

## CONTRIBUTED PAPERS

# A standard approach for including climate change responses in IUCN Red List assessments

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**Article state impact:** Standardizing measures of the effects of climate change on species improves extinction risk assessments.

## Abstract

The International Union for Conservation of Nature (IUCN) Red List is a central tool for extinction risk monitoring and influences global biodiversity policy and action. But, to be effective, it is crucial that it consistently accounts for each driver of extinction. Climate change is rapidly becoming a key extinction driver, but consideration of climate change information remains challenging for the IUCN. Several methods can be used to predict species’ future decline, but they often fail to provide estimates of the symptoms of endangerment used by IUCN. We devised a standardized method to measure climate change impact in terms of change in habitat quality to inform criterion A3 on future population reduction. Using terrestrial nonvolant tetrapods as a case study, we measured this impact as the difference between the current and the future species climatic niche, defined based on current and future bioclimatic variables under alternative model algorithms, dispersal scenarios, emission scenarios, and climate models. Our models identified 171 species (13% out of those analyzed) for which their current red-list category could worsen under criterion A3 if they cannot disperse beyond their current range in the future. Categories for 14 species (1.5%) could worsen if maximum dispersal is possible. Although ours is a simulation exercise and not a formal red-list assessment, our results suggest that considering climate change impacts may reduce misclassification and strengthen consistency and comprehensiveness of IUCN Red List assessments.

## KEYWORDS

climate change, conservation, extinction risk, IUCN, Red List of Threatened Species, species distribution models

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## INTRODUCTION

The International Union for Conservation of Nature (IUCN) Red List of Threatened Species is the most authoritative and comprehensive source of information to monitor species' extinction risk and a central tool for guiding biodiversity conservation and sustainable development (Betts et al., 2020). More than 150,000 species have been categorized on the IUCN Red List and over 42,000 of them are threatened with extinction (IUCN, 2022). On the list, species are placed in different extinction risk categories. The categories are based on 5 quantitative criteria that measure specific symptoms, such as small population size, population declines, and restricted ranges. Each species assessment description is accompanied by required documentation, such as a geographic range map and a list of threats to species (IUCN, 2013). The IUCN Red List influences global conservation planning and spending (Betts et al., 2020; Rodrigues et al., 2006) and is used to measure the progress of international strategic plans and agreements (Brooks et al., 2016; Mace et al., 2018) and the potential biodiversity impact of development projects (Bennun et al., 2018). Thus, it is crucial that IUCN monitor all drivers of extinction consistently and comprehensively.

Climate change is a major threat to biodiversity (Armstrong McKay et al., 2022; Bellard et al., 2012; Kemp et al., 2022; Urban, 2015), the impact of which could surpass that of land-use change over the coming decades (Di Marco et al., 2019; Newbold, 2018). Numerous species and systems have already been affected by climate change (Parmesan & Yohe, 2003). In fact, certain traits, such as low reproductive rates, low dispersal ability, or diet specialization, are expected to increase species' extinction risk because they hinder the ability of species to cope with rapidly changing climatic conditions (Foden et al., 2013; Pacifici et al., 2017; Santini et al., 2016). When this is the case, species might contract their range due to the loss of climatically suitable areas (Pacifici et al., 2020), causing a reduction in population size that can lead to a species qualifying as threatened (IUCN Standards & Petitions Committee, 2022).

