WEUGE: A new metric for ranking locations for biodiversity conservation

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Abstract

Aim: Effective policymaking for biological conservation requires the identification and ranking of the most important areas for protection or management. One of the most frequently used systems for selecting priority areas is the Key Biodiversity Areas (hereafter KBAs), developed by the International Union for Conservation of Nature (IUCN). However, KBAs cannot be used to rank areas, potentially limiting their use when limited funding is available. To tackle this shortcoming and facilitate spatial prioritization, here we develop and validate the “WEUGE index” (Weighted Endemism including Global Endangerment index), consisting of an adaptation of the EDGE score (Evolutionarily Distinct and Globally Endangered). WEUGE allows the ranking of any set of locations according to the KBA guidelines and on a continuous scale.

Location: Global.

Methods: We calculated the EDGE score, Weighted Endemism, Evolutionary distinctiveness, Extinction risk and our newly developed WEUGE index for all terrestrial species of amphibians, mammals and birds accessed by IUCN. We then compared the performance of each of those five indices at prioritizing areas according to the KBA guidelines.

Results: We found that for all taxa surveyed, WEUGE was consistently better at identifying areas that trigger KBA status.

Main conclusions: In our analyses, WEUGE outperformed all other methods and metrics designed for similar purposes. It can serve as a robust evidence-based methodology to prioritize among otherwise equally qualified sites according to the KBA categories. WEUGE can therefore support transparent, evidence-based and biologically meaningful decision-making for conservation priorities.

KEYWORDS
conservation, EDGE, KBAs, Key Biodiversity Area, policymaking, prioritization, WEUGE

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INTRODUCTION

In order to protect biodiversity and promote conservation, the decision-making process should be based on scientific research and data, rather than expert judgement (Sutherland, Pullin, Dolman, & Knight, 2004). Threats to biodiversity, such as habitat destruction, overexploitation, and invasive species, have the potential to completely extirpate species at local scales (Biofund, 2018; Mucova, Leal Filho, Azeiteiro, & Pereira, 2018). Therefore, in recent years, instead of focusing on large extensions of low biodiversity land, there has been an increased awareness of the importance of protecting individual sites of high biological value (Butchart et al., 2012). Such shift of focus may ultimately determine whether species will survive or go extinct. Thus, conservation planning should not only encompass the concepts of global conservation prioritization (Myers, Mittermeier, Mittermeier, Da Fonseca, & Kent, 2000), but also include a more local-scale approach more amenable to policymaking at national and finer political levels.

The Global Standards for the Identification of Key Biodiversity Areas (KBAs) is an attempt to gather a consensus of sites that contribute significantly to the global persistence of biodiversity. The criteria and methodology for identifying KBAs were created by the IUCN World Commission on Protected Areas (IUCN, 2016). KBAs can vary considerably in size, and the criteria aim to address aspects of biodiversity operating from regional to relatively local scales. The categorization of areas is based on criteria such as presence and proportional inclusion of threatened species and ecosystems, species' distribution ranges, ecological integrity and irreplaceability. Using these criteria, together with discussions on the manageability of areas as biodiversity units, the KBA process assesses areas through a binary system, where a particular area will either trigger KBA status or not. However, indices that directly measure biodiversity, such as species richness (SR: Colwell, 2009), phylogenetic diversity (PD: Faith, 1992), weighted endemism (WE: Crisp, Laffan, Linder, & Monro, 2001) and phylogenetic endemism (PE: Rosauer, Laffan, Crisp, Donnellan, & Cook, 2009) are, surprisingly, not included in the KBA methodology.

Although the four metrics cited above are useful in conservation, three of them fail to incorporate information on the threat status of the constituent species—the IUCN’s Red List Assessment parameter. The exception is the Evolutionarily Distinct and Globally Endangered (EDGE) score (Isaac, Turvey, Collen, Waterman, & Baillie, 2007), which combines one biodiversity index—Evolutionary Distinctiveness (ED)—with the threat category of species.

