwater LPI (318 species of birds, 257 fishes, 120 amphibians, 35 reptiles and 24 mammals), and this taxonomic bias is exacerbated by the fact that most of the population trend data are derived from temperate latitudes (Collen et al., 2009). However, Joppa et al. (2016) found that many of the global data sets do not meet a set of key attributes that show they can be reliably used for biodiversity threat assessments. Data on the global distribution and/or conservation status of freshwater species are now readily accessible through the Freshwater Biodiversity data Portal of BioFresh (<http://data.freshwaterbiodiversity.eu/#>). However, overall, information on the distribution and conservation status of freshwater biodiversity still remains insufficient to determine progress towards internationally agreed targets. Revenga et al. (2005) had recommended the use of data for specimens in museum collections around the world, which is a valuable supply of geospatial information. While progress has been made, such as by the Global Biodiversity Information Facility (GBIF), FishBase (Froese and Pauly, 2014) and FishNet2 (<http://www.fishnet2.net/aboutFishNet.html>), these museum records remain a significantly untapped resource for many taxonomic groups and regions. A major, emerging source of new data on freshwater species is citizen science (Dickinson et al., 2012; Chandler et al., 2016). Mobilising all freshwater species observations, including museum data and those made by the public using new tools and analyses (ecoinformatics, Michener and Jones, 2012) is a key priority for assessing change in species populations. Together with improved species distribution modelling (Bush et al., 2014; Domisch et al., 2015), this will help in designing more systematic monitoring programs. Species distribution models can help guide where monitoring efforts should be directed

(e.g., areas where there is a high probability of finding a given taxon under the focus of the monitoring program (Tulloch et al., 2012).

4. Measuring change in species traits

Species traits have widely been used to characterise freshwater assemblages or communities, and may include aspects of morphology, function, physiology, behaviour, habitat use, reproduction and life history (Wellborn et al., 1996). Frequently documented traits include: trophic ecology (or functional feeding group); environmental requirement (especially relating to temperature or saprobial water quality); preference for particular substrates; flow regimes of microhabitats; locomotion or dispersal ability; body form; life span, dormancy, and timing and frequency of breeding (Poff, 1997). Species-trait databases have been developed globally for fishes (e.g., Fishbase, Froese and Pauly, 2014) and in some regions for macroinvertebrates, diatoms and plankton (<http://www.freshwaterecology.info/>; <http://www.epa.gov/ncea/global/traits/>). In principle the response of different taxa to various pressures should be predictable based on the right combination of traits e.g. stenothermic and rheophilic taxa are likely to be “losers” under most climate change projections (Chessman, 2009). In addition, it should also be possible to link changes in ecosystem function to changes in the composition of functional traits (Durance et al., 2016). However, comprehensive trait data are still lacking for many freshwater taxa in most parts of the world, and facts about the basic ecology of many common species are lacking, especially in the tropics. We also lack information on how species traits may adapt in response to climate change (Carr et al., 2014) and other human impacts. These gaps are unlikely to be filled by 2020, but priorities to achieve this by 2030 include collection of trait data focussing on gaps in regional coverage (e.g. tropics) and making these data accessible via open-access databases. Environmental genomics tools mentioned in under genetic composition section above (Section 2) will likely play major role in filling these gaps. For example Meta-omics- the analysis profiles of organisms and genes associated with particular steps in key biogeochemical pathways- could help functional species traits to be identified in environmental DNA samples (Chariton et al., 2016).

5. Measuring change in composition of biological communities in freshwaters

Community composition metrics typically provide a quantitative measure of departure from reference conditions that represent taxonomic completeness (or intactness) of the community (Hawkins, 2006). When the reference condition is represented by extant reference sites, environmental variables thought to be unaffected by human activities may be used to predict the probability of occurrence of a taxon at a site based solely on the local environmental characteristics. This has most widely been applied to benthic invertebrates and fish (Simpson and Norris, 2000; Hermoso et al., 2010). Taxa that have a high probability of occurring at a site are considered to be a natural component of the community if the site condition is equivalent to a relatively unimpaired reference site. Different metrics may then be used to quantify the difference between the predicted and observed community at any putatively-impaired site. A range of metrics may be used to represent this difference.

There are also compositional metrics that do not use reference conditions, such as the various biotic indices used to assess water quality and environmental health based upon the composition of assemblages of indicator organisms, most commonly benthic macroinvertebrates, fishes, and periphytic algae (Friberg et al., 2011). Irrespective of the use of reference conditions, metrics of taxonomic diversity typically assume that the detection of a species at a location is determined by the suitability of habitat and the species' dispersal. Hence species interactions like predation, competition, and parasitism are not incorporated into these assessments.

