

# sRedList platform documentation

*version 1.2*



You can ask questions on the [sRedList platform forum](#)  
and report any error or lack of clarity to [sredlist@conservara.fr](mailto:sredlist@conservara.fr)

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## General introduction

The sRedList platform is a joined effort between the [sRedList working group](#) and [LifeWatch Italy](#), aiming to facilitate and streamline the work of Red List assessors (see Cazalis et al., 2022). By providing an easy and interactive analyses, we aim to improve the consistency of the assessments across experts and taxa, while not limiting expert judgement in the evaluation. Every product of the platform can be directly submitted to SIS Connect or you can use the sRedList\_report file present in the final ZIP file to copy-paste the results directly in SIS (check the “From sRedList to SIS” section and video tutorial).

It currently enables for instance:

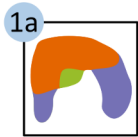
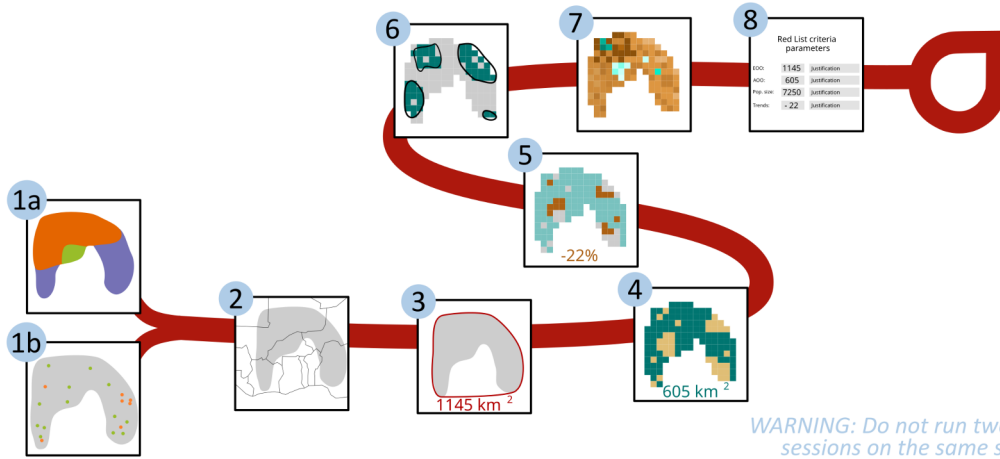
- Creating a distribution from online available or uploaded occurrence records
- Mapping species Area of Habitat and calculating trends in Area of Habitat
- Extracting Countries of Occurrence of the species
- Calculating trends in forest cover in species' range
- Calculating population severe fragmentation

You will find in this document all the information to use the platform (information also available on the platform clicking on the little icons ) and you can also find a Cheatsheet and some video tutorials on the home page of the platform (or directly in the platform with the little icons ). The R code used in the platform can be found [here](#).

Before starting, here are some important points to note:

- All results displayed on the platform should be carefully checked and questioned with your expertise. For instance, before using trends in Area of Habitat (AOH) for criterion A2, you should check that the map of AOH makes ecological sense, that the map trends in AOH fits your regional knowledge, and question if there are other sources of decline (e.g., this estimate does not consider effect of hunting, diseases...).
- The platform does not store your results, so you cannot start using it and come back in a few hours / days on it, everything will be removed after 3 hours of inactivity. So you need to complete the whole process in a short time and you will be able to download everything at the end of the process in a ZIP file.
- It is currently not possible to run two parallel sessions on the same species, you should always have only a single internet page open per species.

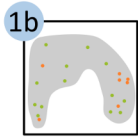
We are always happy to receive your feedback on the platform. This can be done on the forum, or via email at [sredlist@conservara.fr](mailto:sredlist@conservara.fr)



### Charge / edit distribution:

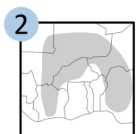
- 1) Either
  - Reuse the Red List published range map
  - Upload your distribution shapefile
- 2) Select polygons to use (presence / seasonal / origin)
- 3 - optional) Restrict to a single country

For National or Regional Red Listing you can enter the name of one country (or "Europe", "EU27" or "Mediterranean")



### Create distribution map:

- 1) Download occurrence records
  - GBIF Limited to 2000 records (if more data we download a spatially representative sample)
  - OBIS All records (for marine species; default: ticked if species last assessed in marine system)
  - Red List Use data points from Red List assessment (default: ticked if data available)
  - Upload Upload your own points with a csv (2 mandatory columns: 'longitude' and 'latitude')
  - Synonym Synonyms to download (for GBIF, OBIS, Red List). If several synonyms, split with semicolon
  - Restrict to a country For National or Regional Red Listing you can enter the name of one country (or "Europe", "EU27" or "Mediterranean") to restrict the distribution
- 2) Filter occurrence records
  - Automated filter Use CoordinateCleaner (e.g., records at countries' centroid, at coords 0,0)
  - Year Filter out data anterior to this date (+ tick to exclude data with no year)
  - Uncertainty Filter out data with high coords. uncertainty (+ tick to exclude data with no uncertainty)
  - Extent Filter out data outside a specific extent (lon/lat)
  - Sea/Land Filter out data made at sea / at land
- 3) Create polygon range map
  - Choose a starting point "Show examples" will help you choose between 1,2,3,4
    - 1) 'Minimum Convex Polygon' will draw a convex polygon including all points
    - 2) 'AlphaHull' will draw an alpha convex hull. Please specify tension parameter below
    - 3) 'Kernel' will draw kernels. Please specify probability parameter below
    - 4) 'Individual localities' will draw a buffer around each occurrence. Please specify buffer distance
    - 5) 'Coast' will draw the coast around points. Please specify buffer distance and crop by land or sea
    - 6) 'Hydrobasins' will map all hydrobasins level 8/10/12 with at least one occurrence, or all hydrobasins of level 8 overlapping with the Minimum Convex Polygon
  - Buffer (in km)
  - Crop by land or sea
  - Crop by altitude Click on "Extract" to visualise the elevation of occurrence records
  - Merge with published map Will merge the polygon created with the published polygon range map (if it exists)
- 4) Smooth polygon range map
  - Choose a smoothing parameter 0 if you do not want to smooth



### Extract Countries of Occurrence:

- 1) Select one or several domains
- 2) Extract realms + countries National / subnational entities following the Red List classification. For marine species, EEZs are used
- 3) Visualise countries Explore countries that are extracted by zooming / clicking. Cannot edit for now.

## Outputs

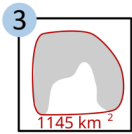
- Criteria estimate
- SIS-compatible file

→ Point range map (.csv)

→ Polygon range map (.shp)

→ Hydrobasins (.csv)

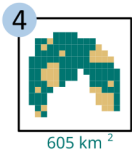
→ Countries of Occurrence (.csv)



### 3 Calculate extent of occurrence:

- 1) Map Minimal Convex Polygon around range
- 2) Calculate EOO

● Extent of occurrence (B1)

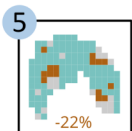


### 4 Calculate Area of Habitat:

- 1) Enter / reuse species information: You can provide uncertainty in elevation limits or density as value1-value2 and in habitat by clicking a box twice
  - **Habitat preferences** Default from Red List (marginal or unknown grouped as "Marginal\_Unknown")  
Click on "Extract" to visualise the habitat distribution of occurrence records
  - **Elevation preferences** Default Red List; if absent we calculate and provide min / max elevation in range
  - **Average density** Enter manually or use calculator. Default density in occupied habitat provided for mammals and birds.
- 2) Calculate lower bound of AOO (if distribution from occurrence records)  
Calculate the area of 2x2km pixels that include known occurrence records
- 3) Calculate current AOH Using the ESA-CCI land-cover map with Lumbierres et al. (2022) crosswalk
- 4) Rescale AOH at 2x2km to get an upper bound of AOO
- 5) Multiply AOH and density to estimate population size

→ Habitat preferences (.csv)

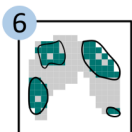
● Area of occupancy (B2)  
● Population size (C-D)



### 5 Calculate Trends in Area of Habitat:

- 1) Enter / reuse generation length  
If available, we display the GL from the Red List (mean when range provided)
- 2) Calculates trends in AOH in last 10 years / 3 generations  
If 3 generations length brings before 1992, we use 1992 data and make an exponential extrapolation to estimate total AOH loss

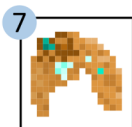
● Population decline (A2)



### 6 Calculate habitat fragmentation:

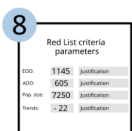
- 1) Provide isolation distance Distance above which subpopulations are considered isolated (this could include uncertainty by typing value1-value2)
- 2) Map and calculate population fragmentation
- 3) Determine severe fragmentation Depending on what is "small" subpopulation
- 4) Determine max subpopulation size and proportion

● Severe fragmentation (B)  
● C2a subparameters



### 7 Calculate trends in remote-sensed products

- 1) Select the remote-sensed product Forest cover, Human modification index, or Human density
- 2) Calculate trends Provides current value, absolute trends, relative trends



### 8 Edit estimates and text:

- 1) Fill or edit taxonomy, parameters and justifications
- 2) Visualise triggered category and criteria
- 3) Download zip file Download, edit files if necessary, upload to SIS Connect. Leave fields empty to avoid overwriting in SIS

→ allfields (.csv)  
→ assessments (.csv)  
→ references (.csv)  
→ sRedList\_report (.html)  
→ Output log (.csv)

## To cite the platform in your assessments:

sRedList (2023). sRedList Platform - a tool to support Red List assessments (Version 1.2). LifeWatch ERIC. <https://doi.org/10.48372/DSKB-JE13>

## Page 0: Select a species for reassessment or add a new species for first assessment

Choose whether you are working on a 'Reassessment' (i.e., the species is already published on the Red List), or a 'First assessment' (i.e., the species has never been published on the Red List yet).