The EDGE score combines ED with values for species' extinction risk in order to generate a list of species that are both evolutionarily distinct and globally endangered ("EDGE species"). The EDGE score is thus tailored to rank species rather than locations. Location scores may be computed as the sum of EDGE scores for all species at a site (Safi, Armour-Marshall, Baillie, & Isaac, 2013). However, this is not guaranteed to maximize conservation importance of individual sites, since the presence of widespread, critically endangered (CR) species produces higher EDGE scores than a vulnerable (VU) or endangered (EN) micro-endemic restricted to very few sites, which could rapidly go extinct if those sites are damaged. One example is the Little Brown Bat (Myotis lucifugus), which occurs across a large portion of the North American continent, but is nevertheless considered an endangered species due to the invasive fungus Pseudogymnoascus destructans causing white-nose syndrome with very high mortality in the species (Solari, 2018).

To tackle the shortcomings described above, in this study, we propose the WEGE index (Weighted Endemism and Globally Endangered), a metric designed to rank any set of locations by their biodiversity importance. WEGE is an adaptation of the EDGE score (Mooers, Faith, & Maddison, 2008), but instead of incorporating the phylogenetic component it uses an endemism score.

We compared the ability of WEGE in ranking areas that trigger KBA status with four other metrics that can be used for similar purposes: WE, EDGE, ED and extinction risk (ER). As the KBA methodology weights all species equally, irrespective of their evolutionary uniqueness, we did not include PD and PE in our benchmarking. We focused on the three vertebrate groups (amphibians, mammals and birds) where global range maps are available for all species. By using spatially coarse grids of 100 × 100 km and 20 × 20 km, we compared the ability of WEGE in ranking areas that trigger KBA status with four other metrics that can be used for similar purposes: WE, EDGE, ED and extinction risk (ER). We found that WEGE outperforms all other metrics in the comparisons we made.

METHODS

Using IUCN’s range maps for all assessed terrestrial amphibians (6,615 species), mammals (5,610) and birds (10,549) (2019-3: IUCN, 2019), we calculated EDGE, ED, ER, WE, WEGE and cells that trigger KBA status for criteria A1b, A1e and B1 in a global scale in resolution of c. 100 × 100 km (10,000 km²) and c. 20 × 20 km (400 km²) grids on a Berhmann projection map. We note that the sizes of the cells are area-true but involve some modifications of the shapes. The actual size is only 100 × 100 km at 30 degrees north or south.

The species composition of each grid cell was obtained by intersecting IUCN range maps that met the following conditions: extant or probably extant, native or reintroduced, and resident or using the area as breeding site. For the 20 × 20 km grids, we only assessed the indices and KBA status of the top left corner cell of a disaggregated 100 × 100 km grid map, although all cells were included in the calculation of range size. This was done to reduce over-estimation of the number of KBAs due to neighbouring KBA-triggering cells.

Key biodiversity areas

The Global Standard for the Identification of KBAs (IUCN, 2016) has five main criteria: A. Threatened biodiversity; B. Geographically restricted biodiversity; C. Ecological integrity; D. Biological processes; and E. Irreplaceability through quantitative analysis. Of these, only...
criteria A and B can be applied to datasets consisting only of species range maps (Table 1).

2.2 | Biodiversity indices

To calculate WE, ED, ER and EDGE values for each grid cell, we summed the values of each metric for every species in a cell. To calculate weighted endemism (WE) for each species, we used one divided by the number of grid cells where a species occurs. The evolutionary distinctness (ED) scores were obtained from www.edgeofexistence.org (EDGE of Existence, 2019) and ER from (Davis, Faurby, & Svenning, 2018). To accommodate taxonomic mismatching, we manually searched for synonyms. Failing to find them, we used the ED median value of the genus or family in case of missing the former. To calculate EDGE, we used the following formula from Mooers et al. (2008):

\[ \text{EDGE} = \ln (\text{ED} \times \text{ER}) \]

In contrast, the WEGE index uses weighted endemism (WE) instead of evolutionary distinctness (ED). Similar to EDGE, WEGE incorporates the probability of extinction (ER).

