Prioritizing the reassessment of data deficient species on the IUCN Red List

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This article has been accepted for publication and undergone full peer review but has not been through the copyediting, typesetting, pagination and proofreading process, which may lead to differences between this version and the <u>Version of Record</u>. Please cite this article as <u>doi:</u> 10.1111/cobi.14139.

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## Data availability statement

All data used to create the different models are provided in Appendix S1. Codes are available at <u>https://zenodo.org/record/8019681</u>.

# **Keywords**

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Ecological knowledge; extinction risk; IUCN Red List; Mammals; Odonata; Amphibians; Reptiles; fish

## Article impact statement

Gathering available knowledge on species helps prioritize reassessment of species currently designated data deficient on the IUCN Red List.

# Abstract

Despite being central to the implementation of conservation policies, the IUCN Red List of Threatened Species is hampered by the 14% of species classified as Data Deficient (DD), either because information to evaluate these species' extinction risk was lacking when they were last assessed or because assessors did not appropriately account for uncertainty. With limited funds and time for reassessment, robust methods are needed to identify which DD species are more likely to be reclassified in one of the data sufficient Red List categories. Here we present a reproducible workflow to help Red List assessors prioritise reassessment

of DD species, and tested it with 6,887 DD species of mammals, reptiles, amphibians, fishes, and Odonata (dragonflies and damselflies). Our workflow provides for each DD species: (i) the probability of being classified in a data sufficient category if reassessed today, (ii) the change in such probability since last assessment, and (iii) whether the species might qualify as threatened based on the recent rate of habitat loss. Combining these three elements, our workflow provides a priority list for reassessment of species more likely to be data sufficient, thus ultimately improving knowledge of poorly known species and the comprehensiveness and representativeness of the IUCN Red List.

## Introduction

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The IUCN Red List of Threatened Species (hereafter Red List) is a central tool in biodiversity conservation, guiding policy implementation and biodiversity monitoring from local to global scales (Betts et al., 2020; Rodrigues et al., 2006; Stuart et al., 2010; Williams et al., 2021). An accurate, updated, and comprehensive Red List is crucial for these goals, but decades of insufficient funding (Juffe-Bignoli et al., 2016; Rondinini et al., 2014) dramatically limit assessment and reassessment rates (Cazalis et al., 2022). For example, 14% of all assessed species (N=20,469) are currently classified as Data Deficient (hereafter DD), meaning that assessors were unable to evaluate their extinction risk (IUCN, 2022). These DD species potentially include many imperilled taxa (Bland et al., 2015; Borgelt et al., 2022; Caetano et al., 2022) that are left out of legislation and policies that only target formally threatened species, and introduce uncertainty in monitoring of extinction risk trends of comprehensively assessed taxa (Bland et al., 2017; Butchart and Bird, 2010). Assigning alternative Red List categories (hereafter "data sufficient" or DS) to species currently classified as DD is therefore a high priority for the conservation community (Bland et al., 2017).

Species are typically assessed as DD when "there is inadequate information to make a direct, or indirect, assessment of its risk of extinction based on its distribution and/or population" (IUCN, 2012). The proportion of DD species may be inadvertently inflated when assessors fail to effectively use indirect information (e.g., habitat loss within the range) or are more precautionary than required by Red List guidelines (IUCN Standards and Petitions Committee, 2022). In birds, systematic efforts to use all indirect information (in addition to all direct information owing to the popularity of birds) have reduced the proportion of DD species to 0.4% (N=47; IUCN (2022)), such that the RL status of remaining DD species may only be resolvable by the collection of new *in-situ* information (Butchart and Bird, 2010). Conversely, many groups likely include DD species that could be reassessed as DS if assessors had more systematic access to recent direct and indirect information on species' distributions, populations, and trends.

Recently, multiple studies have attempted to predict the Red List status of DD species using either category-predictive or criteria-explicit approaches (see review in Cazalis et al., 2022). Category-predictive studies establish correlative models that link extinction risk of DS species with relevant characteristics of the species (e.g., showing that narrow-ranged species exposed to high human pressure are more likely threatened). These models are then used to predict the Red List category of DD species (Bland et al., 2015; Bland and Böhm, 2016; Borgelt et al., 2022; Zizka et al., 2022, 2021). However, uptake of such studies and their use to inform Red List assessments has been limited because their ability to correctly predict Red List categories is often low for categories other than Least Concern (Di Marco, 2022). Additionally, as these correlative studies are not explicitly based on Red List criteria, their results lack the required justification of the criteria that are triggered, and are therefore of limited value to assessors (Cardillo and Meijaard, 2012; Cazalis et al., 2022). Criteria-explicit studies mirror the process of assessments by automatically calculating parameters that are used to apply Red List criteria. For example, recent studies have used geospatial data to measure trends in Area of Habitat from global land-cover (Santini et al., 2019) or global forest cover (Tracewski et al., 2016) to apply criteria on population reduction and suggested a list of DD species that could be reclassified as threatened under criterion A2 under certain assumptions. However, these approaches are not sufficient to prioritise reassessments because land-cover products provide a partial view of extinction risk drivers (i.e., habitat loss).

