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Software Note

KBAscope: key biodiversity area identification in R

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Key Biodiversity Areas (KBAs) represent the largest global network of sites critical to the persistence of biodiversity, which have been identified against standardised quantitative criteria. Sites that hold very high biodiversity value or potential are given specific attention on site-based conservation targets of the Kunming-Montreal Global Biodiversity Framework (GBF), and KBAs are already used in indicators for the GBF and the Sustainable Development Goals. However, most of the species that trigger KBA status are birds and to maximise benefits for biodiversity under the actions taken to fulfil the GBF, countries need to update their KBAs to represent important sites across multiple taxa. Here we introduce KBAscope, an R package to identify potential KBAs using multiple taxonomic groups. KBAscope provides flexible, user-friendly functions to edit species data (population, range maps, area of occupancy, area of habitat and localities); apply KBA criteria; and generate outputs to support the delineation and validation of KBAs. The details of the analysis – such as the spatial units tested or the KBA criteria applied – can be decided according to the scope of the analysis. We demonstrate the functionality of KBAscope by using it to identify potential KBAs in Greece based on multiple terrestrial taxonomic groups and four sizes of grid cells (4 km², 25 km², 100 km², 225 km²).

Keywords: Greece, important sites for biodiversity, key biodiversity areas, R package, scoping analysis

Background

Site-based conservation targets of the Kunming-Montreal Global Biodiversity Framework (GBF; [CBD 2022a](#)) and the EU Biodiversity Strategy for 2030 ([European Commission 2021](#)) give priority to sites that hold very high biodiversity value or potential in order to safeguard the diversity of life on this planet. Key Biodiversity Areas (KBAs) represent the largest global network of sites critical to the persistence of biodiversity, which have been identified against standardised quantitative criteria. KBAs are already used in indicators for the GBF ([CBD 2022b](#)) and the Sustainable Development Goals (SDGs; [United Nations 2017](#)) – therefore countries are expected to report on their KBAs – and they are also used by the private and financial sectors to minimize risk to biodiversity ([KBA Partnership 2018](#)). There are currently more than 16 000 KBAs published in the World Database of KBAs that have been identified solely for birds ([BirdLife International 2023](#)), mainly because important sites for biodiversity until recently had been identified based on individual taxa ([Plantlife International 2004](#), [BirdLife International 2014](#)).

Since the release of the Global Standard for the Identification of KBAs (hereafter KBA Standard; [IUCN 2016](#)), there is now a globally standardised mechanism supporting the identification of KBAs across all taxonomic groups and ecosystems. In recent years, various countries including South Africa ([KBA Partnership 2022](#)), Mozambique ([WCS et al. 2021](#)), Uganda ([Plumptre et al. 2019](#)) and Canada ([KBA Canada Coalition 2021](#)) have begun to apply the KBA Standard. A challenge for all countries was to be able to rapidly identify potential sites that could be formally proposed as KBAs, especially with regards to identifying those sites where species data (from different data types aligned to the KBA Standard) would meet relevant KBA criteria and where sites would also satisfy the requirements of what constitutes a unique KBA as outlined in the KBA Standard (IUCN 2016).

Without a tool to help rapidly scope for potential KBAs across all taxonomic groups, countries cannot identify all opportunities to support biodiversity conservation under the actions outlined within the GBF and other multilateral environmental agreements. Here, we introduce the R package ‘KBAScope’ (www.r-project.org), which generates spatial data layers of preliminary sites meeting KBA criteria, therefore assisting the KBA identification process by automating scoping analysis for sites. We demonstrate the application of KBAScope to Greece, for the identification of potential KBA sites for multiple terrestrial taxonomic groups with differing data sources recognised in the KBA Standards. Given two key parameters – proportion of global population size at a site and size of the initial spatial unit considered as a site – ultimately affecting whether a potential KBA meets the requirements of a site to be considered as a KBA as recognised in

the KBA Standard, we also demonstrate the application of KBAScope across a range of differing size spatial units and recognise implications of initial spatial unit size choice for final KBA assessment.