### Reassessment

Enter the scientific name of a species that is already published on the Red List and click on the name. Sometimes the information on this page will not appear and the history plot will display the message “The Red List API is not working, sorry! We cannot provide the usual information on this page, but you can click Next”. This is because the Red List API is not working at the moment and we are waiting for the Red List Unit to fix the issue. You can click next and keep working on your assessment though.

### General information:

Basic taxonomic information on the species. This has been extracted from the Red List database with the *rredlist* R package (Chamberlain, 2020).

### Last assessment:

Basic information on the last Red List assessment; includes date of assessment, Red List category, assessor(s), reviewer(s), population trends, and a link to the assessment. This has been extracted from Red List database with the *rredlist* R package (Chamberlain, 2020).

### Assessment history:

Plots Red List categories of last assessments; former Red List categories (i.e., those different from LC, NT, VU, EN, CR, EW, EX, DD) are grouped into the 'Former' category. Note that the trend does not necessarily represent a genuine change in the Red List category. This has been extracted from the Red List database with the *rredlist* R package (Chamberlain, 2020).

### Distribution:

Plots the polygon distribution published in the last assessment (colours as in the interactive plot from step '1. Distribution').

### First assessment

Enter a species name. Be careful to spell it correctly, and avoid double spaces.



## Page 1a. Select or upload polygons

### Select a species

Select the distribution to use for spatial analyses. The distribution offered as 'Genus\_species\_RL.shp' is the distribution published in the last Red List assessment (if it is not listed, this means it is not available on the platform). You can also upload an existing shapefile distribution from your computer, or create a distribution (see next section).

### Upload a distribution

To upload a distribution map, use the 'Upload' section and select a shapefile (including the 4 files with extension shp, shx, dbf, and prj; of a size of maximum 5MB; using WGS84 lat/lon coordinate reference system). No columns are required but we recommend uploading the shapefile that you will use for published assessment. Once uploaded, the distribution will appear in the distribution lists above (with the date of upload) and you will be able to select it. This distribution will be kept on the platform for 15 to 30 days so you can reuse the distribution without needing to upload it again.

### Edit distribution

Select the polygons that you want to use in further analyses. After this step, all selected polygons will be merged and used indifferently in the following analyses (extraction of countries of occurrence, calculation of extent of occurrence or Area of Habitat...).

### Restrict to a country (for National Red List only)

For national and regional Red Listing, you can restrict species' distribution to a single country by selecting its name in the 'Country to crop' box. Make sure that the country you select is overlapping with the species' distribution. For European Red Listing, you can select 'Europe', which will restrict the distribution to the geographical boundaries of Europe, or 'EU27', which will restrict the distribution to the geographical boundaries of the European Union (as in <https://www.iucnredlist.org/regions/europe>). If you are working on Mediterranean assessments, you can select "Mediterranean" which will restrict your distribution to the Mediterranean Basin biodiversity hotspot (<https://www.iucnredlist.org/regions/mediterranean>).

## Page 1b. Create distribution from point records

In this step, the platform automatically downloads and filters occurrence records, and creates a point and a polygon range map from it (that will be available for download in the Zip files in Step 7). This polygon distribution will be kept on the platform for 15 to 30 days so you can reuse the distribution without needing to create it again.

### Step 1: Download occurrence records

Select the sources of your data between GBIF (Global Biodiversity Information Facility; [www.gbif.org](http://www.gbif.org); downloaded with the *occ\_data* function from the *rgbif* R package, Chamberlain et al. 2022), OBIS (Ocean Biodiversity Information System; [www.obis.org](http://www.obis.org);

downloaded with the *occurrence* function from the *robis* R package, Provoost and Bosch 2021), Red List point range map, or your own uploaded data.

For some species, records can be very numerous and slow down the analyses so we download samples of the data only (this is specified in the plot legend for dots colours as 'sample'). If the number of occurrence records in OBIS or Red List is above 2000, we keep the most recent 2,000 records and discard the others. If the number of georeferenced occurrence records in GBIF is above 2000 (measured with the *occ\_count* function from the *rgbif* R package), we download a sample geographically representative (using the map of GBIF records density available with the *map\_fetch* function from the *rgbif* package). This is notified on the plot produced in this first step by 'GBIF sample'. If the geographical extent of GBIF records is large (i.e., either latitude extent or longitude extent  $\geq 100$  degrees), we divide the extent in cells of 10x10 degrees; otherwise, we divide it in about 100 square cells. We then download data equally from the cells (taking all data for cells with fewer data than 2000 divided by the number of cells, and a sample in the other cells to reach a total of ca. 2000 data).

### Synonyms

If you add a species name here, and that selected sources include GBIF, OBIS and/or Red List, the platform will download and combine occurrence records from the species you are assessing as well as the entered synonyms. This is useful when the species you are assessing correspond to two different species in GBIF or OBIS taxonomies, or when you are reassessing a species that was first published in the Red List with another scientific name. If you want to include several synonyms, you can use semicolons (e.g., 'Parus ater;Periparus ater').

### Restrict to a country (for National Red List only)

For national and regional Red Listing, you can restrict species' distribution to a single country by selecting its name in the 'Country to crop' box. Make sure that the country you select is overlapping with the species' distribution. For European Red Listing, you can select 'Europe', which will restrict the distribution to the geographical boundaries of Europe, or 'EU27', which will restrict the distribution to the geographical boundaries of the European Union (as in <https://www.iucnredlist.org/regions/europe>). If you are working on Mediterranean assessments, you can select "Mediterranean" which will remove occurrence records outside the Mediterranean Basin biodiversity hotspot (<https://www.iucnredlist.org/regions/mediterranean>).

### Upload records

You can upload your own records using the box 'Upload records'. Click 'Choose' to select the csv file to upload (please use comma, semicolon, or tabulations as csv separator); it must include at least two columns including longitude coordinates (names can be 'longitude', 'Longitude', 'x', 'X', 'lon', 'Lon') and latitude coordinates (names can be 'latitude', 'Latitude', 'y', 'Y', 'lat', 'Lat'). Optionally, more columns can be included to inform the point range map shapefile (see the template provided in the 'Upload records' box). If there are more than 6,000 records, we will keep only the first 6,000 rows to ensure analyses go smoothly.

## Step 2: Filter occurrence records

You can filter the occurrence records with the different parameters detailed below.

### Edit points manually

Since version 1.2, point records can be edited manually by clicking on the button “Edits records manually”. You can then manually include or exclude individual records by clicking on an individual record and action the button “Make valid” / ”Make invalid”; the record will then change colour and be included or excluded from the valid records. You can also remove multiple records at once by drawing an area (with the rectangle or polygon drawing tools) and clicking on “Save from map”; all records within those polygons will be excluded. You can add records manually by selecting the marker drawing tool and clicking directly on the map; you can pre-fill some attributes (year and source) for those records. Finally, you can drag existing records if you know they are misplaced by clicking “Allow dragging” and then clicking on individual records to move them around. When you are done click on “Save from map” and continue with Step 3.

Note that in this interactive map we slightly displace records (jitter) that have strictly the same coordinates to enable you clicking them individually. When several records seem overlapping, you can then zoom in at maximum level to see them individually.

### Automated filter

An automated filter is by default applied to all records using the *CoordinateCleaner* R package (Zizka et al. 2019) but this can be unselected. This flags records with coordinates strictly equal to capitals coordinates, countries centroids coordinates, GBIF and other institutions coordinates, or with equal longitude and latitude.

### Year

All records made before this year will be flagged. By default, records with no information on the year of observation will not be flagged, but you can tick the 'remove missing data' to exclude them.

### Uncertainty

All records with localisation uncertainty higher than this value (in km) will be flagged. This is used to filter GBIF data that sometimes come with an uncertainty measure on records coordinates (i.e., measuring from how many kilometres the coordinates could be wrong). By default, records with no information on the coordinate uncertainty will not be flagged, but you can tick the 'remove missing data' to exclude them.

### Extent

All records outside this lon/lat extent will be flagged. This is for instance useful if you want to exclude a whole continent or region. You can use the interactive map that will appear after you clicked on 'Run Step 2' to find the values that correspond to what you need to exclude.

### Exclude Sea/Land records

If “Exclude sea” is selected, all records made at sea are removed (for purely terrestrial species). If “Exclude land” is selected, all records made at land are removed (for purely marine species). The map used to determine if points are at land or at sea is a simplified

version of the map of Red List countries v.2023.1:  
[https://github.com/victorcazalis/RedList\\_countries/releases/tag/v2023.1](https://github.com/victorcazalis/RedList_countries/releases/tag/v2023.1).

## Map

You can then visualise the records that were gathered in the interactive map in which you can zoom in and out. It displays if records are considered valid (yellow) or not (purple) depending on the filtering parameters. You can click on each record to visualise the source of the record (GBIF, OBIS, Red List, or your own data), the year of observation, the record id (which links to the url of the observation for GBIF and OBIS observations), and, if the observation is considered not valid, the reason why it was flagged ('Year' if the record was made before the minimal year you set; 'Coordinates\_uncertainty' if the record coordinates are more uncertain than you specified; 'Outside\_extent' if the record coordinates are outside of the extent you set; 'Sea' if the record was made in the domain you chose to exclude (sea or land); 'Equal\_LonLat' if the record strictly has equal longitude and latitude; 'Zero\_Coordinates' if the record was located at coordinates (0,0); 'Capitals' if the record is located at a country capital coordinates (which can result from mistakes when data was contributed); 'Country\_centroids' if the record is located at a country centroid coordinates; 'GBIF\_headquarters' if the record is located at GBIF headquarters coordinates; 'Institutions' if the record is located at biodiversity institution headquarter coordinates; "Presence\_456" if the presence code of the occurrence record is 4, 5, or 6).