An avenue better aligned with Red List assessors' needs may be to help them identify which species are more likely to become DS if they were reassessed, thus helping assessors to prioritise reassessments. This can be done by training models to predict species' probability of being DS from variables directly representing available knowledge (e.g., number of available occurrence data), proxies of available knowledge (e.g., road density within species range), or species' ecological characteristics that make them harder to monitor (e.g., nocturnality). The main difference to the category-predictive approach described above is that covariates are not expected to correlate with species' extinction risk, but rather with the knowledge available on them. If such models can accurately predict which species are DS, they could in turn be used to predict (i) which DD species have the highest probability of being classified in a DS category if reassessed, and (ii) for which DD species such probabilities have substantially increased since the last assessment. This enables ranking species based on the information currently available (e.g., a species could be prioritised because of the high number of occurrence records available) as well as the gain in information since the last assessment (e.g., a species could be prioritised because the number of occurrence records has grown recently), thus providing complementary valuable information for prioritizing reassessments.

Here, we present a reproducible workflow to prioritise reassessment of DD species based on three complementary analyses and we apply it to 6,887 DD species of mammals, reptiles, amphibians, freshwater and marine fishes, and dragonflies and damselflies. First, we model the probability that a species is classified as DS with a Random Forest algorithm and use this model to predict which DD species are the most likely to be classified in a DS category if reassessed. Second, we use the same model to predict by how much DD species increased their probability of being DS since last assessment. Third, we calculate change in Area of Habitat using two global land-cover products for each terrestrial DD species and identify some species that potentially qualify as threatened or Near Threatened based on the data we provide with our workflow. Gathering the information from these three analyses in a single index, we provide assessors with a priority list of DD species likely to be reassessed as DS, as well as information that can directly inform these reassessments.

### **Methods**

Our workflow includes the calculation of species' probability of being DS if reassessed (*pDS*), the change in this probability since last assessment ( $\Delta pDS$ ) and the change in Area of Habitat ( $\Delta_{AOH}$ ). These three estimates are then combined in an index (*PrioDS*) used to create the priority list that is provided to assessors, along with some additional information to guide their work.

Here we applied this workflow on animal groups assessed in the Red List with at least 10% of species classified as DD (e.g., excluding birds in which DD species are too few to build a model;  $\sim 0.4\%$  of all species, IUCN (2022)) and with published range maps for at least half of the species. From these groups we then selected species with a range map available, which is needed to calculate many covariates used in our model (and we eventually removed all species for which at least one covariate could not be calculated). Our selection included mammals (5,663, 14% DD), reptiles (8,294 species, 13% DD), amphibians (7,051 species, 15% DD). fishes (including classes Actinopterygii, Chondrichthyes, Myxini, Cephalaspidomorphi, and Sarcopterygii; 14,023 species, 19% DD), and Odonata (4,511 species, 29% DD). We refer to these five groups as "broad taxonomic groups". We used species' current Red List category (IUCN, 2022) to separate species into DD and DS, excluding those Extinct or Extinct in the Wild.

### Covariates

We gathered covariates deemed relevant to predict species' probabilities of being DS. Definition, source and rationale for each covariate are given in Table 1; detailed methods are given in Appendix S3. First, we gathered direct measures of available knowledge: number of occurrence records available from the Global Biodiversity Information Facility (hereafter "GBIF records"; also including records from the Ocean Biodiversity Information System

OBIS for fishes); proportion of the species' range that is covered by GBIF records; as a proxy for sampling effort, the density of occurrence records for the broad taxonomic group within a focal species' range; number of articles in Web of Science mentioning the focal species' Red List name; number of traits known for the species; spatial overlap with DD species from the broad taxonomic group occurring in the range; whether the species is present in at least one zoo or aquarium; and time since description of the species. Second, we gathered a number of proxies of knowledge: average Gross Domestic Product and frequency of armed conflicts in species' countries of occurrence; remoteness of species range; road density in species range; human population size in species range; proportion of rural population in species range; and fishing intensity in species range (marine fishes only). Third, we included ecological characteristics of species: habitat preference; order of magnitude of their range size; altitude or depth of occurrence of the species; main realm where the species occurs; as well as other potentially relevant traits that we could readily retrieve from existing trait datasets that use the Red List taxonomy (body mass and nocturnality for mammals, body length for amphibians). Finally, we retrieved the Red List Authority of each species (i.e., the expert group appointed to assess or review assessments for each taxonomic group) to control for possible differences in assessment behaviours between expert groups working on different taxa (Caetano et al., 2022). Four variables were calculated for two time-steps, at the time of assessment (to fit the model) and at present time (to predict the current probability of being DS, pDS). These variables (hereafter called "temporal variables") are: number of GBIF records, coverage of GBIF records, number of published scientific articles, and time since description.

### Statistical analyses

### Modelling data sufficiency

We modelled the probability of a species being DS independently for each of the five broad taxonomic groups. Mammals that are strictly marine according to Red List systems classification (i.e., 73 cetaceans, 1 dugong, and 2 seals; including 3 DD) were removed from the analyses as they could not be modelled together with terrestrial species (covariates such as human density, remoteness or altitudes could not be calculated), and there were too few DD species to be modelled independently (N=3). Conversely, strictly marine reptiles (i.e., sea snakes; 48 species including 20 DD) were modelled together with terrestrial reptiles as these are mainly coastal species (see Appendix S3). For fishes, we fitted two models, one including all species occurring in freshwater domain (N=10,160), and another one including all species occurring in marine domain (N=4,987), with 942 species being present in both (e.g., anadromous or catadromous species; Appendix S7).

For each broad taxonomic group and domain, we fitted a Random Forest model with 1,000 trees using the *ranger* function from the *ranger* R package v.0.13.1 (Wright and Ziegler, 2017) with covariate values from the year of last assessment for temporal variables. As our samples were unbalanced, we attributed to DD species a weight corresponding to the proportion of DS species, and to DS species the proportion of DD species, using the 'class.weights' argument. We measured the relative importance of covariates with the 'impurity\_corrected' argument, which provides a sampling-size corrected measure of the Gini impurity index.