Methods and features

Overview

KBAScope can utilise all assessment parameters recognised in the KBA Standard – except for distinct genetic diversity – that are used to identify KBAs. Parameters include population data in mature individuals (need to have estimates of numbers mapped across the global range of the species), and the spatial proxies of populations: area of occupancy (AOO); extent of suitable habitat (ESH; now consistently referred to as ‘Area of Habitat’ or AoH; [Brooks et al. 2019](#)); range maps; and number of localities ([KBA Standards and Appeals Committee of IUCN SSC/WCPA 2022](#)). When range maps from the IUCN Red List are used as an assessment parameter, KBAScope can deal both with breeding and non-breeding ranges of species by selecting the appropriate polygons. It also integrates all the available resources from the KBA website (Tools page) to calculate in the background all information needed to apply KBA criteria; namely the appropriate taxonomic group level, restricted range species and ecoregion and bioregion restricted species.

The KBAScope package comprises 16 functions which can be divided into four main groups 1) preparation functions; 2) functions that generate parameters needed to test KBA criteria; 3) functions that test data against KBA criteria; and 4) functions that generate results and summary outputs ([Table 1](#)). They can be used either to scope a single/few sites or perform a scoping analysis nationally using any type of spatial units (i.e. existing sites, grid cells, hexagons, hydro-basins). KBAScope applies the species specific KBA criteria (threatened biodiversity A1; geographically restricted biodiversity B1, B2 and B3; and biological processes D1, D2 and D3) which are the ones that are mainly used to identify KBAs ([BirdLife International 2023](#)) and require an automatization tool to speed up the process, due to the amount of data. The remaining KBA criteria 1) are applied to ecosystems (threatened ecosystem types A2; geographically restricted ecosystem types B4) using data from the IUCN Red List of Ecosystems which are available mainly for Europe and North America ([IUCN 2024](#)); 2) are identifying areas of at least 10 000km² in size, requiring many qualitative parameters in addition to the quantitative ones (ecological integrity C); and 3) are still being tested/developed (irreplaceability through quantitative analysis E).

KBAScope can be used both with data of species that are assessed against the IUCN Red List criteria (IUCN 2012;

Table 1. The KBAScope functions separated into four main groups and their description.

Function	Description
Preparation	
<code>create_repo()</code>	Creates the required folder structure to run the scoping analysis
<code>spatial_units_edit()</code>	Edits the spatial units to a certain format
<code>red_list_info()</code>	Combines information of species taxonomy, assessment and common names from the IUCN Red List
<code>species_info()</code>	Creates a file with all information needed to apply KBA criteria
<code>species_edit()</code>	Packages species population data in a format that KBA criteria can be tested
Parameters for KBA Criteria	
<code>eco_bio_check()</code>	Evaluates if a species is ecoregion or bioregion restricted
<code>site_calculation()</code>	Calculates site population size
KBA Criteria	
<code>criterion_A()</code>	Checks threshold for criterion A and qualitative requirements
<code>criterion_B()</code>	Checks threshold for criterion B and qualitative requirements
<code>criterion_D()</code>	Checks threshold for criterion D
<code>criteria()</code>	Wrap up function to create one column for all criteria
<code>save_triggers()</code>	Writes output of each species and the sites it triggers KBA criteria
Results	
<code>potential_kbas()</code>	Generates GIS file of potential KBAs
<code>results_summary()</code>	Generates results summary information
<code>view_results()</code>	Generates a graph to visualise results
<code>kba_dataforms()</code>	Pre-populates KBA data form

relevant to KBA A criteria) and those that are not yet assessed (relevant to KBA B and D criteria). KBAScope generates two types of outputs, 1) GIS outputs (i.e. geopackages) of the spatial units used in the analysis, for which KBA criteria are triggered (i.e. which spatial units satisfy KBA criteria for species, potential_KBAs.gpkg); 2) the species distribution within the potential_KBAs (i.e. the KBA 'element layers' as defined in the KBA Guidelines, ptrigger_species.gpkg); 3) an Excel file of all the information needed to apply KBA criteria for the species that trigger KBA criteria (pttrigger_species.csv); and 4) a results summary Excel file which includes the number of species per taxonomic group that trigger KBA criteria in each spatial unit and the spatial units that criteria B2 and B3 are triggered (results_summary.xlsx).

In order to install the package a standard installation of R (ver. 4.3.1, www.r-project.org) is required. KBAScope mainly depends on the 'sf' (Pebesma 2018) and 'dplyr' (Wickham et al. 2020) packages. The package core is open-source and available on GitHub (www.github.com/.../KBAScope), where users can contribute and/or submit issues. KBAScope uses the internal storage of a computer and applies functions to each species separately to speed up the analysis. There are no computer specifications required; however, the more RAM and CPU threads a computer has, the faster the analysis will be completed.