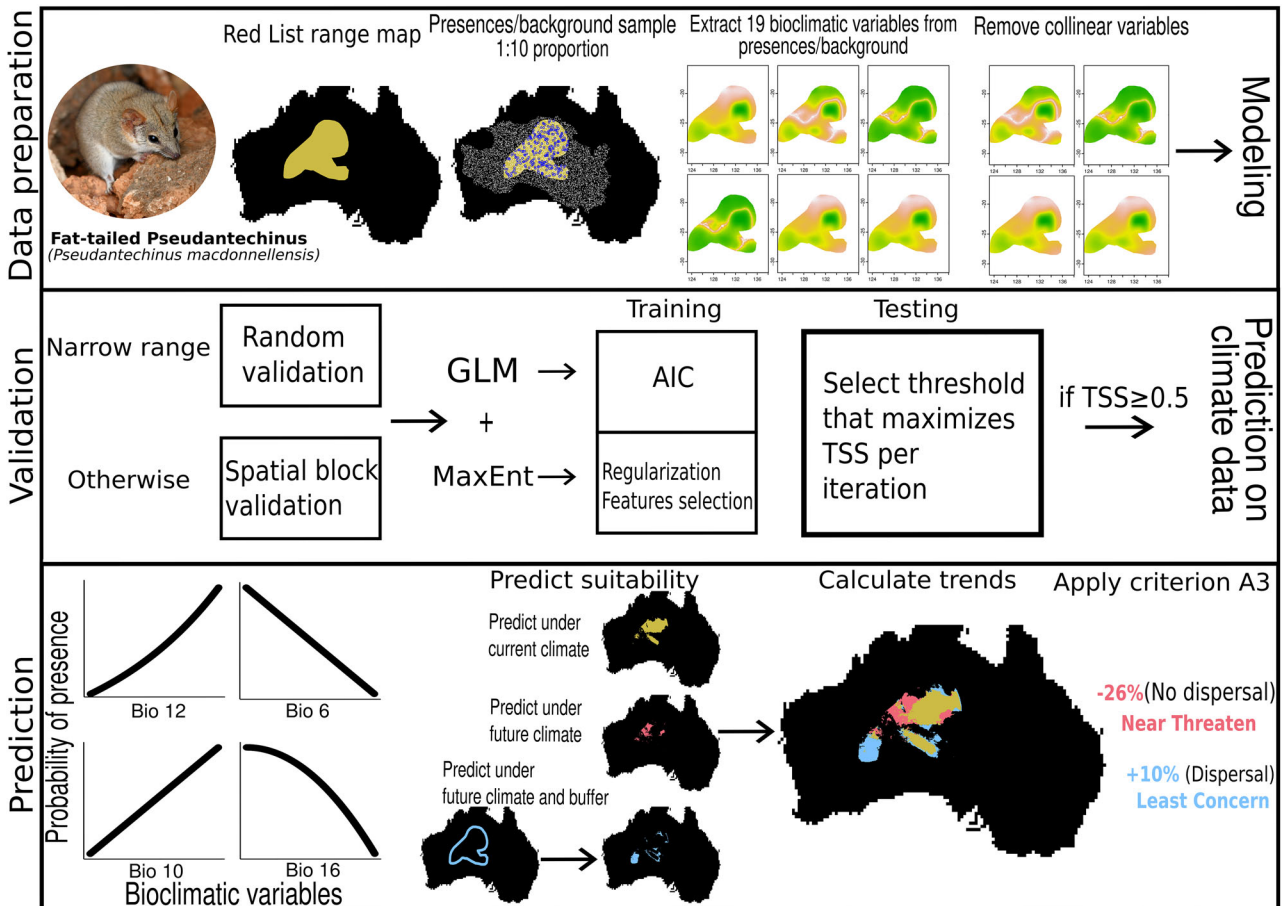
Despite the recent, and projected, acceleration of climate change globally, the use of climate projections to quantify population trends for application of IUCN Red List criteria remains difficult and limited to a minority of species. Similarly, the percentage of species for which climate change is documented as a threat, based on the IUCN Red List Threats Classification Scheme, differs among taxa: 30% for threatened and near-threatened birds compared with 11% for reptiles (IUCN, 2022). The IUCN Red List Threats Classification Scheme is applied separate from the red-list criteria. Thus, such differences do not necessarily imply that climate change was considered differently in the application of the criteria. However, they may suggest differences in expert knowledge of groups. For example, reptiles are expected to be particularly sensitive to climate change due to high dependency on temperature for activity and reproduction and low-range shifting ability (Thurman et al., 2020). Projections of changes in species distribution obtained from species distribution models, including those determined by climate, can

be used to infer “population reduction” under red-list criterion A or “continuing decline” under criteria B or C2 (respectively, decline in species extent of occurrence or area of occupancy and small population size) (IUCN Standards & Petitions Committee, 2022). Although best practices for developing such models have been proposed (e.g., Araujo et al., 2019), data preparation, modeling approaches, and parameter settings still vary substantially across authors, hampering modeling output reliability and comparability (Santini et al., 2021). Additionally, occurrence data needed to build species distribution models are not evenly available across taxonomic groups (e.g., Global Biodiversity Information Facility points) (Troudet et al., 2017). The lack of standardization of species distribution modeling techniques comes from multiple sources, such as the use of background versus pseudoabsence sampling, uneven data availability, and reporting of model uncertainty. All these factors can affect red-list assessments when distribution models are used to assess the impact of climate change (see section 12.1.12 “Using Bioclimate Models” in IUCN Standards & Petitions Committee [2022]). Moreover, the development of such models requires advanced technical skills that assessors might not possess and might not have access to when performing red-list assessments (e.g., during thematic workshops). This generates an implementation gap between the volume of data and modeling approaches available and their application into the red-listing process (Cazalis et al., 2022). Therefore, a standard framework that produces ready-to-use estimates of species' symptoms that assessors can modify based on species-specific information could be of great value in reducing this gap.