Despite being integrated into large bio-monitoring programs, the data available on the composition of freshwater biological communities are biased and patchy with large geographic gaps. Because models of compositional turnover include all observed species in a community, they do not suffer the weakness of standard techniques where rare species, or as many as half the total taxa, are dropped from the analysis (Ferrier and Guisan, 2006; Linke et al., 2008). The species omitted can be combined with spatially-continuous remotely-derived environmental layers to model community-level properties of biodiversity such as richness (alpha diversity) and compositional turnover (beta and gamma diversity) across large regions (Ferrier, 2011).

6. Measuring change in the structure of freshwater ecosystems

The persistence of freshwater species and communities depends on the spatial arrangements of suitable habitats in the landscape and the presence and location of barriers to movement, including those introduced by humans. Advances in remote sensing technologies offer increasingly frequent and finer scale data on the structural attributes associated with persistence of species, e.g. different wetland types, floodplains, pools, riffles and runs (MacKay et al., 2009). More comprehensive global datasets are now available for both natural and artificial barriers although there are still gaps of coverage (Lehner et al., 2011; Lehner, 2013).

While much in situ data on ecosystem structure exists, it is rarely made available at a suitable resolution for all parts of the world. The development of these global platforms for sub-catchments and wetland extent at a high enough resolution for use at national or sub-national scale offers much potential to synergise local, national and global data collection efforts.

Maps of sub-catchments and associated river networks are now available for the world, (HydroBASINS; Lehner and Grill, 2013), and offer an important global platform for coordinating data collection and measuring structural changes in freshwater ecosystems. A globally consistent map of wetland extent is high priority given the rapid rate of wetland decline (estimated at 64–71% since 1900; Davidson, 2014). A globally-applicable method for mapping wetlands has recently been developed using new remote sensing imagery, seasonal time series and downscaling technologies (Fluet-Chouinard et al., 2015). It distinguishes permanent and temporary wetlands, and measures three patterns of inundation (mean annual minimum, mean annual maximum, and long-term maximum). Integration of such methods to generate a wetland layer within high-resolution global land cover products (Chen et al., 2015) offer the possibility of globally-consistent time series of wetland maps for tracking change in extent across the world. A major challenge is on-ground validation of wetland boundaries, but crowdsourcing mechanisms that validate land cover products could help address this challenge (Fritz et al., 2009). Despite increasing availability of land cover time series evolving methodologies for land cover change detection make the use of this seemingly rich data resource challenging, as there is no standardized information source (Joppa et al., 2016). Developing standardized global maps of wetland extent at an appropriate resolution for local users that are comparable through time and space is a major priority for assessing change in the structure of freshwater ecosystems.

7. Measuring change in the functioning of freshwater ecosystems

Functional measures supply information about the condition of biodiversity not provided by community composition or species populations. There are very few examples of the use of ecosystem-function measures as indicators of the condition of freshwater ecosystems, and Geizendorffer et al. (2015) note that the CBD indicators make limited reference to changes in ecosystem function.

Although some important work has been undertaken on the relationship between species diversity and freshwater ecosystem

functioning (Cardinale, 2011; Brooks et al., 2016), we are not yet able, with a few exceptions, to identify the role of individual species in maintaining particular functions. Thus it is not generally possible to predict how function changes with species loss: some species may be 'redundant' so that their loss has little impact on overall function. Conversely, the loss of certain species (e.g. keystone species such as beaver, *Castor* spp.) may have a large effect on functioning (Dudgeon, 2010). Accordingly, it is possible that structure may change and function remain unchanged in response to some anthropogenic stressors, or vice versa. In the latter case, it is possible that changes in ecosystem function (e.g. in response to sub-lethal effects of contaminants) could serve as an early warning of shifts in community composition and declines in species of conservation concern.

The functional attributes that offer the greatest potential for monitoring changes in freshwater ecosystems include rates of organic matter processing and nutrient dynamics (MacKenzie et al., 2013), which have implications for the candidate EBV of nutrient retention. Primary production and rates of ecosystem metabolism are also potential candidates for monitoring, since they vary at different scales (Beaulieu et al., 2013) and respond to disturbance (Cardinale et al., 2005). Simple measures such as water transparency or colour that could be sensed remotely may have potential as surrogates of primary production (Olmanson et al., 2008). Fisheries production is an aspect of secondary production that is relatively tractable to monitor and, because fish yield represents an aspect of ecosystem functioning that is manifested in ecosystem service provision, it has immediate relevance both to biodiversity conservation and to human livelihoods (Brooks et al., 2016). Biodiversity (and not just biomass) is also important here because a wider variety of fish species yields a more valuable food source (in terms of micronutrients and minerals) than a fishery consisting of a narrow range of species (Youn et al., 2014).