Workflow

There are five types of data that need to be acquired for applying KBAScope: 1) species global population/distribution data in tabular/vector format; 2) species taxonomic classification (including phylum, class, order and family); 3) species Red List Category and criteria (necessary only when applying A1); 4) spatial units as vector polygon features (such as protected areas, grid cells and hydrobasins level 12) that will be

tested against KBA criteria; and 5) ecoregion and bioregion vector polygons (Fig. 1; necessary only when applying B2 and B3). Population/distribution data need to be separated for terrestrial, freshwater and marine systems. There are different ecoregion/bioregion layers used to identify KBAs in each system and specifically KBAs for freshwater species are suggested to be identified using HydroBASINS level 12 (Holland et al. 2012, Sayer et al. 2019). It is also important that the assessment parameter input data only contain the scientific name of a species and do not have any redundant information that may cause errors in the application of KBAScope, except from IUCN Red List range maps where information on species 'id' and 'scientific name', 'assessment id', polygon 'presence', 'origin' and 'seasonal' codes and 'legend' should be included.

The first step in the KBAScope workflow is the use of the *create_repo* function to create the folder structure necessary for input and output data. Species data should be stored in the input folder 'raw_species', taxonomy under 'IUCN_Red_List', spatial units under 'spatial_units' and ecoregion/bioregion layers under 'eco_bioregions'.

The second step is the use of the preparation functions (Table 1) to edit all acquired data. For species data, preparation functions need to be used separately for each data type. In this step a separate GIS file for each species with almost all the necessary information to apply KBA criteria – including the calculation of the global population/distribution size – is created in the species folder.

The third step is the use of the parameters for KBA criteria and KBA criteria functions (Table 1) separately for each species. Species data are intersected with spatial units, the proportion of the global population of species present in the spatial units is calculated and KBA criteria are tested against global/site species population/distribution. In this step, GIS files – for which KBA criteria are met – are created under the output folder.