We measured the performance of our models using a taxonomic block validation. To that end, we iteratively fitted models putting aside one family from the training data and then predicting the probability of being DS for the species in that family. We calculated the performance metrics based on a binary categorisation of the probabilities of being DS: sensitivity (proportion of DS species correctly categorised), specificity (proportion of DD species correctly categorised), and True Skill Statistic (specificity + sensitivity - 1; Allouche et al. (2006)). Performance metrics were calculated across all species (rather than per family and averaging values across families) to limit the influence of families with very few DD species (as a family with a single DD species will have a specificity of 0 or 1 depending on whether that single species is correctly or incorrectly predicted; Appendix S6). We used two different threshold rules to binarize these probabilities into DD/DS categories: 1) choosing the threshold that maximises the True Skill Statistic (TSS), and 2) choosing the threshold that maximises the TSS while keeping sensitivity > 0.9. This second rule will minimise false negatives (i.e., DS species incorrectly predicted as being DD), which is a desirable property of our method because it will limit the number of species that we exclude from prioritisation (because predicted to remain DD) while they could be reassessed in a DS category. In addition, we measured variation in performance metrics among families (Appendix S6).

Prior to model fitting we verified the correlation between all continuous covariates, considering that pairs of covariates with a Pearson's correlation coefficient > 0.7 could affect parameters estimates (Dormann et al., 2013). Only the number of GBIF records and the number of articles in the Web of Science in Odonata correlated by 0.79 (Appendix S4); however, this did not impact the predictive performance of our model (full model: TSS = 0.67; model excluding the number of GBIF records: TSS = 0.64; model excluding the number of articles in the Web of Science: TSS = 0.67) nor the shape of the relationship, so we decided to keep both covariates in our model, as they have strong independent rationale and are both important for the temporal analysis.

#### Prioritising reassessments

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Predicting the probability of being DS (pDS)

For each DD species, we predicted the probability of being DS if reassessed today (pDS). To do so, we used the Random Forest model trained with all species and predicted the probability of DD species to be reassessed as DS, after changing the temporal variables to their present-day values (e.g., using the current number of GBIF records rather than the one at the time of last assessment). For the 160 DD fishes that occur in both freshwater and marine domains, we reported the highest probability from the two predictions. We considered this choice more cautious from a practical perspective, as the risk here is to prioritise a species for reassessment that will remain DD (i.e., waste some assessor time), while the opposite would risk not reassessing a species that could become DS (i.e., leave a species DD for years).

To provide assessors with more information on why a species has high pDS, we identified variables contributing most to pDS for individual species using the 'breakDown' R package v.0.2.1 (Staniak and Biecek, 2019).

#### *Predicting change in probability of being DS (ΔpDS)*

We calculated the change in probability of being DS since last assessment ( $\Delta pDS$ ) as the difference between predictions based on models using the past (last assessment) vs presentday values of the temporal variables (see distribution of the increase of temporal variables between last assessment and now in Appendix S5). For fishes occurring in freshwater and marine domains, we reported the change in the domain for which current probability pDS was the highest (most conservative). In rare cases where  $\Delta pDS$  was negative (481 species had negative  $\Delta pDS$  with a median of -0.0019 and a minimum of -0.06; negative values were due to the non-monotony of some covariates effects; Fig.2), we considered it to be 0 as it does not really reflect a loss of knowledge since last assessment.

### Measuring change in Area of Habitat ( $\Delta_{AOH}$ )

We expect that both *pDS* and  $\Delta pDS$  will mostly prioritise DD species that are relatively common (e.g., with many GBIF records, large range, in well-sampled regions) and thus that are mostly not threatened. To increase the proportion of potentially threatened species in the prioritization, we included in the workflow an analysis specifically designed to identify DD species that could be reassessed as threatened or Near Threatened based on habitat loss. This index is not needed to calculate data sufficiency *per se*, but could be very helpful in supporting reassessments of some species (Tracewski et al. 2016; Santini et al. 2019) and should thus be considered in reassessment prioritisation. To that end, we calculated change in Area of Habitat ( $\Delta AOH$ ) for all broad taxonomic groups but fishes, to identify species that could likely be reassessed as threatened under Criterion A2 based on population size reduction (IUCN, 2012; IUCN Standards and Petitions Committee, 2022) after assessors carefully checked if the range map and habitat preferences used in our calculation (i.e., those submitted in last assessment) are thought representative. To map AOH, we extracted species' preferences in terms of elevation and habitat types from the Red List data. We used the ESA- CCI land cover data v.2.1.1 to extract pixels within the range that correspond to a species' suitable habitat, using the crosswalk between ESA-CCI and Red List habitat classification from Lumbierres et al. (2022). From those, we extracted cells within the species' altitudinal limits based on elevation data from the National Geophysical Data Center (1999). We calculated AOH using a Mollweide projection using the R '*aoh*' package v.1.0.0 (Hanson, 2022), at two timesteps: current (using the ESA-CCI data from 2020) and 10 years or 3 generations ago, whichever the longest, following Red List guidelines (IUCN Standards and Petitions Committee, 2022). We used a timeframe of 10 years unless a generation length estimate was included in the Red List database (only included for mammals in our DD subset;  $\Delta AOH$  is therefore possibly underestimated for a few reptile and amphibian species with long generation times).