Brooks et al.'s (2016) study highlighted the need for more data. Indeed, data on freshwater capture fisheries are currently both inaccurate and under-reported (Beard et al., 2011; Youn et al., 2014), but there is scope for enhanced monitoring via community participation in data collection, including nutritional surveys (Beard et al., 2011). Furthermore, the generally positive relationship between fisheries yields and primary production might permit the use of remotely-sensed measures of primary production (Brezonik et al., 2005) to monitor potential fish production, assuming appropriate calibration against actual yields.

8. Global modelling of the regional state of freshwater biodiversity

Models increase the value of direct field-based biodiversity observations, which normally cover only a fraction of the landscape, by increasing the spatial coverage of areas for which ecological state can be estimated. In the longer term it would be desirable to accurately model variables in all EBV classes. Currently, however, community composition variables based on taxonomic diversity (GEO BON, 2015) are probably the most suitable to be modelled by 2020 given the datasets available. There has been some success in predicting the taxonomic composition of riverine biological communities at regional and continental scales, using a set of environmental predictor variables and anthropogenic disturbance indices (e.g. Norris et al., 2007; Esselman et al., 2011). These methods can be combined with those developed for modelling richness and compositional turnover in terrestrial biodiversity (Ferrier, 2011) to produce regional estimates of the state of freshwater biodiversity (Fig. 1). Global maps may then be generated by using the same approach for each region (e.g. Freshwater Ecoregions of the World, Abell et al., 2008).

A major challenge in applying the approach depicted in Fig. 1 is generating spatial layers and models that describe the relevant threats or stressors, either directly or via proxies, including their accumulated effects upstream and downstream (e.g. Stein et al., 2014; Janse et al., 2015). Sub-catchment condition can be inferred indirectly from the combination of multiple threatening processes (i.e. "cumulative threat

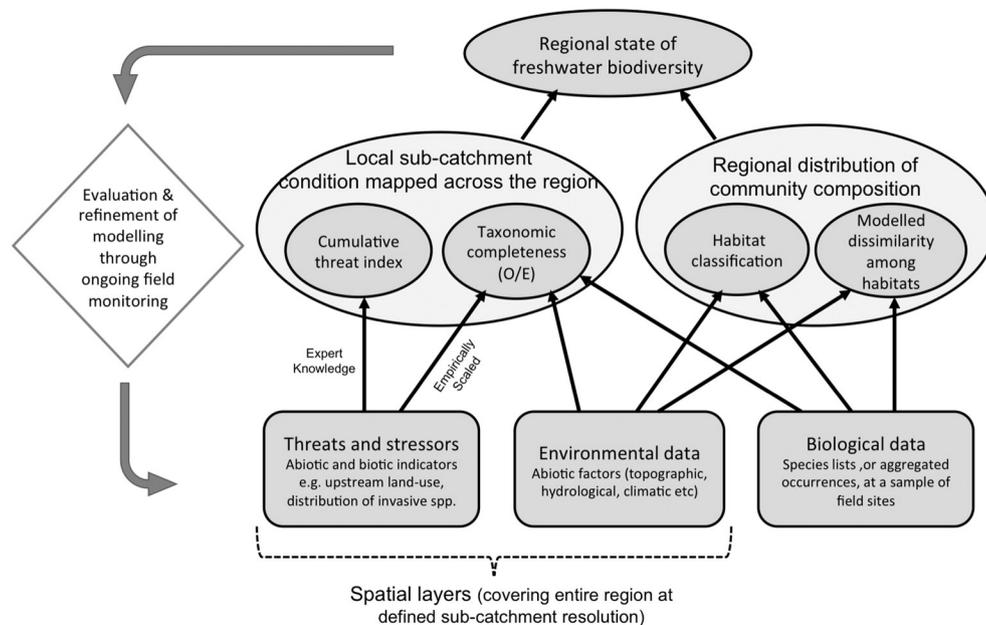


Fig. 1. Modelling framework to estimate the state of freshwater biodiversity within a region, based on the spatial distribution of community composition, and the spatial pattern of sub-catchment condition. Local condition may be inferred directly from the distribution of multiple stressors, or modelled based on observed biological departure from reference communities. The local condition of each and every sub-catchment can then be integrated with information on differences in community composition between sub-catchments (predicted through various methods) to estimate the collective state of biodiversity regionally. To identify change, the model must be repeated with updated information on threats and stressors which are the drivers of change.

indices": Vörösmarty et al., 2010). A more direct approach to assessing the condition of sub-catchments is by using biological data as the baseline of the evaluation. For example, taxonomic completeness (e.g. Observed/Expected taxa, Mean Relative Abundance of Original Species) can be interpolated for un-surveyed sub-catchments using the relationship between stressors and taxonomic completeness at surveyed sub-catchments (e.g. Turak et al., 2011, Janse et al., 2015).