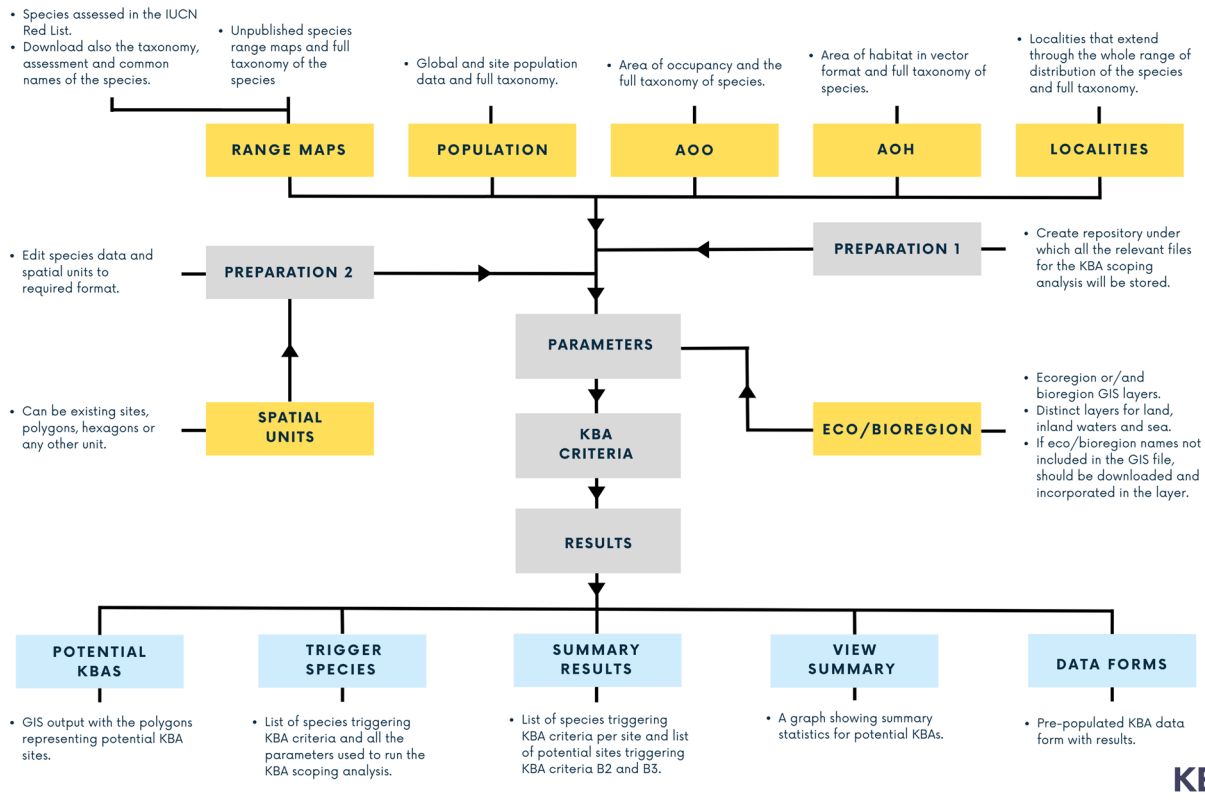


Figure 1. KBAScope workflow. Yellow rectangles represent input data that the user needs to collect (not all yellow rectangles are mandatory; it depends on the data that are being analysed), grey rectangles represent analyses performed by functions in KBAScope and light blue rectangles represent outputs of the scoping.

The fourth step is the use of results functions (Table 1). In this step a GIS file containing potential KBA sites, one with potential trigger species and a results summary file are created under the results folder. There is also the option to view results and pre-populate a KBA data form. A script for the application of KBAScope is available in the Supporting information.

Example applied to Greece

Data

A variety of data types can be used to identify KBAs allowing for the utilization of the best available information for species (KBA Standards and Appeals Committee of IUCN SSC/WCPA 2022). Acquiring data for species in Greece revealed that species data are collected in different data types. We managed to collect 1) range maps for 1853 terrestrial species from the IUCN Red List (IUCN 2023), representing all available maps for terrestrial species in Greece, regardless of the threat category; 2) localities for 189 endemic species (amphibia, reptiles, orthoptera, odonata and the plant family Caryophyllaceae) from taxonomic experts; 3) AoH maps for 21 mammal species (Lumbierres et al. 2022); and d) AOO data for 210 endemic troglobite species (Arachnida,

Diplopoda, Entognatha, Gastropoda, Hexanauplia, Insects and Malacostraca; Paragamian et al. 2018). We used in total 2088 species, representing 57 taxonomic groups – according to the appropriate taxonomic ranking to apply KBA criteria

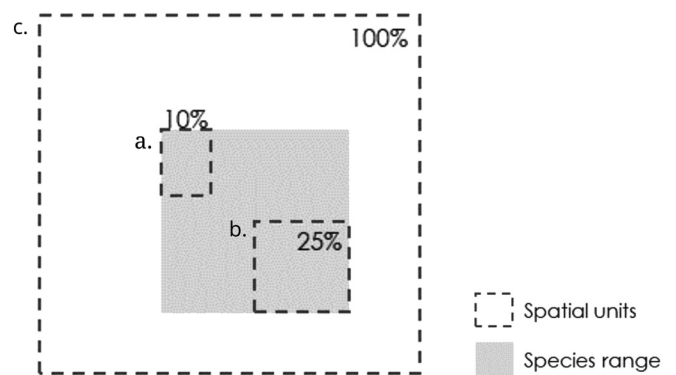


Figure 2. Example of potential KBA sites according to B1 criterion (using species ranges as an assessment parameter). Dashed line areas represent spatial units of varying sizes (a, b and c). The grey square represents a species range. Numbers next to the spatial units represent the percentage of the species global population (here estimated from range) present in each of the spatial units. If the percentage is $\geq 10\%$, the spatial unit can be identified as a KBA (here all three of them). Even spatial unit c, the largest one, can be identified as a KBA.