In addition, because more detailed data are available for forest habitats, we calculated change in forest cover for each terrestrial DD forest specialist (i.e., species for which forests are the only suitable primary terrestrial habitat, disregarding habitat classes 5, 9-13, 15, 17-18) using the Global Forest Change maps (Hansen et al., 2013). We used the 'gfcanalysis' R package v.1.6.0 (Zvoleff, 2020) to download and process the data. We calculated the forest cover in 2021 within a species range as the coverage of 30m-pixels that were covered by forest in 2000 (i.e., with a coverage value > 0.25 which is the default of the *threshold\_gfc* function) and did not suffer from any loss since. We calculated the forest coverage in the initial year (between 2000 and 2011, depending on generation length) using the same method but excluding cells that suffered from loss before the initial year. Forest gains are not considered in this analysis, assuming that regenerated forests do not provide habitat of sufficient quality over the short study period.

For both AOH and forest cover, we then calculated change as the difference between current and initial divided by initial coverage (negative values in case of habitat loss). When generation length was so high that the initial year was before the first year of land-cover products (i.e., 1992 for the ESA-CCI and 2000 for the Global Forest Change), we linearly extrapolated habitat loss. We kept the lowest (i.e., most negative) AOH change among ESA-CCI and Global Forest Changes estimates ( $\Delta_{AOH}$ ) and considered that species with  $\Delta_{AOH} \leq -$ 0.3 could potentially qualify as threatened under criterion A2(c). Additionally, although there is no strict quantitative threshold for Near Threatened (NT), we considered species could potentially qualify as NT if  $\Delta_{AOH} \leq -0.2$ , which correspond to the example given in the Red List guidelines (IUCN Standards and Petitions Committee, 2022).

Prioritising reassessments (PrioDS)

We created an index to identify reassessment priorities:

$$PrioDS = \begin{cases} 1 & if \Delta_{AOH} \le -0.2 \\ \left(1 - \sqrt{0.5 * \left((1 - pDS)^2 + (1 - \Delta pDS)^2\right)}\right) & if \Delta_{AOH} > -0.2 \end{cases}$$
(1)

where pDS is the current probability of being DS,  $\Delta pDS$  is the change in probability of being DS since last assessment, and  $\Delta_{AOH}$  is the AOH change in the last 10 years / 3 generations. *PrioDS* ranges from 0 to 1 with higher values indicating higher reassessment priority, with a value of 1 if  $\Delta_{AOH} \leq -0.2$  (i.e., maximum priority as the species could likely be reassessed as NT or threatened with that information) and a value based on pDS and  $\Delta pDS$  otherwise. The index gives equal importance to pDS and  $\Delta pDS$  and takes a value of 1 when both pDS and  $\Delta pDS$  are 1, and 0 when both are null. We then used the index values to create a priority list (of 10, 25, and 50% species with highest priority score) and mapped the distribution of these priority species.

#### Application and performance of the priority list

While all analyses were run on Red List version 2021-3, we used Red List version 2022-2 to perform an ex-post validation of our models. In this new version, 180 DD species included in our analyses were reassessed, of which 73 remained DD and 107 were moved into a DS category. We checked the agreement between the new category (i.e., remained DD or became DS) and our reassessment priority score (*PrioDS*). This provided an independent validation of our approach and proposed priority list, although it was based on a small sample size and, importantly, reassessments were conducted without the information provided by our workflow.

### **Results**

Our models showed good performance at predicting DS species of mammals, reptiles, amphibians and Odonata from taxonomically independent samples (Fig. 1; Appendix S8) with some important variation among families (Appendix S6). When we used the threshold that maximises TSS to binarize predictions, we obtained a TSS > 0.5 for these four groups, with a maximum of 0.67 for Odonata, and a specificity slightly higher than sensitivity. Models for fishes performed slightly worse with a TSS of 0.47 and 0.41 for freshwater and marine fish species, respectively. Using the binarization threshold that maximises TSS but keeping a sensitivity > 0.9 (i.e., to ensure that we correctly identify the species that could be reassessed in a DS category) led to a drop in specificity (falling to 0.39 for marine fishes and

0.71 for amphibians) but TSS remained relatively high (between 0.31 for marine fishes and 0.61 for amphibians).

The most important variables to predict species probability of being DS differed among taxa (Fig. 2; Appendix S9). Overall, direct measures of available knowledge were among the most important variables, especially the number of GBIF records, which was among the three most important variables for all taxonomic groups (and was the most important for three groups) and coverage of GBIF records, as well as trait data availability (among the four most important variables for the two groups it was measured). Some proxies of knowledge were also particularly important, especially the spatial overlap with DD species, which was among the four most important variables for all groups but mammals and marine fishes. The median GDP (for freshwater fishes) and the time since description of the species (for marine fishes and mammals) were also important. Finally, the most important variables for four groups (with a positive effect on the probability of being DS), while habitat preferences, nocturnality and body size did not strongly influence the probability of being DS.

Using these group-specific models, we found that 27% of DD species (1,907 of 6,887) had a high probability to be DS now (pDS > 0.5; Fig. 3; e.g., Zamenis lineatus in Fig. 4a). Moreover, 624 species had considerably increased in their probability of being DS since last assessment,  $\Delta pDS > 0.25$  due to for example many new GBIF records (Fig. 3; e.g., *Elattoneura campioni* in Fig. 4b). Although pDS and  $\Delta pDS$  correlate (Pearson's correlation coefficient of 0.68), there is great variation in  $\Delta pDS$  for a same pDS, often ranging from 0 (i.e., no new information since last assessment) to a value close to pDS (i.e., all information was gained since last assessment).