## Step 3: Create polygon range map

Create a polygon range map from non-flagged records (it will be available for download in the Zip files in Step 7). Currently, the platform does not enable differentiating polygons with different presence / origin / seasonality coding and they are all assumed to be 1 (i.e., that the range is the extant, native, and resident range).

### Starting point

Choose what base method you will use to create the first polygon between the options below (see Fig. 1 in sRedList documentation). You can click on "Show examples" to get some examples of what different starting points will enable for your species (note that these examples do not include hydrobasins and any of the further options to buffer, crop, or merge your polygons).

1) Minimum Convex Polygon: will create the MCP around all records (see Fig. 1 in sRedList documentation).

2) Alpha hull: will calculate the alpha hull around points using the *convexHull* function from the *spatialEco* R package (Evans & Murphy, 2022; see Fig. 1 in sRedList documentation). This will connect points (note that we subsample points closer than 10m to avoid calculation problems) similarly to the MCP but enabling concave shapes where no occurrence points are found, and splitting the distribution in several polygons. Please specify a parameter [0-10] that will impact the tension of the polygon. A high parameter will provide an output very close to the MCP; conversely a small parameter will provide a shape with more concavity and can be split in several polygons (see Fig. 1 in sRedList documentation). There is no scientific recommendation on the choice of this parameter; you should choose the one that

best fit the distribution of the species as you know it. Note that we remove occurrence records that are very close to each others in order to avoid the function to crash, which can create minor discrepancies between occurrence records and polygons (to avoid this you can buffer your distribution by 10 or 100m). If you are an alpha hull expert, note that the parameter provided here differs from the alpha parameter *per se* as we scale it by the length of the diagonal of the geographic extent of the points (in meters) in order to have a reasonable range of values that work for species with different range sizes ( $\text{true\_alpha} = (0.5 * \text{alpha\_parameter})^2 * \text{length\_diagonal}$ ). The true unscaled alpha parameter is then displayed as a caption at the bottom of the plot.

3) Kernel: will calculate a Kernel around points (see Fig. 1 in sRedList documentation). This is mainly relevant for species with many occurrence records with relatively homogeneous density of occurrence points. It maps the probability for a species to be present at a certain location. Please specify the kernel probability parameter in the range ]0-1[, with a default fixed to 0.99. The closer to one is this parameter, the broader will be the range (i.e., including all occurrence points and more area around them); conversely a small parameter will map a distribution not including all points, only keeping regions with high occurrence densities. There is no scientific recommendation on the choice of this parameter; you should choose the one that best fit the distribution of the species as you know it. We use the *getverticeshr* function from the *adehabitatHR* R package (Calenge, 2006) after subsampling to keep only one record with a given set of coordinates.

4) Individual localities: will create a distribution consisting in a 1m circle around each occurrence record (see Fig. 1 in sRedList documentation). This is supposed to be combined with the buffer option to create circular buffers around each individual locality. This is mainly relevant for species with very few occurrence records (e.g., <5) and for which the true distribution is totally unknown.

5) Coast: will create a line of coast around occurrence records. First, we buffer the occurrence records by the distance set in the “Buffer (km)” parameter. Then, we extract the coast line that overlaps with this buffer. We then buffer that coast line by the “Buffer (km)” parameter, crop by land or by sea, and use the resulting polygon as the distribution map.

6) Hydrobasins: will select all hydrobasins (of level 8, 10, or 12 depending on your choice) in which records have been made; the hydrobasins map used is the map made available by the Red List (version 2023\_08; see Fig. 1 in sRedList documentation). Level 8 is the most recommended in general, and the platform thus allows mapping level 10 or 12 only for species with small distributions. If you select ‘within MCP’, the platform will select all hydrobasins of level 8 within the Minimum Convex Polygon of the species (see Fig. 1 in sRedList documentation). Hydrobasins in the MCP but with no occurrence records will be marked with a Presence code of “Possibly Extant”. This is only recommended for freshwater species.

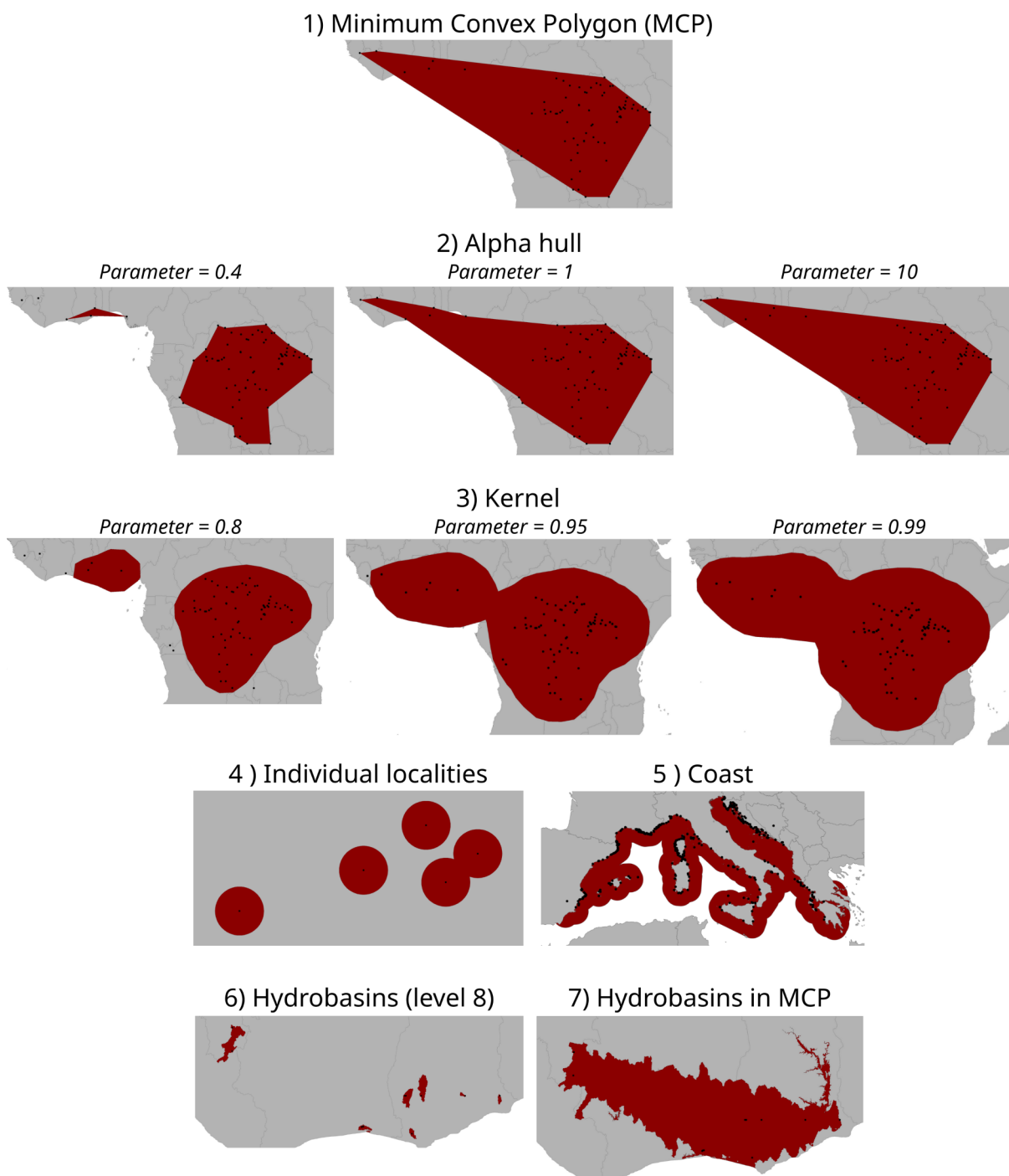


Fig. 1: Example of starting point to map species distribution in a polygon using the different options available on the sRedList platform (with 3 example values of the parameters for Alpha, and Kernel). For graphical purpose, the same data were used for options 1, 2, and 3, but different ones for 4, 5, 6, and 7.

### Buffer

Enter a number (in kilometres) if you want the range map of the species to be buffered (e.g., if you consider that records are not representing the whole range).

### Crop by land / sea

Select 'Keep only land' to crop the range map to land (ie excluding sea from the range). Select 'Keep only sea' to crop the range map to sea (i.e., excluding land from the range). The map used to crop land or sea is a simplified version of the map of Red List countries v.2023.1: [https://github.com/victorcazalis/RedList\\_countries/releases/tag/v2023.1](https://github.com/victorcazalis/RedList_countries/releases/tag/v2023.1). Note that this step can take some time for large-ranged species, so we advise to use it only if polygons include area to remove (e.g., do not select 'land' if the range created so far does not include any sea, the result will be the same).

### Crop by altitude

Enter minimum and maximum values to crop range by altitude. The elevation raster used in the step is the GLOBE data (National Geophysical Data Center, 1999) that we reprojected in Mollweide at the CCI resolution to fasten analyses. Note that this step can take some time for large-ranged species, so we advise entering values here only if you want to exclude significant part of the range (e.g., a mountain peak in the middle of the range where the species does not occur).

### *Extract elevation from occurrences*

You can visualise here at which elevation the species was observed (using valid observations after the filtering step). Note that this plot is highly sensitive to sampling bias (e.g., if a species has been observed 10 times at low elevation and only once at higher elevation, it may be because lower elevations are more sampled rather than because the species prefers them).

### Merge with published map

If ticked, this will merge the polygon you created from occurrence records with the range map published in the last assessment of the species. This will only work if a range map has been published and if it is stored in the platform (check 'Distributions' tab on the left menu bar). Only polygons with presence code 1-2 (i.e., 'extant' or 'probably extant'), of origin code 1-2 (i.e., 'native' or 'reintroduced'), and of seasonal code 1-2 ('resident' or 'breeding season') are considered in this step and are merged; consequently the distribution shapefile that you will get in the ZIP output will have lost some of the information from your uploaded shapefile, you might need to merge these shapefiles manually.