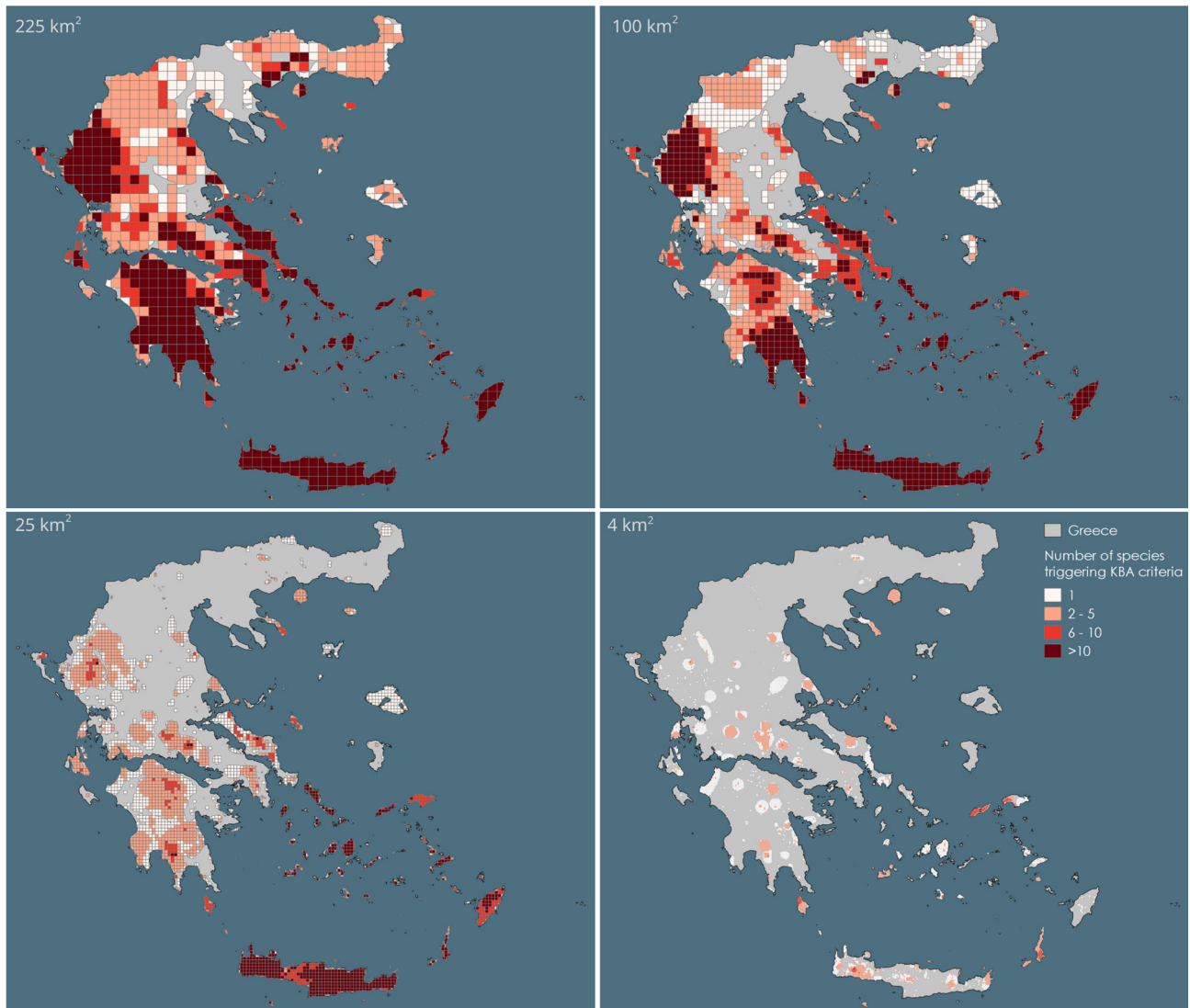


Figure 3. Potential KBA sites using 225 km², 100 km², 25 km² and 4 km² grids. Every cell with colour (not grey) is a potential KBA site. The darker the cell colour, the higher the number of species triggering KBA criteria.

(KBA Standards and Appeals Committee of IUCN SSC/WCPA 2022). The majority of the species are invertebrate (1265 species) and vertebrate (491 species) animals; while plants comprise 332 species (Supporting information).

We stored all species distribution data under the folder 'input/raw_species' in a single file per data type (e.g. range_maps.gpkg and AOO.gpkg). We also downloaded the files 'taxonomy.csv', 'assessment.csv' and 'common names.csv' from the IUCN Red List (IUCN 2023) and stored them under 'input/IUCN_Red_List' to gather information on species taxonomy, conservation status and IUCN Red List criteria triggered, and common names used. For species not assessed in the IUCN Red List, we added their full taxonomy in the 'taxonomy.csv' file downloaded. Grid cells were stored under 'input/spatial_units' and the terrestrial ecoregions layer used (Olson et al. 2001) under 'input/eco_bioregions'.