We devised a method for estimating climate change impact for use in red-list assessments across taxonomic groups. The method is meant to support the work of assessors by providing information on climate change impact in terms of change in habitat quality in a way that complies with the IUCN Red List guidelines. Although to evaluate a large number of species we had to make some assumptions that differ from what is specified by these guidelines, our approach is theoretically simple to understand and easy to customize to incorporate relevant ecological knowledge of the species by red-list assessors. Specifically, our aim was to inform the application of criterion A3 to future population declines, although our framework can be adapted for application to criterion A4 on past and future population declines.

## METHODS

We developed a method to estimate change in future habitat quality due to climate change (Figure 1) and tested it on 1493 nonvolant tetrapod species (amphibians, reptiles, and nonvolant mammals) with available estimates of generation length, reproductive traits, and geographic distribution. We used 2 of the most commonly applied species distribution modeling algorithms, generalized linear model (GLM) and MaxEnt, to predict the potential future distribution of each of these species from



**FIGURE 1** Modeling steps taken to fit and project the species distribution models and to apply International Union for Conservation of Nature Red List criterion A3. The steps are the same for each global circulation model and representative concentration pathway. The fat-tailed pseudantechinus (*Pseudantechinus macdonnellensis*) is shown as an example (photo by loz88woz licensed under <http://creativecommons.org/licenses/by-nc/4.0/>; photo modified for graphical purposes).

bioclimatic variables. We ran our models under 2 representative concentration pathways (RCPs) (4.5 and 8.5) and 4 different global circulation models (GCMs) (ACCESS1-3, CESM1-BGC, CMCC-CM, and MIROC5). We also considered 2 alternative dispersal scenarios, one in which species could not disperse outside their currently suitable area (no-dispersal scenario) and one in which species were able to disperse to newly suitable areas in their geographic range and in species-specific areas around that geographic range (here after buffer area) (maximum dispersal scenario). Overall, we fit 32 models per species (2 algorithms  $\times$  2 RCPs  $\times$  4 GCMs  $\times$  2 dispersal scenarios). We used our predictions to assess species red-list categories based on criterion A3. We also estimated uncertainty in categories based on the above combination of fitted models.

### Selection of species and distribution data

We focused on terrestrial nonvolant tetrapods with relatively available data and varying degrees of climate sensitivity according to the current IUCN Red List database. Nonvolant tetrapods represent a good study case because they have a large

number of species for our purposes and sufficient data; there are published assumptions related to dispersal (Newbold, 2018); and they include species for which criterion A is relatively less applied (i.e., amphibians and reptiles). From all species with available distribution ranges in the IUCN Red List spatial data repository ( $n = 22,710$ ), we excluded all species categorized as data deficient, extinct in the wild, or extinct on the IUCN Red List (excluding 3654 species). We then selected species with available information on generation length, age at first reproduction, and dispersal to predict future climate risk. Due to lack of dispersal data for amphibians and reptiles, we also included all the species with available reproductive or generation length data but with no data on dispersal based on the assumption of a fixed dispersal rate per year (see below) (1659 species: 491 amphibians, 1065 mammals, and 103 reptiles). We excluded all species with a range size of  $<250 \text{ km}^2$  (excluding 166 species) because the resolution we used to retrieve climate data from the species' ranges was too coarse to assess those species (see below). Our final sample included 1493 species (413 amphibians, 1005 mammals, and 75 reptiles).

To ensure equal data availability across all species, we generated species occurrences from species' geographic range

polygons (Hof et al., 2018; Newbold, 2018; Newbold et al., 2020; Visconti et al., 2016). Although range maps were too coarse to capture the influence of small-scale factors, for a large number of species, they offered a sufficient approximation to estimate the species climatic niche at global scale (Visconti et al., 2016). Although such an approach would not be acceptable for official IUCN Red List assessments, which require actual species' presence points, we chose this approach so our analyses would be comparable across species because databases of species occurrence points are inherently biased toward popular and well-studied taxa (Meyer et al., 2016; Troudet et al., 2017). Our purpose here was to provide a representation of species distributions, which one can derive for any species with a spatial distribution polygon provided in the IUCN Red List. We converted the range vector polygons into rasters of 0.049° resolution (~5 km at the equator), matched the resolution of the bioclimatic rasters (see below), and extracted each grid cell's centroid as an occurrence point. We assumed each cell was occupied by the species (Hof et al., 2018; Newbold, 2018; Newbold et al., 2020; Visconti et al., 2016). We then generated a set of background and pseudoabsences for each species that was used in turn to run the algorithms (background points for MaxEnt and background and pseudoabsences for GLM [see below]). We randomly sampled the background points in the ecoregions (Olson et al., 2001) where the species' ranges occurred. We sampled pseudoabsences by selecting points outside the species range and in the same biogeographical realm (from Olson et al. [2001]) with the decay function of Hof et al. (2018):