From the final step of the workflow, assuming that distribution and species preferences data were accurate, we identified 5 mammals, 14 reptiles, 5 amphibians, and 5 Odonata species with an estimated loss of > 30% of their AOH in the last 10 years or 3 generations (i.e.,  $\Delta_{AOH} \leq -0.3$ ), thus being considered threatened under criterion A2 with 24 being VU, 3 EN, and 2 CR (Fig. 3; e.g., *Hypsugo vordermanni* in Fig. 4c; Appendix S1). An additional 11, 28, 9, and 35 species, respectively, could be considered as Near Threatened based on an estimated AOH loss of 20-30% (Figs. 3, 4c; Appendix S1).

Calculated *PrioDS* values suggested that priority DD species for reassessment mainly concentrate in Latin America and South-East Asia (Appendix S10).

The independent validation of predictions (for 180 species based on the recently released version 2022-2) showed higher priority scores for the species that were reassessed in a DS category (0.39 ± 0.17 (mean ± SD) vs 0.24 ± 0.12 for species that remained DD after their reassessment; unilateral T-test: t = -6.97,  $P < 10^{-10}$ ; Fig. 5). Our workflow performed

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particularly well for amphibians (N=107) with *PrioDS* being on average double for species reassessed as DS than species reassessed as DD ( $0.39 \pm 0.16 vs 0.19 \pm 0.10$ ; unilateral T-test: t = -7.53, P < 10<sup>-11</sup>). Results for reptiles (N=45) also showed a significant difference in *PrioDS* ( $0.36 \pm 0.11 vs 0.28 \pm 0.12$ ; unilateral T-test: t = -2.35, P = 0.01). Results for fishes (N=24) confirmed that this group is not as accurately predicted and that caution is required in interpreting our results there ( $0.31 \pm 0.12 vs 0.29 \pm 0.11$ ; unilateral T-test: t = -0.38, P = 0.36). Results for mammals (N=1) and Odonata (N=3) only included species reassessed as DS with relatively high priority scores. Results were similar when looking at *pDS* and *ApDS* independently, showing that *ApDS* was a great predictor of species reassessed as DS for amphibians (Appendix S11).

### Discussion

Our workflow is the first to predict the probability of a species to be DS, aiming at being of practical value for Red List assessors. The covariates we chose for the model show strong predictive power of species classification as DD or DS during taxonomic block validation, performing well (TSS > 0.5) for all groups but fishes, and thus suggesting that this workflow is a powerful tool to prioritise reassessment at least of terrestrial DD species. The independent validation enabled by the recent update of the Red List showed that our workflow performed well for the 107 amphibian species and 45 reptiles in our test group, with newly DS species showing higher priority scores than species retaining DD status. It is worth noting, however, that the sample size of this validation is relatively low and this cannot be seen as a direct test for our workflow, since the assessors did not have access to the workflow outputs (which could potentially have contributed to additional species being reassessed as DS). The genuine performance and utility of our workflow will only be measurable after assessors use it and see if they end up with fewer species remaining DD than without our information. This is particularly true for  $\triangle$ AOH which has proven to be useful in the past (Tracewski et al. 2016, Santini et al. 2019) but could not be tested for our workflow outside of a real assessment process.

The most important variable to predict the probability of species to be DS was the number of GBIF records available at the time of the last assessment, which provides information directly applicable in assessments (Bachman et al., 2020). Across all broad taxonomic groups, we found that the probability of being DS is low for species with no GBIF records, strongly increases as the first records are gathered, before plateauing when a few tens of records are available (Appendix S12), highlighting the utmost importance of increasing the collection and availability of primary occurrence records for poorly known species (Shirey et al., 2019). Other direct indicators of available knowledge were also important, such as the number of

articles published on a species (that can be directly used in Red List assessments; Bird et al. (2020)) or trait data availability (for the two groups for which it was measured; González-Suárez et al. (2012)). Several proxies of knowledge were also important predictors. The spatial overlap with DD species reduced the probability of being DS, highlighting the geographical clustering of DD species (Appendix S10). This means that a DD species cooccurring with many other DD species is less likely to be reassessed as DS, e.g., because the region has been poorly sampled, or because little contextual information is available on threats. In fewer cases, we also found that species described very recently were more likely to be DD, indicating that it takes time to gain knowledge on a new taxon (Morais et al., 2013). Finally, some ecological characteristics were important predictors, with e.g., species with small range sizes more likely to be DD (Bland and Böhm, 2016; Butchart and Bird, 2010). This effect might be partly driven by underestimation of range size for DD species (see example in Fig. 4b), and thus means that species that are known from a smaller area are more likely to be DD (even if their true range size may be larger). Interestingly, variables describing human distribution (e.g., population density, road density, or travel time to cities), or variables related to species altitude or marine depth preferences, were not among the most important predictors (Appendix S9). This could due to the exclusion, in our method, of some poorly known species for which the distribution has not be mapped, which may occure in more remote areas than other DD species. It could also be that our models do not find remoteness important because they have a more direct way of measuring availability of knowledge for the species, which is the number of GBIF records.

The first element of our prioritization index is the predicted probability of being DS if the DD species is reassessed today (*pDS*). This element should help identify species that currently share many characteristics with DS species (e.g., in terms of distribution, available knowledge, traits) and invite assessors to reconsider the status of these species. The snake *Zamenis lineatus*, for instance, is predicted to have one of the highest probabilities of being DS, mainly because of the high number and coverage of GBIF records, its large range, and the fact that it overlaps with few DD species (Fig. 4; Corti et al. (2008)). It could thus be a good reassessment priority, as its last assessment was 14 years ago. Notably, several of the GBIF records of *Z. lineatus* were well outside the known range of the species, an issue with geo-referenced occurrences from public data repositories (Maldonado et al., 2015), which can be reduced with the use of automated tools to filter data (Zizka et al., 2019; Arlé et al., 2021), although this would significantly increase calculation time.