Methodology

The thresholds for KBA criteria are the proportion of the site to global population size. Two parameters affect whether the KBA criteria are met: 1) global population size and 2) spatial unit size against which the site population is considered against the global population. The bigger the spatial unit and the smaller the global population size, the higher the chances of meeting KBA criteria. For example, in Fig. 2, all three sizes of spatial units for assessing the proportion of global population within a spatial unit capture at least 10% of the species global and thus, all three can be identified as KBAs (B1 criterion threshold).

To demonstrate the application of KBAScope and the impact of spatial unit size on identifying potential KBAs, we assessed available data for Greece using grid cells of four different sizes (4 km², 25 km², 100 km², 225 km²), which represent

the size range of the majority of the protected areas and KBAs of Greece (BirdLife International 2023, UNEP-WCMC and IUCN 2023). We could not test over an infinite number of grid cell sizes due to processing power limitations. However, for smaller countries or smaller regions, testing over a smaller grid cell size will be feasible. We tested the grid cells against KBA criteria A1, B1, B2 and B3, which are species specific and can be applied using data types we collected for Greece.

Results

Our results show that scoping for the largest grid size (225 km²) resulted in almost the whole of Greece becoming a potential KBA, covering 86.8% of the country's land (Fig. 3). The 4 km² grid was the only one that produced distinct sites that aligned with the KBA Standards which recognises that sites should be of a 'manageable size'. In all the grid cell sizes, the islands and the southern part of the mainland consistently have the highest density of potential KBAs.

The largest cell had the highest number of species triggering KBA criteria. In total, 977 species met the thresholds for the 225 km² grid; only 880 and 712 did for the 100 km² and 25 km² cell sizes, respectively; and 514 did so for the 4 km² grid. The results from the different grid sizes are highly nested – all species captured by the smaller grids are also captured

by the larger ones. For further details on the scoping analysis results see the Supporting information. A visual representation of summary results is also possible with KBAscope, displaying the number of species per taxonomic group; the number of potential KBAs and their mean and total area; the number of KBA criteria triggered; and the sites with the highest number of species triggering KBA criteria (Fig. 4; depicting KBA scoping analysis summary results using the 25 km² grids as an example).

Invertebrate species and specifically gastropoda (snails) and orthoptera (crickets) were the taxonomic groups with the highest numbers of species triggering KBA criteria in Greece, consistently across all spatial units (Supporting information). These two taxonomic groups, along with aves, have the highest number of species used in our analysis. However, in contrast with aves, they have relatively small distributions and higher number of species threatened with extinction, which trigger KBA criteria A (threatened biodiversity) and B (geographically restricted biodiversity). The caryophyllales plant taxonomic group (represented only by the Caryophyllaceae family) had the third highest number of species meeting KBA thresholds. Vertebrates had the lowest number of species across all spatial units. Within these, the group with the highest number of species were the reptiles. For the number of species per taxonomic group see Supporting information.