## Step 4: Smooth polygon range map

The range map can be smoothed to have less sharp angles and make the polygon look better and closer to a range map (see Fig. 2 in sRedList documentation), using the *smooth* function from the *smoothr* package (Strimas-Mackey, 2023) using the *ksmooth* function with the parameter you selected (0 means no smoothing). If you chose to crop by land or sea in the previous step, this will be applied again after smoothing the polygon. If this function returns an error, set the smoothing parameter to 0.

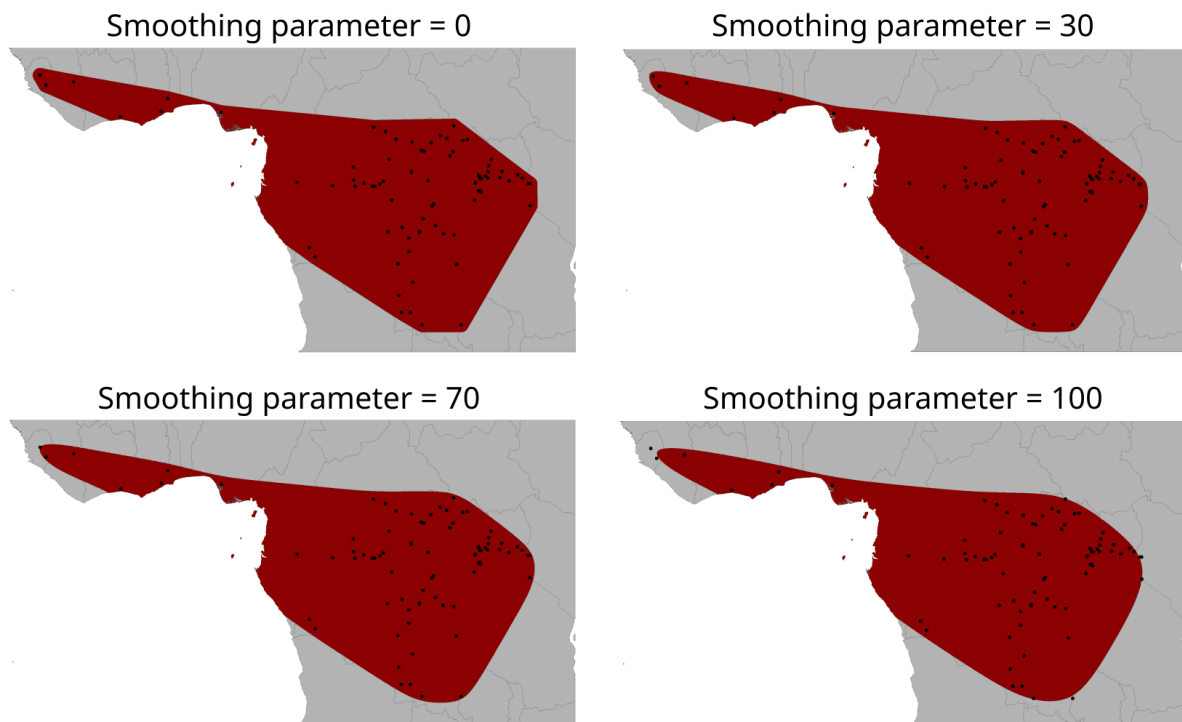


Fig. 2: Effect of smoothing on the shape of the polygon range map created in the sRedList platform (step 4) with four different smoothing parameters.

## 2. Extract countries of occurrence

Automatically extracts the countries overlapping with species' distribution, as well as realms. You can check the list of realms and countries of occurrence by clicking on the small list icon on the left of the map and they will be outputted as a csv file that you can download page 7 and upload directly in SIS. You can skip this step by clicking “Next” without running the countries of occurrence analysis.

This includes all countries that intersect with the distribution, regardless of the proportion of overlap and of the presence / origin / season parameters of the distribution. You can explore the selection of countries of occurrence with the interactive map but so far you can not modify anything here, you will have to edit this later in SIS. Subnational entities noted as 'Absent from subnational' correspond to subnational entities from which the species is absent but belonging to countries from which the species is present. If you created a range map from occurrence records (Step 1b), we differentiate entities that overlap with the distribution range map and with occurrence records (in regular font in the list of countries of occurrence and “Extant” in the SIS output) and those that overlap with the distribution range map but not with occurrence records (in italics in the list of countries of occurrence and “Possibly Extant” in the SIS output).



For terrestrial and freshwater species, we used a map of countries fitting the Red List list of countries (levels 0 and 1), available at [https://github.com/victorcazalis/RedList\\_countries/releases/tag/v2023.1](https://github.com/victorcazalis/RedList_countries/releases/tag/v2023.1) (note that some subnational entities are absent from the scheme used in SIS [Arica y Parinacota (Chile), Nuble (Chile), Los Rios (Chile), Telangana (India)] and will be marked as “Absent\_SIS” and won’t be exported in the output, only the country will be exported). For marine species, we used a map of EEZs fitting the Red List list of countries (level 0 and some level 1), available at [https://github.com/victorcazalis/RedList\\_EEZs/releases/tag/v\\_2023.1](https://github.com/victorcazalis/RedList_EEZs/releases/tag/v_2023.1). Note that shape of countries in this map are greatly simplified to fasten the process. The designation of geographical entities on The IUCN Red List do not imply the expression of, or represent, any opinion by sRedList, IUCN, the Species Survival Commission, or its Partners concerning the legal status of any country, territory or area, or concerning the delimitation of its frontiers or boundaries.

Realms are extracted from a global map of realms similar to the one displayed on SIS, available at: [https://github.com/victorcazalis/RedList\\_realms/releases/tag/v2023.1](https://github.com/victorcazalis/RedList_realms/releases/tag/v2023.1). Note that this map is coarser than the Olson et al. (2001) map so there can be mistakes close to the edge of realms. Realms will be reported in assessments.csv in the final ZIP file.

### Select species systems

Select species systems to report in SIS. This can be any combination of terrestrial, freshwater (i.e., inland waters) and marine.

### Edit COO manually

Since version 1.2, you can edit the list of countries of occurrence manually. Click on “Edit COO manually” above the leaflet table. You can then make a country or subnational entity occupied or empty by clicking on the respective button (either on the map or in the table). You can also edit presence, origin, and seasonal attributes in the table by double-clicking on a attribute (countries of occurrence are then coloured by attributes). When you are done, don’t forget to click on “Save changes” and the map and table will update.

## 3. EOO analysis

Calculates the extent of occurrence, measured as the Minimum Convex Polygon around species' distribution. This can be used to inform criterion B1. When the calculated EOO is very small ( $<4\text{km}^2$ ), the platform outputs an EOO of  $4\text{km}^2$ ; this is because AOO cannot be smaller than  $4\text{km}^2$  and EOO should not be lower than AOO (IUCN Standards and Petitions Committee, 2022). You can click on “Interactive map” to explore that map in more details.

According to the Red List categories and criteria (IUCN, 2012), 'extent of occurrence is defined as the area contained within the shortest continuous imaginary boundary which can be drawn to encompass all the known, inferred or projected sites of present occurrence of a taxon, excluding cases of vagrancy.' Make sure that the polygon you are using is compliant with the Red List guidelines in terms of presence, seasonality, and origin.

## 4. AOH analysis

Calculates the terrestrial Area of Habitat of a species, which can be used as an upper bound for area of occupancy for criterion A2 (Brooks et al., 2019), and population size (Area of Habitat multiplied by density; used in criteria C and D), using the approach developed in Santini et al. (2019).

### Habitat preferences

Select habitat suitable to the species. If available, the habitat preferences of the last published assessment are charged. You can select habitats that are marginal or of unknown suitability (we call them both 'Marginal\_Unknown' in the platform); if you do so, the platform will calculate Area of Habitat with and without these marginal habitats to provide a range of estimates. For now, this calculation does not allow to use different habitat preferences per season / origin / presence.

### Extract habitat preferences from occurrences

If the distribution was built from occurrence records, and the species is terrestrial, you can visualise here in which habitats the species was observed. We extract habitats from Jung et al. (2020) who created a global map of terrestrial habitats using the Red List habitat classification (you can check the raw map here: <https://uploads.users.earthengine.app/view/habitat-types-map>). We display the proportion of occurrence in each habitats. Note that this plot is highly sensitive to sampling bias (e.g., if a species has been observed 10 times in urban area and only once in temperate shrublands, it may be because urban areas are more sampled rather than because the species prefers urban areas over shrublands). Also note that for old records, habitat may have changed between the observation and the creation of the habitat map (which is based on recent data), perhaps biasing the results towards artificial habitats.

### Elevation preferences

Select species elevation preferences of the species (all area outside of these limits will be considered unsuitable). If available, the elevation preferences of the last published assessment are charged; otherwise we calculate and display the minimum and maximum elevation existing in the range from the GLOBE elevation raster (National Geophysical Data Center, 1999). You can provide a range of possible elevation limits by separating both values by a hyphen (e.g., '800-1000') for the analyses on the sRedList platform but not that only the most extreme values will be exported to allfields.csv since SIS Connect does not allow uncertainty in elevation limits.

### Density

Select the average density of the species, which will be used to calculate population size, which should be the average density of mature individuals within the habitat suitable to the species (in individuals per km<sup>2</sup>). You can also use the density calculator to calculate it from the average density of individuals within occupied habitat (i.e., also including non mature individuals), the percentage of mature individuals, and the percentage of suitable habitat that

is occupied. For instance, if a forest-specialist species occupies 50% of the forest within its range, has 75% of mature individuals, and local estimates within occupied habitat reported an average density of 300 individuals per km<sup>2</sup>, you could enter  $300 / 75 / 50$  in the density calculator or directly enter 112.5 in the manual field.