A second output of our model is the change in the probability of being DS since the last assessment ( $\Delta pDS$ ). The dragonfly *Elattoneura campioni* was last assessed in 2010, when no articles in the Web of Science and no GBIF records were available (the species was not reported since 1967 according to the last Red List assessment; Sharma and Dow (2010)),

resulting in a probability of 0.06 of the species to be DS by that time (Fig. 4). Even though the probability of being DS is only intermediate based on current data (pDS=0.54), our workflow suggests that it strongly increased since last assessment ( $\Delta pDS$  =0.48), indicating that the species is of higher reassessment priority than one with similar pDS but lower  $\Delta pDS$ . Indeed, the number of GBIF records for this species now reaches 29 and suggest the species is more widespread than previously thought. Additionally, two articles mentioning the species were published since the last assessment, providing additional records and information on species habitat (Mujumdar et al., 2021). This index of change in probability of being DS is important since we found that the gain in information greatly varies among species independently of the time since last assessment (Appendix S5). It could still gain relevance if more temporal variables, measuring the availability of data directly usable by Red List assessors, were included in the model (e.g., number of specimens in museums, records in citizen science platforms that do not contribute to GBIF, articles published in non-English journals (Nic Lughadha et al., 2019; Bachman et al., 2019; Amano et al., 2021)).

The species prioritised based on the two above-mentioned parameters are more likely to be species with relatively large ranges, that are not rare (e.g., with more GBIF records), and that will thus most likely be reassessed as Least Concern. While this is important in order to reduce the uncertainty around the proportion and distribution of threatened species, it is also very important that our prioritisation helps assessors identify those DD species that are threatened with extinction (Bland et al., 2015; Howard and Bickford, 2014). To do so, we included in our workflow a calculation of species' change in AOH ( $\Delta_{AOH}$ ; Brooks et al., 2019; IUCN Standards and Petitions Committee, 2022) using land-cover time series, which can provide direct input into Red List assessments (IUCN Standards and Petitions Committee, 2022; Santini et al., 2019; Tracewski et al., 2016). This identified 112 species that lost > 20% of their AOH in the last 10 years/3 generations and may thus potentially qualify for threatened or NT. For instance, the last assessment of the bat species Hypsugo vordermanni, made in 2015, mentions that the species lives in forest and may be restricted to mangroves, but that information on population dynamics are lacking to assess its status (Görföl et al., 2015). The loss of 31% of forest habitat within its range ( $\Delta_{AOH} = -0.31$ ), as we calculated here, could be sufficient to classify the species as Vulnerable under criterion A2c based on population size decline inferred from habitat reduction. To use this result though, assessors should evaluate the completeness of the published range map (i.e., that it includes sites of occurrence, but also inferred or projected presences) and habitat preferences of the species, consider the likely relationship between habitat loss and population decline, and acknowledge that the ESA-CCI land-cover and habitat crosswalk used here can have important misclassification errors locally. While change in AOH may be important in prioritising reassessment of potentially threatened species, we acknowledge it only relates to a subset of the reasons to classify a species as threatened, and could in the future be supplemented by other indices of threat that can be directly used by assessors.

Based on these three outputs (*pDS*,  $\Delta_{pDS}$ ,  $\Delta_{AOH}$ ) we created a priority index (*PrioDS*) that can be used to create a priority list for reassessment. Assessors can choose a threshold in *PrioDS* depending on their resources and the rate of false positives and negative they are willing to accept (e.g., a group with very limited resources will select only the top priority species, which will likely include mostly species that can be reassessed as DS, but will be incomplete; Appendix S8). In addition, our workflow provides outputs directly usable by assessors, to prioritise and inform reassessments (Fig. 4). It contrasts with previous studies that aimed at reducing the number of DD species by estimating their extinction risk (Bland and Böhm, 2016; Borgelt et al., 2022; Howard and Bickford, 2014) but that were not widely used by Red List assessors (Cardillo and Meijaard, 2012; Cazalis et al., 2022). While being so far restricted to groups with polygon range maps, it could in principle be extended to groups with point data but no polygon range maps (most of vascular plants and some invertebrates) by adding an automated approximation of polygon range maps from points (e.g., using alpha-hulls), which would enable spatial covariates to be calculated. This would only be feasible if point coverage within the species distribution is adequate.

To maximise its utility though, our workflow will have to be effectively shared with assessors. For example, integrating our workflow in an interactive platform (e.g., as a Shiny App; Bachman et al. (2020)) would enable assessors to create their priority list from their own criteria (e.g., choosing if they want to use the priority index *PrioDS* or if they give more weight to *pDS* or  $\Delta pDS$  individually, or a single variable of interest such as the new number of GBIF records) and filtering conditions (e.g., species last assessed before a given year, from a given family or region). Such platform could also provide easy-access to the additional information provided by our workflow (e.g., list of published articles, map of GBIF records, or map of change in AOH; Fig. 4), which may be used by assessors as supplementary decision support in their assessments.

Allowing flexibility in the use of the outputs, as well as updating them regularly (e.g., as the number of GBIF records can increase rapidly for some species), will be key to enable uptake of this workflow by the Red List community (Cazalis et al., 2022). It should help assessors to make better use of their limited time and resources by targeting the reassessment of DD species that will most likely be reassessed in a DS category. It should also help them finding and making use of "whatever information is available and relevant to make assessments" as required by the guidelines (IUCN Standards and Petitions Committee, 2022). Eventually, we expect our approach to enable the proportion of DD species in the Red List to be reduced, which would reduce the uncertainty of products that are based on the Red List and help

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focusing research efforts on the remaining DD species, thus helping future conservation efforts to be based on more robust foundations.