To calculate WEGE, we applied the formula:

\[ \text{WEGE} = \sum_{i=1}^{3R} \sqrt{\text{WE}_i \times \text{ER}_i} \]

We calculated the WEGE index for each site as the sum across all local species of the square root of the partial weighted endemism value (WE) for each species (i) multiplied by its probability of extinction value (ER). The square root transformation was chosen to improve the normality of the weighted endemism data.

We used species range and conservation status in the WEGE formula as those parameters are also used in the KBA methodology, and as we aimed to rank areas that are also highlighted by the KBA methodology (rather than introducing other metrics such as phylogenetic diversity). In order to calculate WEGE values for a given spatial unit, we created a package in R – WEGE (https://CRAN.R-project.org/package=WEGE). We used the IUCN50 transformation for the ER as in (Davis et al., 2018), which scales the extinction risk over a 50-year period using the following extinction probabilities: LC = 0.0009, NT = 0.0071, VU = 0.0513, EN = 0.4276, and CR = 0.9688. We assigned the extinction risk of the “DD” (Data Deficient) species with the VU probability following Bland, Collen, Orme, and Bielby (2015).

To test our newly developed WEGE index (see above for equation), we built a global gridded map of cells that would trigger KBA status based on criterion A1a, A1b, A1e or B1, hereafter referred to as “KBA-triggering cells”, and calculated the percentage of cells triggering KBA status on the worldwide top-ranking cells for WE, ER, ED, EDGE and WEGE. We used hypothetical KBA-triggered cells to avoid areas that trigger KBA status but are not yet considered KBAs, or areas that are considered KBAs due to other criteria not analysed in this study. We conducted separate analyses for amphibians, mammals, birds and one combining the three groups.

The KBA-triggering cells were the ones that conformed to the criteria A1a), A1b), A1e) and B1 of the KBA guidelines (Table 1). We assumed the presence of ≥10 reproductive units, as stated in the KBA guidelines, whenever a species range intersected with a grid cell. This extrapolation still holds for extremely demanding species such as the tiger (Panthera tigris), where a female tiger has a territory of ~20 km² (Carter, Levin, Barlow, & Grimm, 2015).

### 2.3 | Performance across indices

To test the performance of our newly developed index, we calculated the WEGE index, EDGE, ER, ED and WE globally and compared the percentage of KBA-triggering cells in the highest ranked cells of each metric. A score of 100% means perfect overlap between the highest-ranking cells and the KBA-triggering cells in their top-scored cells, while a score of 50% means that in the top-ranked cells for a particular index, only 50% are KBA-triggering cells. We first identified the number of KBA-triggering cells (K). Following this, we identified how many of the KBA-triggering cells were contained within the K highest ranked cells for the other metrics. In this main analysis, we used the threshold 1 and analysed the 1 × K highest ranked cells. We also tested five other thresholds (0.5, 0.75, 0.9, 1.2 and 1.5).

| Criteria | Conditions in the KBA guidelines | Coded conditions to trigger KBA status |
|----------|-----------------------------------|--------------------------------------|
| A1a)     | The site regularly holds ≥ 0.5% of the global population size AND ≥ 5 reproductive units of a CR or EN species | If at least one CR or EN species is present and has a range of 200 grid cells or fewer |
| A1b)     | The site regularly holds ≥ 1% of the global population size AND ≥ 10 reproductive units of a VU species | If at least one VU species is present and has a range of 100 grid cells or fewer |
| A1e)     | Effectively the entire global population size of a CR or EN species | If any CR or EN species with a range of 1 grid cell is present |
| B1       | The site regularly holds ≥ 10% of the global population size AND ≥ 10 reproductive units of a species | If any species with a range of 10 grid cells or fewer is present |

### TABLE 1 Criteria and conditions used to produce the world KBA-gridded map
1.5), where we, for example in the 0.5 threshold tested how many KBA-triggering cells were found in the $0.5 \times K$ highest ranked cells (Figure 1). All thresholds produce identical patterns, and the results can be found in Appendix S1. Our measure of performance thus means that the higher the percentage of KBA-triggering cells in the top cells, the better the index performs at ranking KBAs.