For birds and mammals, we provide a default density of individuals within occupied habitat the estimates from Santini et al. (2022) for mammals and Santini et al. (Under review) for birds. Note that these estimates often come with great uncertainty (see more in the corresponding papers); they are just meant to be used as a guide if you do not have better data.

All values can be provided as a range by separating two values with a hyphen (e.g., '1.2-5.1') and are assumed constant across the species Area of Habitat.

According to the Red List categories and criteria (IUCN, 2012), 'The number of mature individuals is the number of individuals known, estimated or inferred to be capable of reproduction.'

#### Area of occupancy based on known occurrence records

If the distribution was created from occurrence records (Step 1b), we calculate the area of occupancy based on occurrence records by calculating the area of 2x2km pixels that include known occurrence records. Note that if your species has a large range, you might not see the grid cells (plotted in green) because 2km is very small on the map, but you can still see the estimated value below the plots. You can click on “Interactive map” to explore that map in more details.

This estimate gives a lower bound estimate of area of occupancy (i.e., the area of occupancy if you assume that all sites where the species is present are represented in your occurrence sample; note that the platform downloads only a sample of GBIF records when there are more than 2000 records, which might underestimate known area of occupancy). If you consider that the species is more widespread than your occurrence sample suggest, you can use the upper bound of area of occupancy (next plot) to visualise where suitable habitat is present, the true area of occupancy is likely between those two estimates.

#### Area of occupancy based on suitable habitat

##### AOH Calculation

Terrestrial Area of Habitat (AOH) is generally calculated as the area within the range of a species that is covered by suitable habitat and within suitable elevation limits. For habitat, we use the ESA-CCI land cover maps of 1992-2020 (ESA, 2022) which you can visualise here <https://maps.elie.ucl.ac.be/CCI/viewer/> and the crosswalk from Lumbierres et al. (2022) but restricting rocky habitats (IUCN habitat code 6) to bare areas (ESA-CCI codes 200-202). For elevation, we use the GLOBE raster (National Geophysical Data Center, 1999). Both were previously projected in Mollweide projection using the resolution of the ESA-CCI layer to fasten analyses.

For species with small range sizes (i.e., the polygon range size used in the analyses is smaller than 10,000 km<sup>2</sup>), we calculate AOH using the 'aoh' package (Hanson, 2022). For species with large range, in order to provide faster calculations, we use pre-processed aggregates of our land-cover and elevation rasters (a cell of the aggregated rasters correspond to an aggregate of 30x30 cells of the ESA-CCI raster; ~10x10km). You can click on “Interactive map” to explore that map in more details.

In case Marginal\_Unknown habitat preferences are provided, or extreme elevation limits, two AOH (and rescaled) are calculated: minimum AOH excluding Marginal\_Unknown habitat preferences and using the strictest elevation preference limits, and maximum AOH including Marginal\_Unknown habitat preferences and using the broadest elevation preference limits. It can happen that both estimates are equal if the selected Marginal\_Unknown habitat / extreme elevation are not present in the range or if the selected Marginal\_Unknown habitat overlaps in the habitat crosswalk with other habitat types in habitat preferences (e.g., if habitat 1.1 is already listed in habitat preferences, adding habitat 1.2 will not lead to any change since they correspond to the same ESA-CCI classes according to Lumbierres et al. (2022)'s crosswalk).

#### AOH at 2x2km resolution

We then rescale AOH map at a 2x2km scale in order to get an upper bound of area of occupancy (Brooks et al., 2019; IUCN Standards and Petitions Committee, 2022) which can be used to inform criterion B2. It is crucial to consider this as an upper bound of area of occupancy as it only considers broad habitat suitability (e.g., ecological or human-induced filters that do not translate in habitat transformation are not considered). Note that for species with large range, this might be slightly overestimated because of the use of 10x10km aggregated rasters (if a 10x10km cell includes some suitable habitat, we consider every of the overlapping 2x2km cells to have suitable habitats).

According to the Red List categories and criteria (IUCN, 2012), 'area of occupancy is defined as the area within its 'extent of occurrence' which is occupied by a taxon, excluding cases of vagrancy.'

#### Population size calculation

Population size is calculated by multiplying the Area of Habitat by population density. If density was provided with uncertainty, we calculate a low estimate (using the low density estimate and the minimum AOH if two AOH are calculated) and a high estimate (using the high density estimate and the maximum AOH if two AOH are calculated). In most cases, this should be used with the data qualifier “Inferred”.

## 5. AOH trends

Calculates trends in Area of Habitat between the most recent year of land-cover data and 10 years / 3 generations before, using the same method as explained above. This can be used to inform criterion A2 (as an inferred trend in area of occupancy). This is not of sufficient quality to justify the use of criterion C1, unless you can justify why this decline in AOH results in a similar decline in population size. This might also inform 'continuing decline

habitat quality / area / extent' under criterion B. You can click on “Interactive map” to explore that map in more details.

### Generation length

Select the generation length of the species (in years), to calculate trends. If no value is entered here, a generation length of 1 year will be assumed. If available, the generation length of the last published assessment is charged (or from Pacifici et al. 2013 for mammal species that do not have generation length data in SIS). This field does not support range of possible values so far, only one value should be provided. If you are unsure about the generation length, you will thus have to calculate it twice with two different values and see how different the trends in AOH results are.

According to the Red List categories and criteria (IUCN, 2012), 'generation length is the average age of parents of the current cohort (i.e. newborn individuals in the population). Generation length therefore reflects the turnover rate of breeding individuals in a population. Generation length is greater than the age at first breeding and less than the age of the oldest breeding individual, except in taxa that breed only once. Where generation length varies under threat, the more natural, i.e. pre-disturbance, generation length should be used.'

### Extrapolation

If 3 generations ago was before 1992, we do not have the land-cover data to map past AOH. In this case, we used the raster from 1992 to calculate the trends over the last 3 decades and extrapolate assuming an exponential relationship:  $Trends\_extrap = 1 - (1 - Trends\_period)^{((1992-Year1) / (2020-1992))}$ . Where *Trends\_period* is the estimated trends between 1992 and 2020 and *Trends\_extrap* is the extrapolated trends estimate for the period *Year1-2020*.

## 6. Fragmentation

Calculates the fragmentation of suitable habitat following the Red List guidelines, using the method developed in Santini et al. (2019). You should use the results of this analysis only if you consider that the clusters mapped on the left plot make ecological sense as 'subpopulations'.

The fragmentation is calculated based on the Area of Habitat calculated in Step 4 (see Fig. 3 in the sRedList documentation). In case a minimum and a maximum Area of Habitat have been calculated, we use the minimum one. For species with large ranges (as defined in the AOH step), the Area of Habitat map created in Step 4 is not binary (each cell has a value of proportion of suitable habitat); we binarized Area of Habitat considering that each 10x10km cell with at least 10% of suitable habitat was a suitable cell.

We then identified each patch of suitable habitat that was distant by at least a dispersal distance from any other patch of suitable habitat. We calculated the number of individuals in each patch (subpopulations size) by multiplying the area of each patch of suitable habitat by the population density and considered the patch unoccupied if this subpopulation was below 2 individuals.

We then calculate the proportion of the population that is found in small and isolated subpopulations depending on what is considered a small subpopulation. We report this in the plot provided at the end of the fragmentation calculation (see Fig. 3 in the sRedList documentation). The dashed lines on the plot indicate the size of subpopulation for which half of the population lives in subpopulation smaller than this; if you consider this size of subpopulation as small (as defined in the guidelines), you can consider the population as severely fragmented. Note that severe fragmentation is not ticked by default on the Summary step, so if you consider the population as such you have to manually tick and add the justification.

Using the subpopulation sizes calculated in that step, we also calculate the maximum number of mature individuals in a subpopulation (used in criterion C2a(i)) and the % of mature individuals in one subpopulation (used in criterion C2a(ii)). These should only be used if you consider that each cluster mapped on the plot above indeed correspond to subpopulations.

According to the Red List categories and criteria (IUCN, 2012), ‘the phrase ‘severely fragmented’ refers to the situation in which increased extinction risk to the taxon results from the fact that most of its individuals are found in small and relatively isolated subpopulations (in certain circumstances this may be inferred from habitat information). These small subpopulations may go extinct, with a reduced probability of recolonization.’

#### Density

See ‘Density’ paragraph in section ‘4. AOH analysis’.

#### Isolation distance

Enter here the isolation distance of the species (in km), i.e., the distance above which patches of suitable habitat should be considered isolated and hosting isolated subpopulations. You can include uncertainty by separating two estimates with a hyphen (e.g., ‘10-50’ if you are unsure whether the isolation distance is 10 or 50km)). Note that dispersal barriers (e.g., water, mountains, human infrastructures) are not taken into account in this fragmentation calculation.