$$P_{\text{sampling}} = \frac{1}{\text{distance from range}^2}, \quad (1)$$

which exponentially decreases the probability of sampling a point as the distance from the range boundary grows. This approach favors the contrast of presence areas with unoccupied areas that can be reached by the species, in contrast to areas that are unlikely to be colonized in the short term, remaining in the biogeographic realm domain. We set a maximum number of 10,000 pseudoabsence and background points to be sampled. We then extracted the values of the bioclimatic variables from each background and pseudoabsence point for 2022 and for the future based on 10 years or 3 times generation length of the species. We used the presence (1) and pseudoabsence or background (0) status as a binary response variable for our models.

### Selection of bioclimatic variables

We selected primary climatic variables (mean precipitation, minimum temperature, maximum temperature) from CHELSA database (Karger et al., 2020) for each month from 2013 to 2100. The CHELSA database provided monthly rasters of primary climatic variables calculated using 4 different GCMs (ACCESS1-3, CESM1-BGC, CMCC-CM, MIROC5) under 2 different RCPs (4.5 and 8.5) in a WGS84 geographic coordinate system with a spatial resolution of 0.049° (~5 km at the

equator). We used these primary variables to calculate 19 bioclimatic variables (Appendix S1) for each year (2013–2100). Bioclimatic variables should be selected based on the biology of the species to avoid including spurious correlates (Fourcade et al., 2018; Santini et al., 2021; Synes & Osborne, 2011). However, to demonstrate the application of our framework on a large number of species, we used the same set of standard bioclimatic variables across all because we did not have access to species-specific expertise for all 1493 species. We represented the climatic condition experienced by each species in a given year by averaging the annual bioclimatic variables of the 10 previous years (Lucas et al., 2023 [preprint]). We extracted the values of the bioclimatic variables from each presence and background or pseudoabsence point for the present (year 2022) and for the future based on 10 years or 3 times generation length of the species (whichever was longer, as per criterion A3). Our aim was to demonstrate the application of a standardized climate risk assessment in IUCN Red List assessments across many species. To do so, we extracted climate variables from within the entire species' ranges despite IUCN Red List guidelines suggesting use of a filter based on habitat variables. Such an approach would likely have reduced the generalizability of our framework (e.g., land-use preferences are available for only some groups [Powers & Jetz, 2019]).

### Species distribution modeling

We ran species distribution models with 2 different algorithms: GLM and MaxEnt (Phillips & Dudík, 2008). These 2 algorithms are widely used in species distribution modeling because they have consistently good performance relative to other available models (Elith et al., 2006; Santini et al., 2021; Wisz et al., 2008). Moreover, for climate change analysis, it is advisable to use models that reduce overfitting; thus, we used these algorithms over other more complex machine learning approaches (Merow et al., 2014). We used the same methodological framework for both algorithms (Figure 1). We excluded collinear variables among the present bioclimatic variables (year 2022) with a variance inflation factor (VIF) >3 (Figure 1, data preparation). We repeated the VIF calculation and excluded 1 variable at a time (that with highest VIF) until none of the variables exceeded the threshold (Santini et al., 2021). We followed previous work that showed the GLM and MaxEnt perform better when the proportion of background points is higher than the number of presences (Santini et al., 2021). Therefore, we set a 1:10 proportion for presences:background. For the GLM, we weighted the response variable by assigning a different weight to the presences and the background so that the sum of their weights was equal. We also included second-order polynomial features to consider nonlinear relationships between the predictors and the response variable. We applied the Akaike information criterion to select the best model. For MaxEnt, we also included linear and quadratic features and we scaled the regularization function iteratively by 0.5, 1, 2, and 10 to calibrate the model (Radosavljevic & Anderson, 2014).

We performed a spatial block validation to evaluate model performance (Figure 1). We divided the sampled data set into blocks with 1° sides (~111-km side at the Equator) and systematically aggregated blocks into 5 groups (Roberts et al., 2017). We iteratively ran our algorithms on a training set consisting of all data in 4 of the groups, leaving 1 group out for validation. We then validated the GLM and MaxEnt models on a test set based on the data from the remaining group. This procedure was not applicable to species with a narrow range (e.g., because most points were included in a single block), and we proceeded with a random 5-fold cross-validation in that case. To make predicted probabilities binary (presence or absence), we selected the probability threshold that maximized the true skill statistic (TSS) (Allouche et al., 2006).