Aggregating estimates of sub-catchment condition offers a practical, and therefore appealing, approach to global assessment in which there have been major advances (Vörösmarty et al., 2010; Janse et al., 2015). However, just as estimates of local species richness (alpha diversity) cannot simply be summed to estimate regional richness (gamma diversity) without knowing the degree of overlap in species composition between locations (beta diversity), sub-catchment condition cannot simply be averaged to estimate the regional state or gamma diversity. In regions that are well studied, beta diversity can be estimated as observed compositional dissimilarity among biological communities using species occurrence data. In other regions inputs from methods such as species distribution models or habitat classification systems could also be used (Linke et al., 2008; Bush et al., 2014). In assessing the state of regional biodiversity it is desirable to use species-area relationship (SAR) coefficients to account for the non-linear relationship between species richness and the area of intact habitat (Ferrier and Drielsma, 2010; Turak et al., 2011).

The state of freshwater biodiversity at ecoregional or global scales will primarily be driven by changes in the distribution and intensity of threats (Fig. 1). Further, the distribution of biodiversity, and potentially its exposure to threats will also be affected by compositional shifts under climate change as was demonstrated by Nelson et al. (2009) in relation to urban development and by Radinger et al. (2016) in relation to multiple land uses. The accuracy of global assessments would be improved if these compositional shifts under climate change can be incorporated into the approach shown in Fig. 1.

9. Outlook and priorities for 2020 and 2030

There has been notable progress towards assessing the state of global freshwater biodiversity since the review by Revenga et al. (2005) and the Millennium Ecosystem Assessment (MEA, 2005). This includes new concepts and approaches (e.g. EBVs), as well as new knowledge on all major components of freshwater biodiversity, advances in data acquisition and management technology, as well as a new toolkit for assessing and implementing environmental flow allocations (Poff et al., 2010). The priorities in Table 1 set the future direction for assessing global freshwater biodiversity guided by the EBV Framework. Important new elements of this direction include use of crowdsourcing and citizen science to expand the coverage of data collection and validate remote sensing products, advancements in environmental DNA methods and sequencing technologies, and the use of ecoinformatics to link observations on species occurrences with other types of data, e.g. species traits and genetic information. Models that combine in-situ and remote sensing data can help to generate a globally-continuous map of the state of freshwater biodiversity.

Effective action towards priorities for 2020 (Table 1) will enable estimating variables in three EBV classes: species populations, community composition and ecosystem structure. Priorities include a globally systematic approach to collecting and assessing species data, collating existing and new data within global platforms (e.g. BioFresh, GBIF, FishBase, FishNet2), coordinated effort towards mapping wetland extent at high spatial resolution, linking in-situ data to modelling across regions, and mobilising citizen science for collection and verification of data. This will allow assessment of the state of global freshwater biodiversity by 2020 using the Red List index, an improved freshwater Living Planet Index, indices of alpha diversity (e.g. local species richness averaged across all locations in a region) and gamma diversity (e.g. collective number of species occurring in a region), and globally-consistent estimates of wetland extent. Assessing variables in the remaining three EBV classes (genetic composition, species traits, and ecosystem function) will be feasible by 2030 if certain priorities are achieved,

Table 1
Short- and medium-term priorities for measuring change in different components of freshwater biodiversity.