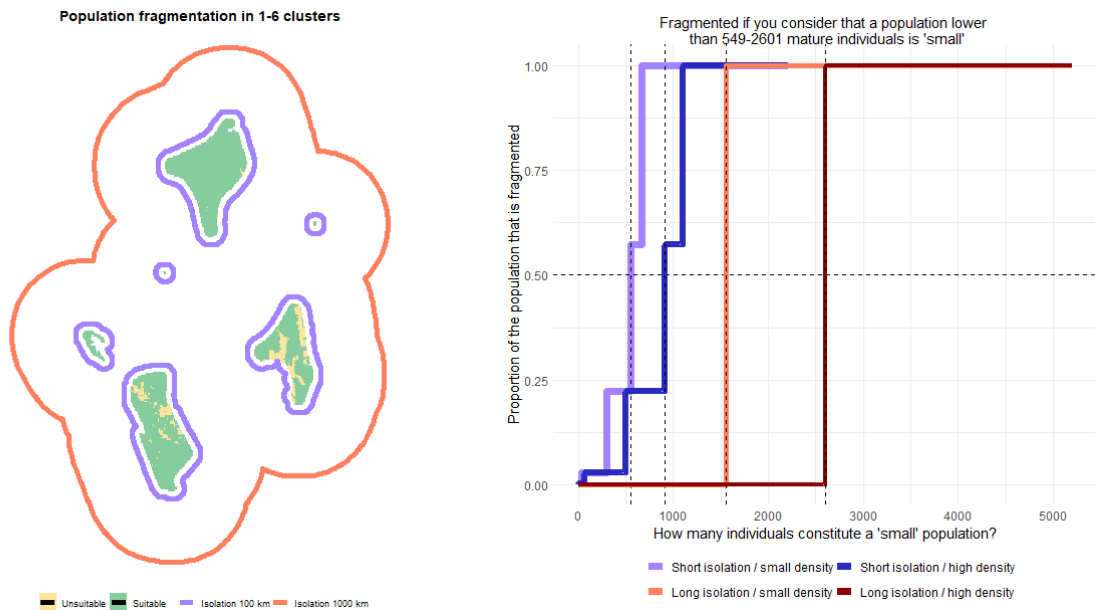


Fig. 3: Example result from the fragmentation analysis when both density and isolation estimates are provided with uncertainty (density is 0.3-0.5 and isolation distance 100-1000km). The left plot shows that if subpopulations are considered isolated from 100km there are 6 isolated subpopulations; if they are considered isolated > 1000km there are no isolated subpopulations. The right plot shows that if you consider isolation distance of 100km and a density of 0.3 (light blue line), you can consider the population severely fragmented if you consider that a subpopulation of 549 individuals is small (see plot title); the dark blue represents results with short isolation distance and high density, the light red with long isolation distance and small density, and the dark red with long isolation distance and high density.

## 7. Trends in Remote Sensing products

The platform enables mapping and calculating current value and trends in some remote-sensed products in species range. For each of them, the platform will return absolute trends (current-former values) and relative trends ((current-former)/former values). You can click on 'Interactive map' to explore maps in more details.

### Forest cover

We use the Global Forest Change maps (Hansen et al., 2013) version 1.9 that we pre-processed to enable fast calculation of forest cover and forest loss since 2000, using a resolution of 0.05 degrees (ca. 6km at equator). To calculate forest cover in 2000, we calculated for each 0.05 degree cell the number of pixels from the original raster with a forest cover > 25%. To calculate forest cover in following years, we calculated the number of pixels from the original raster that had a forest cover > 25% in 2000 and did not loose forest cover since. If you need more details (e.g., very restricted species), you can check the original data here: <https://earthenginepartners.appspot.com/science-2013-global-forest>.

We calculate trends in forest cover over a 10 years / 3 generation time period using the generation length provided in Trends in AOH (note that you need to actually calculate trends in AOH if you want the platform to use the generation length value). If no generation length was provided or if the generation length is < 3.3 years, the platform calculates trends between

2012 and 2022, otherwise it calculates over a 3 generation time period (with a limit to 2000 as the data we used are not available before 2000).

#### Human modification index

We use the Global Human Modification maps created by Theobald et al. (2020) version1\_4 for the years 1990 and 2015. This index combines 14 stressors (urban and built-up, cropland and pasture-lands, grazing intensity, oil and gas production, mining and quarrying, power generation, roads, railways, power lines, electrical infrastructure, logging and wood harvesting, human intrusion [a combination of human accessibility and human density], reservoirs, air pollution) into a single value that is comparable across years. We aggregated the rasters to a resolution of ca. 4km at the equator to enable fast calculations. This does not provide any information directly applicable to the Red List but gives you additional information on the regional context.

#### Human density

We use the Global Human Settlement dataset (Florczyk et al., 2019) v.4.11 at 2.5 arc-minute resolution. We calculate the 'current' value from the 2020 map and the 'former' value from either the 2000, 2005, or 2010, whichever is the closest from 3 generations / 10 years before 2020. This does not provide any information directly applicable to the Red List but gives you additional information on the regional context.

## 8. Assign Red List Category

#### Species taxonomy

The species taxonomy should be specified here if you want to be able to upload this file through SIS Connect. If the species, or another species with the same genus name, is already published in the Red List, the platform displays automatically the one from last published assessment. Otherwise, we try to retrieve it in the GBIF taxonomy database using the *taxize* R package (Chamberlain et al., 2020).

#### sRedList calculated parameters

Parameters calculated in the platform are automatically reported here. You can use the fields to edit the values and justifications that you want to export to SIS (e.g., complete justification, add uncertainty boundaries...) or delete any value you do not want to be passed on to SIS. You can also complete some information (e.g., qualification of trends).

#### Other parameters

You can also fill in other parameters that are used to apply Red List criteria. If you do, these will be used to calculate the category triggered and will be exported in the ZIP file. If you do not, these fields will remain empty.

#### Apply Red List criteria

Based on the parameters filled in the previous fields, the platform calculates the category triggered by the species. The category (or range of categories) is reported for each criterion on the figure, with a colour intensity that depends on subcriteria (full colour if subcriteria are met; light colour if the quantitative threshold is met but not subcriteria). The highest triggered



category (including subcriteria) is reported in the plot title. Note that this plot will never suggest a species a Data Deficient, this is left to your judgement and will be better covered by the Criteria Calculator from SIS.

If the plot includes the warning “The taxonomy information is incomplete, this will cause issue if you want to push the output ZIP file to SIS Connect.” it means that you did not complete all taxonomy fields (on the top of the Summary page). This will likely prevent you from uploading your species to SIS Connect. If the plot includes the warning “Some of the entered taxonomy does not correspond to any of the published species. Make sure it fits with the Red List taxonomic backbone before pushing to SIS Connect.” it means that the taxonomy information is complete but that some of the taxonomy information you provided does not correspond to any of the published taxon. This can indicate 1) that there is a spelling mistake or a mismatch with the Red List taxonomy, in which case you should edit the taxonomy to ensure consistency with the Red List, or 2) that this taxon is not yet covered by the Red List, in which case you can ignore the warning.

*Note: If a mismatch appears between the category we display here and the category displayed by SIS Criteria Calculator, you should trust SIS and report this mismatch to [sredlist@conservara.fr](mailto:sredlist@conservara.fr).*

#### Download ZIP

You can download the zip file that summarises your assessment. This includes different files that can be directly exported to SIS Connect: allfields.csv includes assessment parameters, assessments.csv includes the systems, realms and current trends information, countries.csv includes a list of countries of occurrence, habitats.csv includes a list of habitat preferences, references.csv includes a list of references used for the assessment (including sources of occurrences points downloaded from GBIF and OBIS), taxonomy.csv includes the taxonomy of your species. You can then edit these files before exporting them to SIS (e.g., filling the presence / origin / seasonal parameters of COO and habitat preferences) or do so directly in SIS. If a distribution has been created, the ZIP file will also include the polygon range map (as a shapefile), the point range map (occurrences that were not filtered out from the analyses, as a csv file) and, if you used hydrobasins to create the range map, a list of hydrobasins.

You will also find a file called ‘sRedList\_report\_SPECIES\_NAME.html’ which reports all the choices made during your use of the platform and all the plots that have been created (which you can use to remember what has been done on the platform, but also to communicate with other assessors and reviewers) and '00.Output\_log.csv' which includes the parameters used in the platform. This does not need to be exported to SIS.

### From sRedList to SIS

There are two main ways to use sRedList results in the platform: manually copy-pasting information directly in SIS or using SIS Connect to push automatically information to SIS.

### Manually adding information in SIS

After completing the process on sRedList, you can go to your assessment draft on SIS as you normally do, and manually add the information from the platform that you find useful. We advise you to open the sRedList\_report.html file, where you can find all the results from the platform, and copy-paste the fields that you want to include in SIS. In that case, please don't forget to manually include the citation to the sRedList platform in the references (under the References function search on Author = sRedList and the current year, then select the appropriate reference from the list)!

### Uploading information to SIS through SIS Connect

In order to use the SIS Connect option, you need special permission from the Red List Unit to upload working sets. If you are wanting to use the same login details that you use for SIS, please send an email to [craig.hilton-taylor@iucn.org](mailto:craig.hilton-taylor@iucn.org) requesting permission to upload assessments in SIS Connect. You can use the following template:

Dear Craig,

As a user of the sRedList platform and assessor of [Taxa you are assessing], I am requesting access to SIS Connect Upload function in order to push sRedList results directly to SIS.

Thank you in advance for your help! All the best,

[Your name]

Note that uploads to SIS Connect need to be manually checked and validated by the Red List Unit. This means there will be a delay between your upload and their import into SIS. If you cannot wait, we advise you to add information to SIS manually.

### Uploading first assessments

In case of first assessments, you should first complete all the assessments you want to push to SIS Connect. You can then use the Merge ZIP function from the platform to create a single ZIP file that will include all your assessments. You can then upload this single ZIP file to SIS Connect. After uploading your zip file, the system runs a series of validation checks (it can take a while depending on the size of the file and how busy the system is), refresh your screen periodically to see if the validation is completed or you can wait to receive an email confirming that the validation is complete and your working set is uploaded.

### Uploading reassessments

In case of reassessments, using SIS Connect is feasible but trickier (so we advise manually adding information to SIS in most cases). After uploading your zip file, the system runs a series of validation checks (it can take a while depending on the size of the file and how busy the system is), refresh your screen periodically to see if the validation is completed or you can wait to receive an email confirming that the validation is complete and your working set is uploaded.