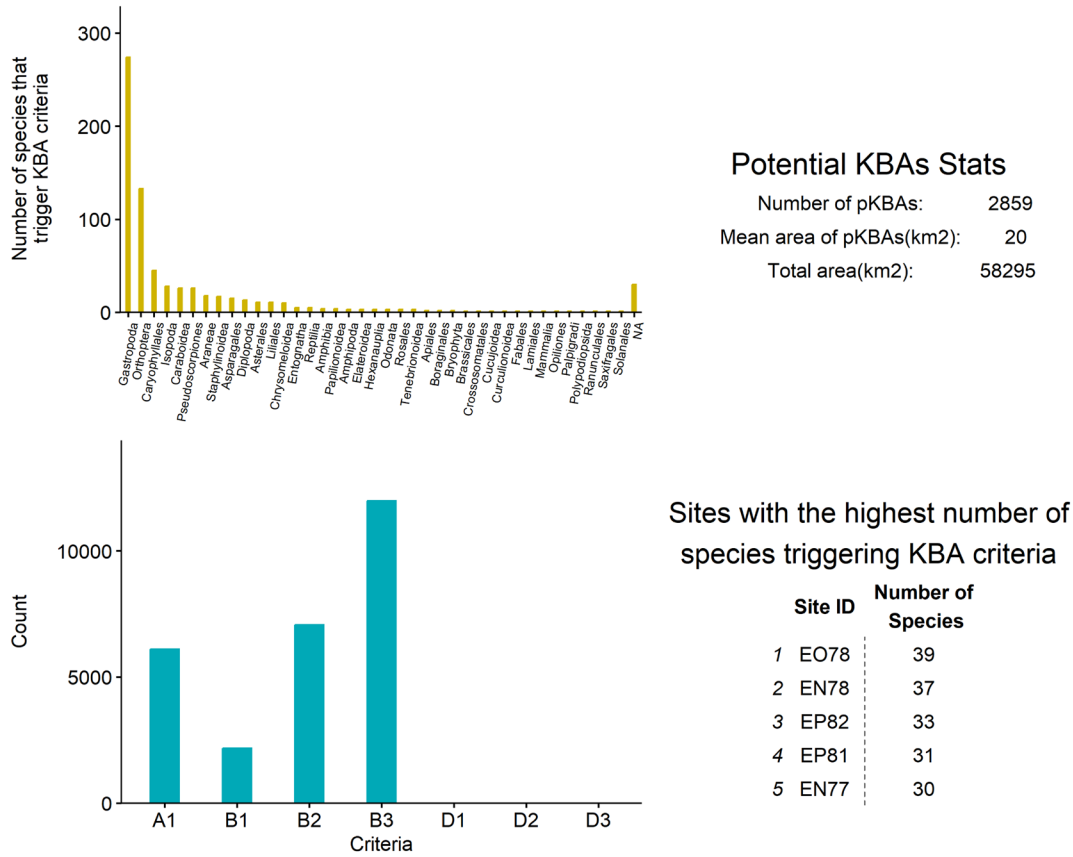


Figure 4. KBAscope output of the *view_results* function, displaying summary results for the potential Key Biodiversity Areas (KBAs) in Greece using terrestrial species and the 25 km² grid cells.

Conclusions

KBAScope helps users to perform rapid scoping analysis for KBAs at the national or site level in terrestrial, freshwater and marine systems. Critically, KBAScope offers this opportunity across all major data types which can be used for assessing proportion of global population within different spatial units. This provides the opportunity for any user to test different methodologies across realms and assess (i.e. scope) for which areas might have sites that could qualify as KBAs and would warrant further investigation. Our results, in the simple example applied to Greece, have shown that scoping for KBAs using multiple taxonomic groups can provide a lot of added information. However, site delineation cannot take place without considering the aspect of manageability – the possibility of effective management across a site considering socio-economic factors (IUCN 2016) – and essentially the choice of initial size of spatial units will determine the number and size of potential KBAs and thus their manageability potential. Therefore, countries should scope for KBAs at different scales to help identify where to focus the identification process.

Ultimately, a scoping analysis is only the first step to the KBA identification process and stakeholder engagement is a key to site delineation. KBAScope also creates results to assist national workshops and the official proposal of sites to the World Database of KBAs. Currently, KBAScope cannot utilize raster data and cannot test KBA criteria A2, B4, C and E. However, KBAScope will be regularly updated to incorporate updates of the resources available on the KBA website (Tools page), and future updates will incorporate all KBA criteria.

To cite *N-SDM* or acknowledge its use, cite this Software note as follows, substituting the version of the application that you used for ‘version 1.0’:

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Author contributions

Konstantina Spiliopoulou: Conceptualization (equal); Data curation (equal); Formal analysis (lead); Methodology (equal); Software (lead); Validation (equal); Visualization (equal); Writing – original draft (lead). **François Rigal:** Software (supporting); Validation (equal); Visualization (equal); Writing – review and editing (equal). **Andrew J.**

Plumptre: Writing – review and editing (equal). **Panayiotis Trigas:** Data curation (equal); Writing – review and editing (equal). **Kaloust Paragamian:** Data curation (equal); Writing – review and editing (equal). **Axel Hochkirch:** Data curation (equal); Writing – review and editing (equal). **Petros Lymberakis:** Data curation (equal); Writing – review and editing (equal). **Danae Portolou:** Writing – review and editing (equal). **Maria Th. Stoumboudi:** Writing – review and editing (equal). **Kostas A. Triantis:** Conceptualization (equal); Methodology (equal); Supervision (lead); Writing – review and editing (equal).

Transparent peer review

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Data availability statement

Data are available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.1ns1rn90h> (Spiliopoulou et al. 2024).

Supporting information

The Supporting information associated with this article is available with the online version.

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