3 | RESULTS

In this study, we used 6,615 species of amphibians, 10,549 of birds and 5,610 of mammals (Figure 2a). Using IUCN’s range polygons and a threshold of 50,000 km$^2$ for range-restricted taxa, we grouped the different species in four main groups: (a) wide-ranging threatened, (b) range-restricted threatened, (c) wide-ranging non-threatened and (d) range-restricted non-threatened. We find that the vast majority of the threatened amphibians are range-restricted while a relatively larger fraction of threatened mammals or birds are wide-ranging. Due to different thresholds on the KBA criteria (Table 1), numerous threatened species were unable to trigger KBA status on our 10,000 km$^2$ grid cells.

When assessing whether a grid cell would trigger KBA status, on a $100 \times 100$ km grid, we found 3,347 cells triggering KBA status for amphibians, 6,649 for mammals and 6,327 for birds. On a $20 \times 20$ km grid, we found 613 cells triggering KBA status for amphibians, 734 for mammals and 660 for birds. When combining all taxa, we found 9,228 cells on a $100 \times 100$ km grid and 1,480 on a $20 \times 20$ km grid triggering KBA status, out of a pool of 17,283 terrestrial grid cells.

There was overall similarity in the spatial patterns between the three taxa but also some taxon-specific patterns. Most KBA-triggering cells were triggered by all three taxa (2,280), followed by grid cells triggered only by mammals (2,161) and only by birds (1,914) (Figure 3).

We identified the number of cells that were classified as KBAs (K). We then looked at the K top-scoring cells for each metric and identified how many of these were KBAs (K values for the $100 \times 100$ km grid amounted to 3,347 cells for amphibians, 6,649 for mammals, 6,327 for birds and 9,228 for all taxa). By comparing the percentage of KBA-triggering cells on the top-scoring cells of each tested index, WEGE consistently outperforms ED, ER, EDGE and WE for all terrestrial amphibians, mammals and birds at both tested resolutions (Figure 4). The second-best performer for all groups, as well as for the taxa combined, was WE, followed by ER (Figure 4). The higher number of KBA-triggering cells for mammals and birds compared to amphibians is explained by the existence of many wide-ranging threatened species in those two groups (Figure 2b).

According to the global spatial distribution of the WEGE index, the most important WEGE hotspots of amphibians are concentrated in the western United States, Central America, Andes, West Africa, Eastern Arc Mountains in East Africa, eastern Madagascar, China and south-eastern Australia. The most important WEGE hotspots for mammals are found in Central America, Andes, Atlantic Forest, West and Central Africa, Madagascar and Southeast Asia. For birds, the WEGE hotspots comprise Central America, Andes, most of Brazil, India, Southeast Asia, New Zealand and most of sub-Saharan Africa (Figure 5).

![FIGURE 1](Colour figure can be viewed at wileyonlinelibrary.com)
3.1 Regional comparisons

To assess the behaviour of the WEGE index in relation to the other tested indices, we selected three different regions where differences between the indices are more visible. Global maps of all indices can be found in Appendix S1.

As the first example, we illustrate the pattern in amphibians in Africa (Figure 6). Here, EDGE and ED were unable to highlight important grid cells for amphibians, such as the Eastern Arc Mountains, unlike WE, ER and WEGE. Amphibians in this hotspot are often both under threat and restricted to mountain tops, thus driving WE, ER and WEGE scores higher.
As the second example, we illustrate the pattern in mammals in the Americas. Unlike amphibians in Africa, mammals in North America (Figure 7) show an overlap of high evolutionary distinctiveness and narrow ranges that stretches from Central America to the West of North America. However, these areas house fewer threatened species when compared to the East side of the continent. The WEGE index was able to use information from both WE and ER and score grid cells in both west and east of the continent with high values.