Finally, we fitted the models on the full data set. For GLM and MaxEnt, we ran the model selection as we did for the validation. Then, we predicted species climatic suitability for the present (year 2022) and for the future based on the generation length of the species for each GCM and RCP. We used the averaged thresholds resulting from the spatial 5-block validation or the 5-fold cross-validation to make the predicted probabilities binary (1, presence; 0, absence). As a sensitivity test, we also repeated GLM with pseudoabsences rather than background points to evaluate the difference in predictions between 2 alternative sampling strategies (both adopted for GLMs) (Santini et al., 2021).

## Scenarios of climate adaptability via dispersal

We measured the current versus future species bioclimatic range size under 2 alternative assumptions of species' adaptability to climate change (Figure 1, prediction). First, we calculated the proportional change in bioclimatic range between the present (2022) and the future without considering dispersal, which complies with the strictest definition of climate change exposure as the difference between present and future climatic conditions in the species' range (Foden et al., 2019). We considered only the areas classified as suitable in the current species' range and measured the proportion of such areas that were retained or lost in the future. In this case, we assumed that the currently suitable areas could be lost to climate change and that new areas (currently unsuitable) could not be colonized within the time frame of IUCN Red List assessments (i.e., 10 years or 3 generations, whichever is longest, see below). In other words, the species could only retain its current distribution or lose part of it in the short term (no-dispersal scenario).

We then calculated the proportional change in species ranges between the present (2022) and the future under the assumption that species can disperse toward newly suitable areas in their existing range and in a buffer around that range (maximum dispersal scenario). We selected 3 species traits to calculate the buffer for species: generation length, dispersal distance, and age at first reproduction. We retrieved generation length data from IUCN Red List (IUCN, 2022) and other traits from public databases: COMBINE (Soria et al., 2021) for mammals, Lucas et al. (2023 [preprint]) for amphibians, and Etard et al. (2020)

for reptiles. We used the age at first reproduction in combination with dispersal to determine the maximum distance that a species can disperse within a single generation (Bateman et al., 2013; Pacifici et al., 2020; Schloss et al., 2012). We used generation length to represent the time horizon of climatic projection and population trend, which is in line with the IUCN Red List guidelines for examining change in the course of "three generations or 10 years, whichever is the longest." We then assumed that species can expand their range by up to 1 dispersal buffer for each reproduction event:

$$\text{buffer} = \frac{\max(10 \text{ years}, 3 \text{ generation length})}{\text{age at first reproduction}} \times \text{dispersal}. \quad (2)$$

For this scenario, we calculated the proportional range change as the difference between total suitable area in the future (in the range and in the buffer) and suitable area in the present, divided by the latter. This way we accounted for originally suitable areas and newly suitable areas (i.e., area gained). Due to the lack of reproductive and dispersal data for amphibians and reptiles, we assumed a 0.5-km dispersal distance per year for both groups (Newbold, 2018) and used it as a buffer around the species' range. Generation length is also available for a few amphibian species. We excluded all amphibians with body mass >4 kg or no data on body mass, and for the remaining sample, we assumed a 3 times generation length of 10 years if the species had no data on generation length.

These 2 dispersal scenarios are extreme and unrealistic, although similar to those applied in previous assessments (Thuiller et al., 2019). One is based on the assumption of no range shift and the other on the assumption of maximum dispersal potential. We considered these scenarios plausible boundaries (minimum and maximum) around habitat loss predictions.

We explored the relative influence of species' dispersal distance, generation length, and range size on the predicted habitat change. We expect species characterized by short dispersal, long generation times, and small geographic ranges (generally narrow niche) to be those with the highest proportional habitat loss. Conversely, we expected species with small ranges, short generations, and long dispersal to potentially exhibit the highest habitat gain.

## Application of IUCN Red List criterion A3

We used estimates of species climate risk to apply criterion A3c, which is based on "population (size) reduction projected, inferred or suspected to be met in the future (up to a maximum of 100 years)" based on subcriterion c that refers to "a decline in area of occupancy (AOO), extent of occurrence (EOO) and/or habitat quality" (IUCN Standards & Petitions Committee, 2022) (Figure 1). We assumed a linear relationship between habitat loss and population decline (IUCN Standards & Petitions Committee, 2022). Although this relationship is not always true, in absence of species-specific information it is an allowable assumption (IUCN Standards & Petitions Committee,