EBV class	Priorities for 2020	Priorities for 2030
Genetic composition	<ul style="list-style-type: none"> Expand reference DNA sequence databases for vertebrates and selected macro-invertebrates. Improve methods for characterizing DNA from water samples. Integrate environmental DNA into freshwater biodiversity monitoring programs Integr Nviron 	<ul style="list-style-type: none"> Complete the barcoding library of known species. Develop standard molecular markers to widely assess intra-population diversity Establish a global database, and protocols for intra-population genetic diversity change. Build a global network of genetic monitoring sites
Species populations	<ul style="list-style-type: none"> Expand the geographic scope of Red List assessments to complete the global baseline for freshwaters Repeat Red List assessments for those groups that are already globally assessed (e.g. crabs, crayfish and shrimps) to create the first freshwater Red List Index (RLI) of change in status over time Repeat assessments of those freshwater groups that already have baselines in place as part of the Sampled Red List Index (SRLI)– to provide an interim measure of progress towards meeting targets Broaden the geographic and taxonomic coverage and phylogenetic range of the freshwater Living Planet Index Refine species distribution modelling for freshwater species, including validation of models Improve tools and opportunities for public participation in recording freshwater species occurrences 	<ul style="list-style-type: none"> Repeat Red List assessments at 5–10 year intervals for all of the freshwater groups included in the global baseline to generate time series data for monitoring progress towards meeting targets. Integrate new sources of remotely sensed data (at high temporal and spatial resolution) with biodiversity data measured in-situ for modelling species distribution across temporal and spatial scales Generate global networks of citizen scientists and taxonomic experts, collectively recording and verifying occurrences of freshwater species
Species traits	<ul style="list-style-type: none"> Collect trait data for more freshwater species, especially in the tropics Build a global, open-access species trait database Define freshwater species traits to assess species vulnerability to climate change 	<ul style="list-style-type: none"> Further develop models to predict susceptibility of freshwater species to climate change impacts Complete trait descriptions in the global traits database for all species included in Red List Index
Community composition	<ul style="list-style-type: none"> Map sub-catchments for richness and turnover to assess state of freshwater biodiversity globally Develop guidelines for globally consistent monitoring of freshwater fish and invertebrate assemblages. Include species interactions into assessment methods for biological communities in freshwaters 	<ul style="list-style-type: none"> Establish global reporting structure to repeat assessments with updated threat and stressor data every 3–5 years and additional sampling to improve spatial resolution in data-poor regions.
Ecosystem structure	<ul style="list-style-type: none"> Develop global standards and programmes for non-expert citizen scientists to make observations on wetland extent to support automated high resolution mapping of wetlands. Complete globally consistent mapping of wetland extent at high spatial resolution Develop a hierarchical framework for globally classifying 	<ul style="list-style-type: none"> Automate high spatial and temporal resolution mapping of wetlands calibrated by crowdsourced ground observations Connect habitat structure and species models to a hierarchical system for freshwater ecosystem bio-regionalization. Develop capacity to enable access to increasingly

Table 1 (continued)

EBV class	Priorities for 2020	Priorities for 2030
	<ul style="list-style-type: none"> wetlands for monitoring biodiversity change, informed by combining remote sensing technologies and in-situ observations. Test new and cost-effective remote sensing methods for fine-scale mapping of specific habitat features Develop and test structural change indicators for freshwater ecosystems including those that can integrate crowdsourced data 	<ul style="list-style-type: none"> complex data resources, including those provided by ecogenomics and remote sensing.
Ecosystem function	<ul style="list-style-type: none"> Identify functional attributes of freshwater ecosystems that can be readily quantified (preferably by remote-sensing methods) and directly linked to changes in species composition or population size Develop survey and monitoring methods for assessing temporal trends in fishery yields 	<ul style="list-style-type: none"> Undertake global scale assessments of temporal trends in fishery yields from rivers and lakes Establish pilot monitoring programs of ecosystem functioning in freshwater ecosystems, underpinned by understanding of the mechanisms that link species diversity with ecosystem functioning.

which include the development of environmental DNA methods and relevant reference sequences, inexpensive methods to reveal allelic diversity, species traits databases, eco-informatics and modelling. These activities will also greatly improve assessments achieved for the other three EBV classes.

Implementing the identified priorities requires coordinated effort to collect, process, analyse and interpret existing and new data, as well as developing the capacity to use new technologies. The main question is who will take responsibility for these actions and provide suitable repositories for the increasing amount of data and portals to access these? The answer may lie partly in emerging multi-national initiatives. The Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES) contains an objective to support regional/sub-regional assessments on biodiversity and ecosystem services (Díaz et al., 2015). Also significant are the Joint Work Plan (JWP) between the CBD and Ramsar Convention and the decision of the Ramsar Convention Secretariat to report on the state of the world's wetlands and their services to people (Gardner et al., 2015). The legitimacy provided by the conventions and the global program under IPBES provides a new opportunity to take action to implement the priorities identified in Table 1 at national to international scales. Ultimately, determining success or failure in achieving the high-level commitments to the Aichi targets will be impossible without concerted effort to advance the priorities outlined here.

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