As the third and final example, we illustrate the pattern in birds in Australia. Most Australian birds have relatively narrow ranges particularly along the coast, but some of those areas particularly in the northwest are remote and the species occurring there are generally not threatened. Thus, WEGE ranked those cells lower and highlighted instead most of south-eastern and south-western Australia as the most important areas, as well as a few grid cells in the north of Queensland which house threatened species (Figure 8).

**FIGURE 4** Web plot showing the percentage of presence of KBA-triggering cells in the top cells with resolutions of c. 100 x 100 km and c. 20 x 20 km, for ED, EDGE, ER, WE and WEGE. The ED and EDGE values were very similar, rendering the ED line almost indistinguishable (table of values can be found in Appendix S1). Our analyses show that WEGE outperforms all metrics consistently across all tested taxa and resolutions [Colour figure can be viewed at wileyonlinelibrary.com]

**FIGURE 5** Global WEGE maps for all terrestrial amphibians, mammals and birds. Overall, WEGE hotspots were constant through taxa, where, Central America, the Andes, West Africa, East Africa, Eastern Madagascar, China and Eastern Australia registered higher values. For visualization purposes, the values in the cells were divided in 10 quantiles, where blue represent low quantile values, yellow medium and red high. This means that all the same number of cells are shown in the same colour for all four metrics irrespective of the skewness of the distribution of values for the metric [Colour figure can be viewed at wileyonlinelibrary.com]
4 | DISCUSSION

4.1 | KBA-triggering cells

The IUCN's KBA system uses a set of guidelines to decide whether a particular site triggers conservation status, unlike biodiversity metrics which simply quantify different aspects of biodiversity and are therefore expected to weight sites differently. Out of the 9,228 KBA-triggering cells for the three taxonomic groups surveyed, most were triggered by mammals (6,649) and birds (6,327) and fewer by amphibians (3,347) (Figure 2). We interpret this as a result of the higher numbers of wide-ranging threatened species of mammals (104) and birds (97) but whose ranges are nevertheless small enough to trigger KBA status (Table 1) when compared to amphibians (6) (Figure 3). The Western Gorilla (Gorilla gorilla) and the Saiga (Saiga tatarica) are examples of such, by having a range of 104 and 106 grid cells and being CR species.

Despite spatially coarse grids having implications in our interpretations and should be reviewed in light of practical applications of WEGE, that would tend to use much higher resolution data inputs, the fact that most KBA cells were triggered by all three taxa (Figure 2), suggests that important biodiversity areas tend to overlap between different vertebrate groups rather than being taxon-specific. Finally, as more than half of the terrestrial cells were triggered by at least one taxon, this may represent an impractical implementation of the KBA methodology, which may have also been overestimated due to the coarse scale resolution used in this study.

4.2 | The WEGE index

WEGE is capable of ranking locations on a continuous scale and ranks higher the areas that according to current criteria trigger KBA status. The WEGE index adds the component of conservation status of each species to the WE index in order to combine a conservation scoring of each species with a measure of the relative importance of the site in question for each species. This could also be achieved by combining a conservation score while incorporating evolutionary history such as PE rather than WE, but since KBAs by design weight all species equally (irrespective of their evolutionary uniqueness) we chose to select a measure with the same lack of taxonomic weighting. The main rationale for incorporating WE in the EDGE formula to create WEGE was to obtain an index in line with the widely used IUCN KBA framework, which none of the other metrics are able to achieve—WE, ED, ER, WE or EDGE.
Applicability of WEGE

WEGE can be used to rank areas or as a complementary tool in the KBA assessment process—by weighting the importance of biodiversity of sites so that they can be ranked objectively according to their biodiversity importance. The ranking of locations can bring important advantages when prioritizing efforts with limited resources. IUCN’s criteria lack this aspect by attributing a binary system where one particular site either triggers KBA status or not. A policymaker may then focus conservation resource based on insufficiently supported or subjective decisions. WEGE therefore outperforms KBAs when dealing with the A1 and B criteria, by ranking sites within the same category and thereby facilitating the decision-making process with greater objectivity and transparency.