2022). We did not have this information for all 1493 species; thus, we used the same assumption for the entire sample to ensure the consistency of the approach among all species. For example, a species' habitat change of  $-30\%$  corresponded to a  $30\%$  decline in population size in our analyses; this is the threshold to trigger the vulnerable category under criterion A3. Because there is no quantitative threshold for near threatened category, we assumed habitat losses of  $20\text{--}30\%$  represented near threatened category because this is close to the  $30\%$  threshold for vulnerable under criterion A3. For 14 reptile species, the 3-generation period used to apply criterion A3 exceeded the time range of climatic data available until 2100 (see above). For these species, we assigned a category based on a linear extrapolation (IUCN Standards & Petitions Committee, 2022). This is based on the assumption that a species lost the same amount of habitat every year from the year until we had data (year 2100) to the end of the 3-generation period, based on the habitat reduction rate (or habitat expansion rate for the dispersal scenario) calculated from the present (2022) to 2100. Therefore, if a species with a 30-year generation length had its habitat reduced by  $30\%$  over 78 years (i.e., from 2022 to 2100), we assumed it would lose an additional  $\sim 0.4\%$  area every year until the end of the 3-generation period (90 years), up to a maximum of 100 years.

To ease visualization and interpretation of the results, we averaged the proportion of bioclimatic range change between the 2 algorithms (GLM and MaxEnt), the 2 RCPs, and the 4 GCMs. This resulted in separate estimates of habitat change (and category) for each dispersal scenario, provided that the TSS of the 2 algorithms was  $>0.5$ . If only 1 of the algorithms had a TSS  $>0.5$ , we used only that as our prediction. We used only predictions based on background sampling to ensure comparability among the results. We also reported prediction uncertainty for each species (min and max estimates of risk across all 32 prediction settings). We then produced a scatterplot of the averaged prediction for dispersal and no-dispersal scenarios for GLM to test the difference between predictions based on background and pseudoabsence sampling.

All spatial analyses were performed in GRASS GIS 7.8.6 (GRASS Development Team, 2020), and all statistical analyses were performed in R 4.2.1 (R Core Team, 2022) with RStudio 2022.2.0.443 (RStudio Team, 2022) and the following packages: caret (Kuhn, 2022), data.table (Dowle & Srinivasan, 2021), ggbreak (Xu et al., 2021), MASS (Venables & Ripley, 2002), maxnet (Phillips, 2021), patchwork (Pedersen, 2022), raster (Hijmans, 2022), scales (Wickham & Seidel, 2022), tidyverse (Wickham et al., 2019), and usdm (Naimi et al., 2014).

## RESULTS

### Climate change impact assessment

Both modeling algorithms had acceptable performance on average across all GCMs and RCPs. The average TSS for the GLM was 0.56 (SD 0.22), and the average TSS for Maxent was 0.57 (SD 0.22). For 989 species out of 1493 analyzed (322 amphibians, 613 mammals, and 54 reptiles;  $66\%$  of the total), the average TSS for the GLM or the average TSS for Maxent was

$>0.5$ , and it was possible to make a prediction. Therefore, all analyses were based on this subset of species. A table of all predictions for each GCM, RCP, algorithm, and dispersal settings is in Appendix S9.

When combining all predictions to define an average value of habitat change for each species, more species were at risk compared with any single combination of RCPs, GCMs, and algorithms. In the no-dispersal scenario, 155 species were predicted to lose  $20\text{--}30\%$  of habitat ( $82\text{--}120$  species for individual combinations of models and scenarios [Appendix S9]). Further, 144 species were predicted to lose more than  $30\%$  of habitat (Figure 2) ( $99\text{--}201$  species for individual combinations of models and scenarios [Appendix S9]). In the dispersal scenario, 18 species were predicted to lose  $20\text{--}30\%$  of habitat ( $23\text{--}35$  species according to different combinations of models and scenarios [Appendix S9]), and 16 species were predicted to lose  $30\%$  or more of their habitat ( $25\text{--}72$  species for individual combinations of models and scenarios [Appendix S9]). Overall, 282 species out of 989 (125 amphibians, 143 mammals, and 14 reptiles) were predicted to reduce their habitat in the dispersal and the no-dispersal scenarios (Figure 2) ( $225\text{--}291$  species for individual combinations of models and scenarios [Appendix S9]). Conversely, 707 species were predicted to gain habitat under the dispersal scenario (Figure 2) ( $599\text{--}685$  species for individual combinations of models and scenarios [Appendix S9]). A sensitivity test with GLM using pseudoabsences showed qualitatively similar results but a generally higher contraction of habitat, especially in the no-dispersal scenario (Appendix S2).