## **Acknowledgments**

Accepted Article This paper is a joint effort of the working group sRedList kindly supported by sDiv, the Synthesis Centre of the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, funded by the German Research Foundation (FZT 118, 202548816), which also funded positions for V.Ca.. M.D.M. and L.S. acknowledge support from the MUR Rita Levi Montalcini program. C.M. acknowledges funding by the Volkswagen Foundation through a Freigeist Fellowship (A118199), and additional support by iDiv, funded by the German Research Foundation (DFG-FZT 118, 202548816). A.B.L. was supported by a Juan de la Cierva-Incorporación grant (IJCI-2017-31419) from the Spanish Ministry of Science, Innovation and Universities and an EMERGIA grant (EMERGIA20 00252) from the Junta de Andalucía. P.C. is supported by Kone Foundation. B.E.Y. acknowledges Chevron, Inc. We thank the four photographers who allowed us to use their picture in Figure 4.

## Supporting Information

Additional supporting information may be found in the online version of the article at the publisher's website.

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**Table 1:** Variables used to predict the probability of species being data sufficient (pDS). Variables marked as Temporal were also used to estimate change in probability of being data sufficient since last assessment. Types of variables are Binary (Bin), Numeric (Num), Categorical (Cat). More details in Appendix S3.

Variable	Group	Туре	Short	Temporal	Rationale	Source
			definition			
Number of GBIF records	All	Num	Number of records found for the species name. For fishes, we kept the maximum number of records between GBIF and OBIS.	Yes	Species with many GBIF records are regularly observed and thus more likely to be well-known. GBIF records can directly help assessing a species (e.g., measuring the Extent of Occurrence).	Chamberlain et al., (2022); Provoost and Bosch (2021)
Coverage of GBIF records	All	Num	Proportion of $\sim$ 80km grid cells with $\geq$ 1 record.	Yes	GBIF records are less informative if concentrated in a very small part of the species' range.	Chamberlain et al., (2022)
Intensity of GBIF sampling effort	All	Num	Median density of records for the broad taxonomic group in the range.	No	Species in heavily sampled regions are likely to be better known, even if they are not often reported (e.g., limited records in intensively sampled areas might indicate rarity).	Chamberlain et al., (2022)
Number of Web of Science articles	All	Num	Number of search hits when looking for the species name in the Web of Science.	Yes	Published data can provide information usable for assessments (e.g., population monitoring, point	

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					locality data, population size estimates).	
Trait availability	Mammals + Amphibians	Num	Number of traits available in two combined trait databases.	No	A high number of traits available for a species is a direct indicator that the species is well-known (e.g., morphologically, demographically, etc).	Soria et al. (2021) ; Lucas et al. (2023)
Spatial overlap with DD species	All	Num	Overlap of species' range with DD species from the broad taxonomic group, measured as the proportion of Red List gridded distributions that are from DD species.	No	Cluster of DD species can indicate poor knowledge of the region.	IUCN (2022)
Presence in zoos and aquaria	All	Bin	Whether at least one specimen is known in zoos or aquaria.	No	Presence of species in zoos and aquaria may lead to better knowledge on the species from individuals kept in captivity.	Species 360 (2021, p. 360)
Time since description	All	Num	Difference between 2022 and the year reported in the species taxonomy authority.	Yes	Species recently described had less time to accumulate data; however, they might have been described with more in-depth information.	IUCN (2022)
GDP	All	Num	Median GDP of the species Red List Countries of Occurrence.	No	Countries with high GDP might be more likely to fund biodiversity monitoring.	World Bank (2021)
Frequency of armed conflicts	All	Num	Median number of years of armed conflicts in species' Red List Countries of Occurrence in the last 20 years.	No	Regions where armed conflicts are frequent are less likely to be monitored.	Gleditsch et al. (2002); Pettersson et al. (2021)
Remoteness	All	Num	Median travel time to cities across the species range (terrestrial) or median distance to nearest port	No	Species close to human populations are more likely to be observed regularly.	Weiss et al. (2018); Zeenatul Basher et al. (2019)

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				(marine).			
	Road density	Terrestrial +	Num	Highest quartile	No	Species whose	Meijer et al.
		freshwater		of road density		distribution includes	(2018)
		species		within species'		some areas with high	
				range.		road density are more	
						likely to be well	
						sampled.	
	Human	Terrestrial +	Num	Human	No	Species occurring in	Florczyk et al.
	population	freshwater		population		areas with high	(2019)
	density	species		density across		human population	
				the species		density are more	
				range.		likely to be observed	
						and thus should be	
	D (	T ( 1 )	ЪT		NT	better known.	<b>F1 1 ( 1</b>
	Proportion	1  errestrial +	Num	Proportion of	No	Humans living in	Florczyk et al.
	of rural	freshwater		rural inhabitants		rural areas might be	(2019)
	population	species		within the		more likely to	
				species range.		encounter species and	
						then humans living in	
						urbon areas	
	Marine	Marine	Num	Median of the	No	Species occurring in	Kroodsma et
	fishing	fishes	INUIII	log_transformed	110	areas heavily fished	(2018)
	nsning	1131103		number of		are more likely to be	al. (2010)
				fishing hours		caught which can	
				across the		contribute data	
				species range.		directly used in	
				8		assessments (e.g.,	
						occurrence data, or	
						population dynamics	
						data).	
	Habitat	Terrestrial +	Cat	Cluster of Red	No	Some habitats are	IUCN (2022)
	preference	freshwater		List habitat		harder to sample	
J		species		preferences:		(e.g., caves, forests),	
				"Forest		specialists from those	
				specialist",		are thus likely less	
				"Forest		known.	
				generalist",			
				"Non-Forest			
				specialist",			
				"Non-Forest			
				generalist",			
	D '-	A 11	NT		N	0	
	Kange size	All	INUM	Urder of	INO	species with large	10CN (2022)
	(order of			the area of the		to be observed and	
	magintude)			range polycong		thus well known Wa	
				range porygons.		used order of	
						magnitude to	
						minimise the	
						influence of range	
						size underestimation	
						that is common for	
						DD species.	
	Median	Terrestrial +	Num	Median altitude	No	High altitudes are	National
	altitude	freshwater		across the		more difficult to	Geophysical
		species		range.		sample.	Data Center
							(1999)
	Water depth	Marine	Num	Discrete depth	No	Deeper waters are	IUCN (2022)