Once the validation is complete, open the working set by clicking on the name, that will take you to a screen which shows all the individual csv files that were uploaded. At the bottom of the list on the left is a 'Comments' option, please open that and use the comments box to add additional instructions to the Red List Unit about whether you want the data imported into SIS as a Partial Update (recommended for most cases) (see further details here: [https://connect.iucnredlist.org/partial\\_update\\_instructions](https://connect.iucnredlist.org/partial_update_instructions)) or if you want to Replace the existing draft assessment (only to be used if you do not want anything from the previous assessment, but bear in mind the rules about reassessments needing to build off the most recent published assessment)). Please also include this instruction in the name of your zip file (e.g., "PartialUpdate\_sRedList\_Apus\_apus.zip"). In the case of Partial Updates, we do not advise the use of the Merge ZIP function, meaning that sRedList outputs should be uploaded to SIS Connect species by species. Don't forget to click 'Add Comment' to post your comment.

After posting any instructions in the Comments box, click on the 'Working Sets' function at the top of the screen, this takes you out of the working set back to the list of Working Sets. The status of your Working Set might be a red warning saying 'validation failed' don't worry about that message, click on the Actions option on the right of your working set and from the drop down list select "Submit to Red List Unit". The status of your working set will then change to "RedList Check". That action sends an email to the Red List Unit informing them that you have uploaded a working set for checking and import into SIS. Whoever deals with this in the Red List Unit will get back to you if they have any questions or if there are any issues they discover. They may also give you feedback via the Comments option in the Working Set (the system should email the comments to you). They will also confirm if the import is successful, at which stage the status of your working set will change to "SIS Import Passed" with a green tick next to it.

### Merge ZIP files

You can upload different .zip files that were exported from the sRedList platform at the end of an assessment (e.g., if you prepared the assessment of 10 different species on the platform). The platform will create a single zip file combining all .csv and .shp files from the individual zip files (e.g., creating a single habitats.csv file including habitat preferences of all species assessed). This will enable to upload the data in SIS Connect in one single step. The total size of your input files cannot be above 100MB; if so, you might remove reports from the ZIP files (and perhaps shapefile distributions) to make them lighter.

## DD prioritizer: prioritise the reassessment of DD species

### Scientific basis of the Data Deficient prioritizer

This is the result of a [paper we published in Conservation Biology in 2023](#). The goal is to help you identify which species were Data Deficient in their last assessment but could most likely be assessed in another category if you reassess them today. We have applied this method to odonates, amphibians, reptiles and mammals. We prioritise species based on 3 different indices:

- pDS: this is how likely we estimate the species could be reassessed in a non-DD category. It will be high for instance, for a species with many GBIF records, that lives in an area with few other DD species, and that has a relatively large range size.
- dpDS: this is how much the probability pDS increased since last assessment. It will be high for instance, for a species that gained many GBIF records, or for which many scientific articles have been published since last assessment.
- dAOH: this is how much habitat was lost in the last 10 years / 3 generations. If it's below - 20%, it means you can probably reassess the species in a threatened or NT category based on this information.

We merged these different indices in a global priority index called PrioDS: we suggest species with highest PrioDS should be the first to be reassessed.

### How to use the Data Deficient prioritizer:

You can access the Data Deficient prioritizer directly from the sRedList platform clicking on "DD prioritizer" in the menu on the left of the platform. First you have to select a group among mammals, amphibians, reptiles, and odonates. Then you will see a space cut in 3 parts: top left is a scatterplot to visualise priority species, bottom is a table to filter species and explore priority species, to right is a place to visualise more information on single species.

### Scatterplot

On the left you can see a scatterplot where each point represents a species of the group you selected with the 3 indices I was talking about: pDS (the probability to be reassessed in a different category than DD) in x-axis, dpDS (the increase in this probability since last assessment) in y-axis, and if the species lost >20% of its area of habitat with the dark points. In other words, species far on the right are considered more likely to be reassessed in a non-DD category. Species high on the plot are considered to have gained probability to be reassessed in a non-DD category since last assessment. Species in dark losts >20% of their habitat and we suggest it might thus be classified as threatened or NT.

On the plot you can see species names and priorities by positioning your mouse on the point, you can zoom in and out and also isolate a certain priority category by clicking on the legend. Finally you can select species you want to include in the table, by default all species are in the table but you can select on the plot with these tools and the table will only include the selected subset.

#### Table

In this table, you can find the scientific name of the species, its family, realm, the year of last assessment, the different metrics we calculated, the number of GBIF records (in 2023, at the time of the last assessment, and a score telling you the increase), same for the number of articles published in the Web of Science mentioning that species. For each of these columns you can subset the table. For mammals and reptiles you can also select by Red List Authority. You can then order the table by the column you are interested in; for instance, if you want to prioritize species that gained most GBIF records since last assessment you can order by this column. Note that you can also select species rows to see them appear on the scatterplot.

#### More information

While exploring the table, you might want to know more on the occurrence records or the articles that were gathered on a particular species. You can then click on the “More” button and some information will appear on the top right panel of the app. This section will include a sentence explaining if and why we think this species is a reassessment priority. Then a list of the articles we found in the Web of Science where you can click on the link (note that google scholar will likely have more references). Then a map of occurrence records we found in GBIF where you can see records that were made after the last assessment in red. Note that there may be new records since we published the paper, they will appear on the map but are not counted in the table). If available, we also display the range map from the last published assessment. For species that lost >20% of their area of habitat in the last 10 years / 3 generations, you will be able to visualise it on the map (note that we reduced the resolution of these maps in case of large range, for computing reasons). Sometimes you will see that the high number of records we found are actually due to a mismatch of names between the Red List and GBIF and that some of the records are not of your species of interest.

#### Create your list

With the 3 panels detailed above you can then explore what we suggest are reassessment priorities and make your opinion on which species you want to assess in priority. When you know that, you can start clicking on these “Plus” buttons. For instance, I want to record that species, then this one, this one, this one, and this one. You can then create your own reassessment priority list. When you are done, you can click on this button to download your list which will include the information for each species, ordered as you prioritised them.

Don't forget that if you have some questions you can write a message on the sRedList forum and we'll be there to answer your question and help you! We would also love to hear if this app helped you prioritise reassessments, so please take some time to write us!

## Version information

### V 1.0 (also named v2023.3)

This was the first public version of the platform, released on the 24<sup>th</sup> of October 2023.

### v 1.1

This version was released in December 2023. The changes since v1.0 were:

- The Red List data (list of assessed species, point distribution, range distribution) were updated following the Red List update 2023-1
- The way to crop distribution for National Red Listing was changed. In v1.0 this option was included in Step 2 (Countries of occurrence) and countries had to be written manually. This has now been moved to step 1a and 1b and countries are listed in a dropdown menu. This dropdown menu now also includes “Mediterranean” for regional assessments.
- To help you select the “Starting Point” parameter in Step 1b-3 to draw polygon distribution maps, the platform now offers a “Show examples” button that will display a few example distributions that can be drawn from your occurrence records depending on the Starting point you select.

### v 1.2

This version was released in April 2024. The changes since v1.1 were:

- The DD prioritiser app was added
- An option to edit manually occurrence records and to edit manually countries of occurrence was added
- A mapping option was added in Step 1b-3 for coastal species
- The structure of the platform was slightly modified by changing step 6a (fragmentation) and 6b (trends in remote-sensed products) to two independent steps. In addition, users can now navigate between steps by clicking on the step summary on top of the assessment page.

## Errors table

Occasionally, the platform will return you error messages when it cannot complete the task requested. This table is here to help you understand why this is not working and what could you possibly do about it. If you encounter errors that are not in this table, please get in touch with us ([sredlist@conservara.fr](mailto:sredlist@conservara.fr)) so that we can fix it.

Step	Error message	Meaning	What to do
Any	The distribution must be completed in Step 1 to access this step!	You accessed the page for a step 2-8 before completing step 1 but none of these steps can be completed without a valid distribution.	Run step 1 (either using a polygon distribution or creating one from occurrence records) and come back to that page only after step 1 is completed.
Any	The session was inactive for more than 60 minutes so all files have been deleted... We are sorry but you have to start again from the beginning	If a session was inactive for >60 minutes, the platform deletes everything that was created on your session.	You have to start again and avoid long breaks during your time on the platform.
0	The Red List API is not working, sorry!", subtitle="We cannot provide the usual information on this page, but you can click Next.	We cannot access Red List API information at the moment to extract details from previous published assessment. We are waiting for the Red List Unit to fix the API access.	You can click Next and continue with your assessment with no further consequences as this step was just to display some information on past assessments.
0	Species name must be binomial	The species name you entered is not valid because it is not binomial (composed only of a genus name and a species name separated by an empty space).	You can change the species name entered and not use genus or subspecies levels.
1a	The species is not present in the shapefile, there may be a mistake in column 'binomial'	You probably uploaded a distribution range map that does not include the name of the species as written in sRedList platform.	Edit your shapefile so that species name matches exactly with the one you used in the platform.
1a	The distribution could not be loaded; check if it includes the 4 files required (.shp, .shx, .prj, .dbf)	There is a problem with the file you uploaded as distribution. This might come from a problem within the file or because you only uploaded the .shp file (while the platform also requires .shx, .prj, .dbf files)	You must check your file and try upload again with all required extensions.
1a	The uploaded distribution is not valid; maybe you uploaded points instead of	The platform does not accept the distribution uploaded. It may be that the distribution you uploaded is a point distribution while the	Either upload a polygon distribution or use points (in a csv