KBA sites which are triggered either by a single threatened or a single range-restricted species will change their status if re-assessed after the species goes extinct, becomes non-threatened or expands its range considerably. Consequently, lower scoring WEGE sites have higher odds of losing their KBA status. One example that illustrates this scenario could involve the Bramble Cay Melomys (Melomys rubicola), a rodent restricted to the island of Bramble Cay which was recently declared extinct (Waller, Gynther, Freeman, Lavery, & Leung, 2017). This species by itself would meet the requirements for the island to trigger KBA status, regardless of its IUCN status, as it was an accepted species entirely confined to a single small island, hence triggering criteria A1.e) (the whole range of a species in a site) and B1 (10% of the range of any species inside the site). Despite the fact the island may have the minimum requirements to trigger KBA status, the island would get a low WEGE value when compared to WEGE values of areas with numerous triggering species. Using only three vertebrate groups and 100 x 100 km grids, most grid cells are classified as KBAs based on presence of endangered or range-restricted species of at least one of these groups. If the KBA framework is expanded to large species-rich groups like angiosperms, we expect that the number of KBAs would further increase to a point where targeted conservation may not be realistically possible on all.

**Figure 7**  Plot illustrating the prioritization of cells for the different indices tested in this study for mammals in the Americas. KBAs were triggered primarily in the west but also in some eastern grids. EDGE and ED exhibit similar gradients, and neither of them highlighted particular cells in the east. Both WE and ED scored eastern United States as a low priority area. In contrast, WEGE was able to highlight areas in both western and eastern North America, by also incorporating the ER information. Percentage of KBA-triggering cells in each top metric: WEGE—85%, EDGE—74%, WE—84%, ER—76% and ED—74%. For visualization purposes, the values in the cells were divided in 10 quantiles, where blue represent low quantile values, yellow medium and red high. This means that all the same number of cells are shown in the same colour for all four metrics irrespective of the skewness of the distribution of values for the metric [Colour figure can be viewed at wileyonlinelibrary.com]
KBAs. Using WEGE, we are, however, able to quantify the importance of different KBAs, enabling a better prioritization of the limited available conservation funding.

4.4 | Comparison between WEGE and other indices

For all tested taxa (amphibians, mammals and birds) and for both spatial resolutions (100 × 100 and 20 × 20 km), the WEGE index outperformed WE, ED, ER and EDGE by detecting a higher percentage of KBA-triggering cells among the its top-ranking cells. Under such test conditions, we therefore find that WEGE ranks biodiversity according to the KBA criteria better than all other tested metrics. The second-best metric was WE, followed by ER in the case of amphibians and mammals but not in birds. We interpret the low ER scores as due to the fact that IUCN assessments of amphibians and mammals (excluding bats) tend to reflect their range to a greater extent than in birds (Figure 2a); therefore, threatened amphibians and mammals tend to trigger KBA status to a greater extent in comparison with birds.

EDGE and WEGE combine two clearly distinct metrics. EDGE combines phylogenetic information and threat status to highlight important species for biodiversity conservation (Isaac et al., 2007), while WEGE makes use of species distributions and IUCN conservation status, as does the IUCN’s KBA criteria. Although range and threat status are not completely independent, as range size is one of the criteria for the IUCN status assessment, when we analysed species' ranges and threat statuses from the IUCN's polygons, we saw that 50% of all species of amphibians, 49% of mammals and 29% of birds are both range restricted and non-threatened. Therefore, by explicitly using range in its calculation, WEGE is better able to incorporate the high conservation value of species such as the widespread but endangered Saker Falcon (Falco cherrug), a species that occurs in a wide range across the Palearctic region from eastern Europe to western China (BirdLife International, 2017), or species that are highly restricted but currently considered of Least Concern, such as the Broadley’s Writhing Skink (Mochlus lanceolatus) (Conradie et al., 2019). As per our tests, we obtained a better measure combining WE and ER in one metric than solely relying on range or threat status to rank the biodiversity value of a grid cell in accordance with the KBA criteria.