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	fishes		class based on habitat preferences 1 (0-200m), 2 (200-1000m), 3 (1000-4000m), 4 (>4000m).		more difficult to sample.	
Main realm	All	Cat	Identity of the realm covering the biggest part of species range: 8 classes for terrestrial; 18 for marine.	No	Some realms have been less studied than others over the last centuries.	World Wildlife Fund US (2004); The Nature Conservancy (2012)
Body Mass	Mammals	Num	Body mass from the published database (includes some imputed data).	No	Large species are usually easier to observe and monitor.	Soria et al. (2021)
Nocturnality	Mammals	Bin	True for species strictly nocturnal.	No	Nocturnal species are harder to observe and monitor.	Soria et al. (2021)
Body length	Amphibians	Num	Snout to Vent Length from the cited database (including some imputed data).	No	Large species are usually easier to observe and monitor.	Lucas et al. (2023)
Red List Authority	Mammals + Reptiles + Fishes	Cat	Name of the Red List Authority of the species: 36 classes for mammals, 13 classes for reptiles, 11 classes for fishes.	No	Groups of assessors and reviewers might treat uncertainty in assessments slightly differently and thus differ when assessing species as DD.	IUCN (2022)
Taxonomic Order	All	Cat	Order of the species.	No	Some Orders may be more likely than others to be DD (e.g., because they share specific traits or because species-level identification is harder in that group)	IUCN (2022)



Binarization threshold: maximise TSS (●); maximise TSS with sensitivity > 0.9 (●)

**Fig. 1:** Performance of the Random Forest models to predict data sufficient (DS) species per group (mammals, reptiles, amphibians, freshwater fishes, marine fishes, Odonata) with four metrics resulting from a taxonomic block cross-validation with two different binarization rules. The performance metrics are: sensitivity (proportion of DS species correctly categorised by our model), specificity (proportion of Data Deficient species correctly categorised by our model), and TSS (specificity + sensitivity -1). Variation in performance among families is shown in Appendix S6.



**Fig. 2:** Main covariate effects on the probability of being data sufficient (DS), measured as partial dependence, per group (mammals, reptiles, amphibians, freshwater fishes, marine fishes, Odonata). Lines represent the respective group's four most important covariates, sorted by decreasing importance (relative importance of covariates indicated by size of the grey bubbles). Plots are limited to the 95th quantile of the covariate on the right for visualisation purposes (and are transformed by square-root function where it helps visualising); the covariate distribution is represented at the bottom of each facet.



Fig. 3: Scatter plot of predicted probability to be data sufficient currently (pDS) and change in probability to be DS since the last assessment ( $\Delta pDS$ ) for current DD species per group (mammals, reptiles, amphibians, fishes, Odonata). Colours and isoclines show the species to prioritise for reassessment depending on the proportion of species that can be reassessed (10% species with highest PrioDS in purple and black, 25% in dark pink, or 50% in light pink); black dots show species that could be reassessed based on change in AOH (terrestrial realm only; PrioDS=1; closed dots: species with  $\Delta_{AOH} \leq -0.3$  potentially qualify as threatened; open dots: species with  $\Delta_{AOH} \leq -0.2$  potentially qualify as Near Threatened).



**Fig. 4:** Four example species currently classified as DD with different types of available information. Our analyses suggest that species in panels (a-c) are higher priority for reassessment because of a high probability of being DS (*pDS*; a), a large increase in probability of being DS (*dpDS*; b), or a relatively large decrease in AOH (*d*<sub>AOH</sub>; c), while (d) has a lower reassessment priority. The 'additional information' column shows examples of information made available to assessors, which can include main contributions explaining models' results, maps of GBIF records or AOH loss, and list of articles available in WoS. Main contributions were extracted with the '*breakDown*' R package v.0.2.1 (Staniak and Biecek, 2019). Maps of GBIF records show the species' range in yellow, records gathered before last assessment in blue and after in red, the forest loss map shows current forest in green and forest lost in the last 16 years (3 generations for this species) in red. Credit photo: (a) Benny Trapp, (b) Shantanu Joshi, (c) Chien C. Lee, (d) Jos Kielgast.



**Fig.5:** Priority score comparison of the 180 DD species that were reassessed in a data sufficient category (DS, N=107) or as Data Deficient (DD, N=73) in an update of the Red List subsequent to our analyses per group (reptiles, amphibians, fishes). Black dots show raw data and purple violins show their distribution.