	polygons?	platform requires a polygon distribution.	file) to create a polygon on the platform with step 1b.
1b-1	No data found! Check whether the scientific name of the species has been typed correctly or select other data sources.	We did not find any occurrence record with coordinates from the sources you selected.	First check if you spell the species name correctly and, if so, select other sources or upload occurrence records.
1b-1	The csv uploaded is invalid. Check the separator you used.	The platform cannot read the csv. It might be because of the separator used (the platform supports comma, semi-column, or tabulations) or because some special characters are included.	Try saving your file with another separator and uploading again. If this does not change anything, you can also try uploading a file with fewer columns (using only those strictly needed).
1b-1	Longitude (dec_long) and latitude (dec_lat) columns were not found in uploaded data	It is absolutely mandatory to have columns with coordinates and this was not found in the csv file you uploaded. The platform can accommodate some variations in column names but ideally these columns should be named 'dec_long' for longitude and 'dec_lat' for latitude.	You should rename the column with longitude data (in decimals) 'dec_long' and the column with latitude data 'dec_lat'.
1b-1	Coordinates should be in decimal with longitude (dec_long) between -180 and 180 and latitude (dec_lat) between -90 and 90. Make sure you used dots and not commas to write decimals in your csv file, this may cause issues.	Some record coordinates were not valid, probably in the csv file you provided.	Check that all longitude and latitude use dots as decimals; check that all longitude coordinates are between -180 and 180; check that all latitude coordinates are between -90 and 90.
1b-1	At least one of the uploaded observations has a different species name (sci_name) than the name of the species you are assessing. Please edit your csv file before uploading again.	All observations uploaded should concern the species you are assessing. In the uploaded csv file, the platform detected at least one line where the scientific name does not match the name used on the sRedList platform.	You should edit your file to ensure that all observations match the species name used in the platform. You can either remove some lines if they concern another species, or edit the scientific name if you want them to be included.
1b-3	All records have been excluded in Step 2	The platform cannot create a range map because all records were filtered out of the data (they all appear purple on the previous interactive plot).	You could either change your filtering rules to enable keeping more occurrence records, or add some points yourself in step 1 'Upload records'.
1b-3	You need to run Step 2 (filtering records) once again before creating range map since you updated Step 1	The Step 1 (downloading data) has been called a second time and step 2 was not run after that, meaning that occurrence records were not filtered since you downloaded occurrence records.	You need to click on “Run Step 2”
1b-3	There are not enough occurrence records to create the distribution with mcp, alpha hull,	When you have a single or two occurrence records (or more but with the exact same coordinates), Minimum Convex Polygon,	You can either add more occurrences by changing your filtering rules in Step 2 or by uploading some additional



	or kernel. Please add some occurrence records or choose another starting point.	Alpha hulls, or Kernels cannot be drawn.	records with the 'Update records' function, or you can choose another Starting point (Individual localities or hydrobasins will work with 1 or 2 single occurrences).
1b-3	Kernel parameter should be positive	Kernel value entered is negative, only positive value are supported.	Change kernel parameter value.
1b-3	Alpha parameter should be positive	Alpha value entered is negative, only positive value are supported.	Change alpha parameter value.
1b-3	At least 5 relocations are required to fit a home range	Kernel cannot be calculated with too few occurrence records and so it is not possible to calculate it for that species.	Use another starting point (e.g., alpha hull) or alternatively, add some occurrences with the 'Upload records' function in step 1.
1b-3	Alpha hull could not be calculated, try with a higher alpha parameter value or use another Starting point	Some alpha values are not valid for alpha hulls and prevents the platform from calculating the alpha hull. It is likely that the alpha parameter you provided is too small for the calculation. This error can also appear when you have a single occurrence, in which case it is not possible to map an alpha hull and you should rather use the 'Individual site' option.	You can try increasing the alpha value you entered. If this does not work you should choose another starting point to create your range map (e.g., Minimum Convex Polygon, or Individual localities).
1b-3	To use the coastal option, you must enter a non-null buffer value and crop by land or by sea	The coastal option buffers the coast line around occurrence records either on the sea side or land side. You must thus provide a buffer value and crop either by land or sea.	Update your buffer and crop settings accordingly.
1b-3	The coast line is not overlapping with your distribution. Increase buffer size or change starting point	The coast line does not overlap with the buffer around points that was set based on your buffer input.	You can increase your buffer size (to reach the nearest coast) or use a different starting point.
1b-3	The distribution of that species is too large to use hydrobasins level 10 or 12, please use level 8 instead	Hydrobasins should be mapped with level 8 unless the distribution is very small. The platform does not allow to map level 10 or 12 if the number of hydrobasins (level 8) with occurrence records is larger than 10.	You should select level 8.
1b-3	The distribution of that species does not overlap with hydrobasins map	We are not able to map hydrobasins since none of the occurrence records falls in the map of hydrobasins used on the platform.	Choose another starting point or try with another set of occurrence records.
1b-3	The distribution does not overlap with land	The distribution created from the starting point and the buffer does not overlap with land, it only includes sea area.	You can either change the starting point or increase the buffer size, or remove the “crop by land” option.
1b-4	Smoothing was not possible with the	The function we use to smooth does not accept your parameter for	You need to change your parameter, probably by

	parameter you chose. Try another parameter, or set it to 0 to skip smoothing	this specific distribution.	increasing it. If it still does not work you can always skip this step by setting the parameter to 0.
4	We cannot find habitat/elevation preferences because the Red List API is not working. Please add them manually.	We cannot access Red List API information at the moment to extract habitat and elevation preferences from previous published assessment (if they exist). We are waiting for the Red List Unit to fix the API access.	You have to enter them manually. You can check <a href="https://www.iucnredlist.org/">https://www.iucnredlist.org/</a> to find information from last published assessment.
4	At least one suitable habitat must be selected	The Area of Habitat calculation cannot be ran when no habitat preferences are selected.	You must tick at least one box as suitable.
4	This habitat cannot be mapped on the platform (the crosswalk we use to link with land cover data does not include the habitats you selected)	The platform is not able to map any of the habitats you selected as “suitable”. Check the paper from Lumbierres et al. (2022) in Conservation Biology to better understand the crosswalk we use between Red List habitats and ESA-CCI land cover map.	You should tick other habitats or skip AOH step if it does not make sense for that species.
4	Elevation preference is not valid. It should be either a number or two numbers separated by a hyphen.	Elevation preferences cannot be red by the platform, it is not in the right format.	Each value should be either one number (e.g., '100') or a range separated by a hyphen (e.g., '100-140'). Decimals should be separated by a dot.
4	Elevation preference is not valid: minimum elevation higher than maximum	There is a problem with elevation preferences. Either one of the value provided as minimum elevation is higher than the one provided as maximum elevation (e.g., minimum = 50, maximum = 10), or if you provided preferences with uncertainty the upper estimate is lower than the lower estimate (e.g., “100-90”).	Check the values you put in the elevation preference field and check that minimum elevation is lower than maximum elevation and that uncertainty bounds are given in the correct order.
4	Density estimate is not valid. Should be a number or two numbers separated by a hyphen	The density estimate cannot be red by the platform, it is not in the right format.	The estimate should be either one number (e.g., '20') or a range separated by a hyphen (e.g., '20-40'). Decimals should be separated by a dot.
4	One of the percentage values is incorrect, they should always be between 0 and 100	Percentage values cannot be negative or above 100.	Enter a value that is between 0 and 100.
4	Internal server error: Timeout was reached: [apiv3.iucnredlist.org] Connection timeout after 10003 ms	The habitat information cannot be loaded because of a connection issue with the Red List API.	Try again in a few seconds (you can click on 'Reset' to try again loading habitat preferences). If this keeps returning an error, check on the forum if this problem has been reported in the last days (there might be a big issue with the servers)

5	The Generation Length value entered is not valid	The generation length estimate cannot be red by the platform, it is not in the right format.	The estimate should be a single number; decimals should be separated by a dot. Note that uncertainty in generation length is not yet supported by the platform.
5-6	AOH must be calculated in Step 4 to access this step!	You accessed the page for step 5 (trends in AOH) or step 6 (fragmentation) without having completed step 4 (AOH) which is mandatory.	Run step 4 and come back to that page only after step 4 is completed.
6	One of the percentage values is incorrect, they should always be between 0 and 100	Percentage values cannot be negative or above 100.	Enter a value that is between 0 and 100.
6	A density must be provided to perform this step	Fragmentation cannot be calculated without density estimate.	You should add an estimate here (either one number e.g., '20' or a range e.g., '20-40').
6	Either density or isolation distance is not valid	The density or the isolation distance estimate cannot be red by the platform, it is not in the right format. It could also be that you included an estimate with uncertainty but that the first value provided is higher than the second value provided (e.g., "40-20").	The estimate should be either one number (e.g., '20') or a range separated by a hyphen with the minimum value in first position (e.g., '20-40'). Decimals should be separated by a dot.
8	Parameter XX is incorrect; it should be numeric	The parameter specified instead of "XX" text cannot be read as a numeric value.	Modify the parameter in the form.
8	Parameter XX is incorrect; it should not be negative	The parameter specified instead of "XX" text seems to be negative (it starts with "-"), which is not allowed for that parameter.	Modify the parameter in the form.
8	Parameter XX is incorrect; it should be between 0 and 100	The parameter specified instead of "XX" text seems to be above 100, which is not allowed for that parameter which is a percentage.	Modify the parameter in the form.
8	Sign of past trends is incorrect; it should be + or -	The sign of past trends can only be "+" or "-".	Modify the parameter in the form.
Merge ZIP	Only provide files with extension .zip	You probably tried to upload a file that is not directly coming from the sRedList platform and has a different extension (only .zip files are supported)	Try identify this file and upload again without this file.
Merge ZIP	Invalid files size maximum upload size is 100 MB	The ZIP files you uploaded are too big to be managed by the platform (total size > 100MB).	You can remove the sRedList reports and/or ddistributions from individual ZIP files to lower their size. Alternatively, you can merge them in several smaller groups.

Merge ZIP	The mandatory file allfields.csv is missing from at least one ZIP file	At least one of the ZIP files you uploaded on the platform does not include the file allfields.csv, which is mandatory.	Check the individual ZIP files you are uploading and edit or remove those without allfields.csv.
Merge ZIP	Your upload includes at least two ZIP files for the same species	The platform cannot merge two assessments of the same species and we detected that at least two of your ZIP files have the same internal_taxon_name value in allfields.csv.	Only upload one ZIP file per species.

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