Even though both EDGE and KBAs are aimed at the preservation of biodiversity (Isaac et al., 2007; IUCN, 2016), according to our results they prioritize partially different areas. The use of EDGE scores to rank sites is only expected to be efficient when the threats are plausibly mitigated by the protection of a site. However, this may not always be feasible. Threatened species, for instance, may be very widespread under two different scenarios. Some species live in very low population densities, such as tigers (Panthera tigris), meaning that the protection of individual small areas may have little effect. Other species may be threatened by causes that are non-geographic in nature, such as the case of the Tasmanian Devil (Sarcophilus harrisii) which is currently endangered by a sexually transmitted disease (Hawkins et al.,...
Although the species in these two examples are both considered threatened, no single site will be as important for their protection as a site containing the majority of the range of a less threatened, micro-endemic species. This would be the case, for example, for the Near Threatened Mount Mabu Pygmy Chameleon (Rhampholeon maspictus), which has a predicted range of 108 km² (Tolley et al., 2019).

4.5 | The importance of prioritisation

The importance of prioritisation among KBAs for better conservation policy has been previously highlighted (Ferrier, Pressey, & Barrett, 2000; Plumptre et al., 2019; Pressey, Johnson, & Wilson, 1994; Smith et al., 2019). Multiple metrics, including protection status, available funding, “irreplaceability” (Plumptre et al., 2019) and systematic conservation planning (Smith et al., 2019) have been proposed to support the ranking of areas. This methodology, although providing a hierarchy among KBAs, still clusters them in different categories, rather than scoring individual sites as is the purpose of WEGE. In systematic conservation planning, practitioners must choose which conservation features should be used to represent biodiversity (Smith et al., 2019). WEGE represents a simple metric that encapsulates the biodiversity importance of a particular site, highlighting the same areas as the KBA criteria while adding the advantages of continuous scale. Therefore, WEGE may also be used as a feature in systematic conservation planning.

4.6 | Limitations and challenges of the WEGE index

Despite ranking KBA-triggering cells more effectively than other metrics, WEGE uses a simpler methodology by employing only two (A1 and B1) out of seven criteria, as it only uses georeferenced species lists to rank KBAs. We therefore caveat that other criteria like Ecological Integrity (criteria C), Biological Processes (Criteria D) and Irreplaceability Through Quantitative Analysis (Criteria E) are not yet possible to include into our approach. Additional methodological developments would therefore be needed to fully develop a continuous metric fulfilling the full set of goals for the KBAs.

Proposing a particular site as a KBA requires an analysis of the manageability of the site with regard to its physical attributes, such as forest cover or the presence of rivers, and anthropogenic factors, such as roads and existence of human settlements, among other tasks. The WEGE index is not aimed at replacing this process, which we believe is of crucial importance and should be done case by case while involving local authorities and communities. The aim of the WEGE index is to highlight and rank sites, which should be further scrutinized at a local and practical level, as in the KBA process, or to rank already existing KBAs for more effective allocation of resources to maximize biodiversity outcomes.

The selection of sites as KBAs is important in multiple ways, including for conservation planning support and priority setting at national and regional levels (IUCN, 2016). The use of the WEGE index, allowing the ranking of KBAs, is expected to further support a transparent ranking of sites for evaluating conservation priorities.

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BIOSKTECH

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Author contributions: H.F, S.F and A.A conceptualized the project with input from J.A, F.B, C.N and J.M. H.F gathered the data and did the formal analysis with feedback input from S.F and D.B. H.F wrote the original draft H.F, constructively reviewed by S.F, A.A, J.A, F.B, D.B, J.M and A.S.

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