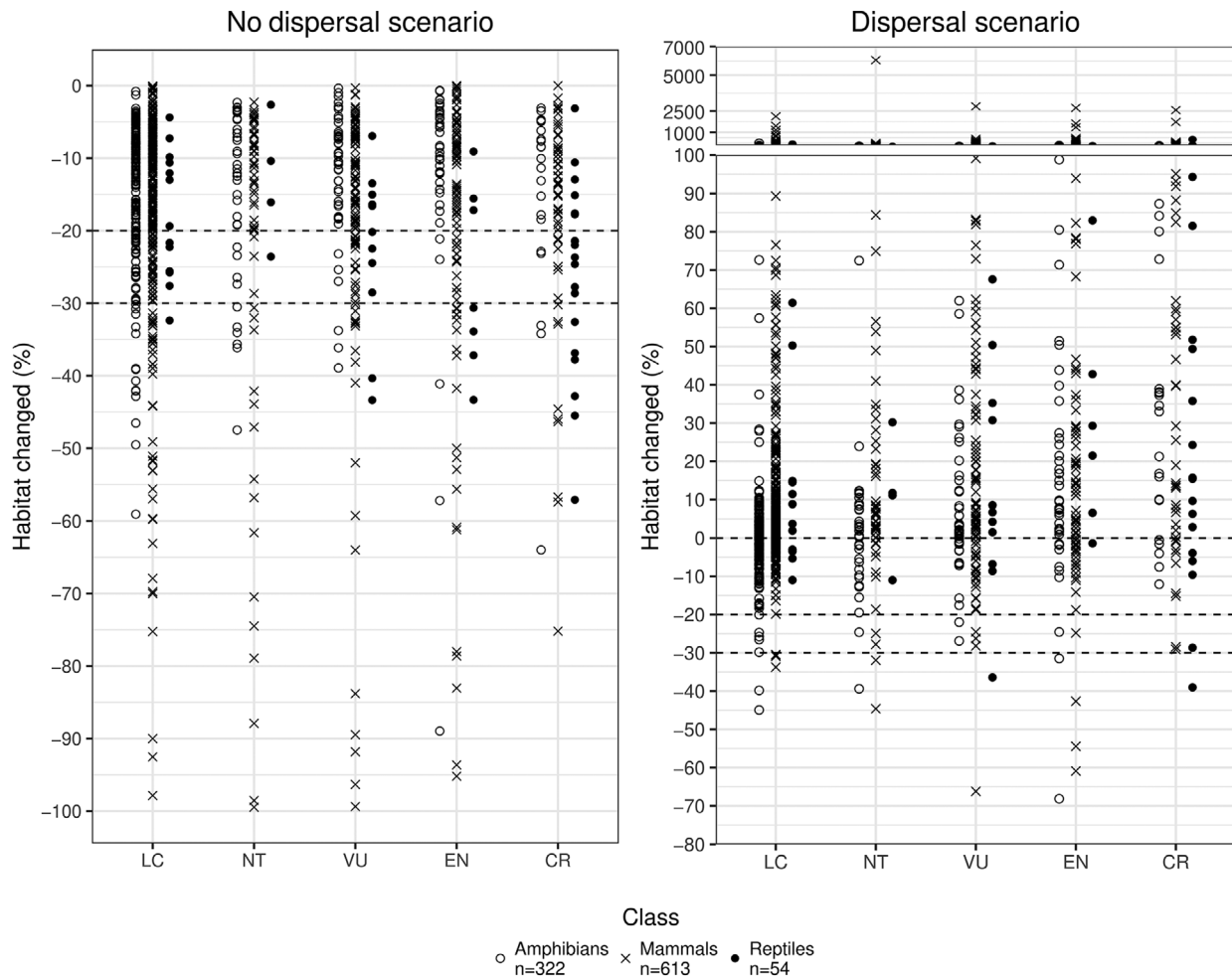
### Application of criterion A3

Overall, 171 species ( $17\%$  out of 989 retained) were predicted to have their category worsen in the no-dispersal scenario, the dispersal scenario, or both scenarios based on criterion A3 ( $116\text{--}185$  species for individual combinations of models and scenarios [Appendices S3 & S5]). Among them, 138 are currently classified as least concern, 21 as near threatened, 8 as vulnerable, and 4 as endangered (Figure 3). Climate change was only documented as a relevant threat for 23 of these species ( $\sim 13\%$ ) in the IUCN Threats Classification Scheme.

For 168 species in our sample, red-list assessors documented climate change as a threat in their application of the IUCN Threats Classification Scheme (Figure 4). For the majority of these ( $n = 167$ ), our analysis predicted the category least concern under criterion A3 in the dispersal scenario. This is not necessarily inconsistent (threats can be documented in the classification scheme as locally affecting least concern species), but nonetheless a surprising mismatch.

### Relative influence of species and range characteristics on impact assessment

Predicted habitat loss was affected by several species' biological traits (Figure 5; Appendices S4–S8). Species with long generation length and large dispersal exhibited large habitat change proportions (habitat gained) in the dispersal scenario



**FIGURE 2** Average habitat change for amphibian, mammal, and reptile species based on future climate change impact relative to International Union for Conservation of Nature (IUCN) status and whether dispersal is possible or not by (dashed lines, thresholds that trigger a category of near threatened [considered 20% decline in this study] or vulnerable [30% decline] under IUCN criterion A3; LC, least concern; NT, near threatened; VU, vulnerable; EN, endangered; CR, critically endangered).

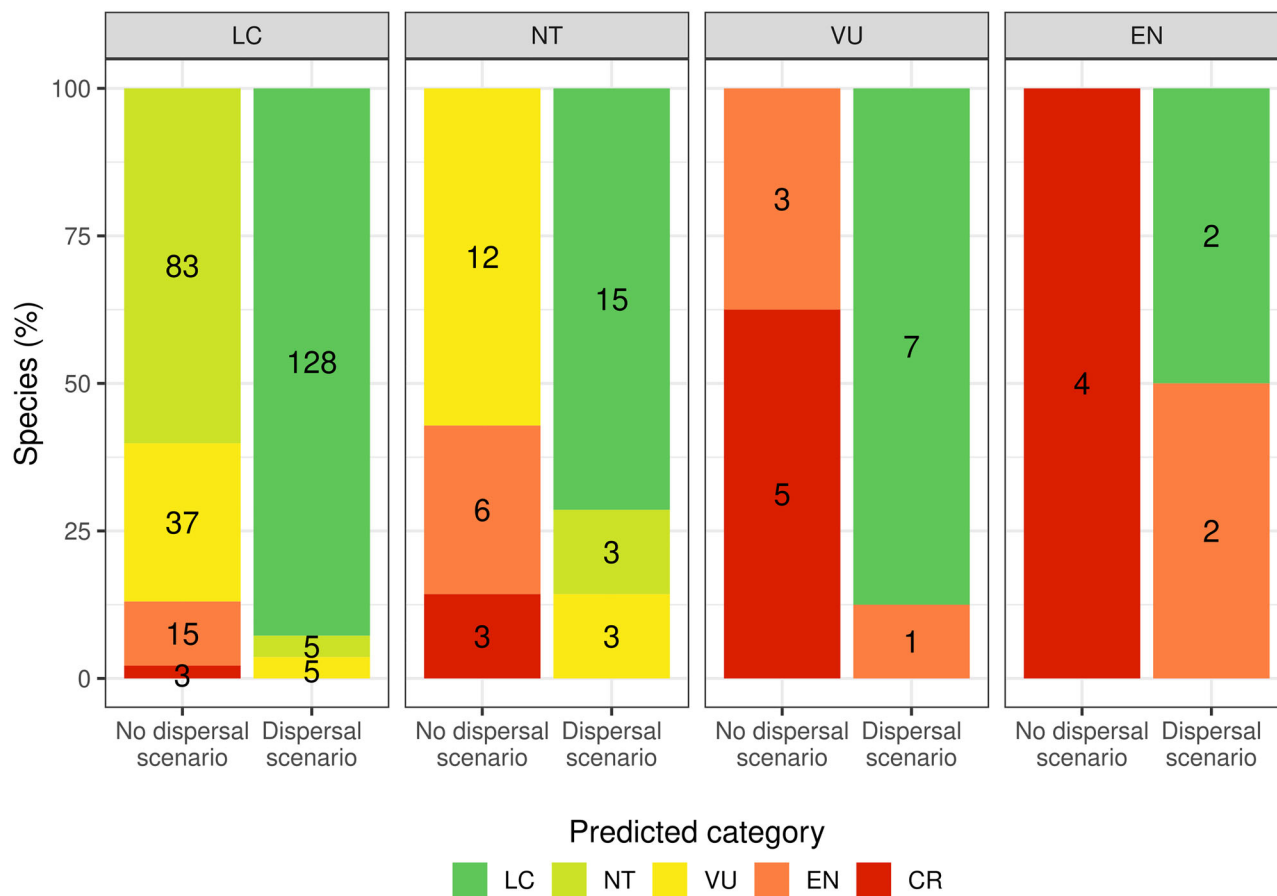
(Appendix S5), whereas short-generation-length and short-dispersal species did not show considerable habitat changes (values around 0) (Figure 5a). Species with small range size and long generation length lost the most habitat (Figure 5b). Species with large dispersal and small range gained the most habitat (Figure 5c). Short-generation-length and short-dispersal species with small range size had the lowest percentage of habitat changes (Appendix S5). With the no-dispersal scenario, species with long generation length had the most habitat contraction (Appendices S4 & S6), whereas species with large range size and short generation length had the least habitat contraction (approximately -0.2 to 0 [Appendix S8]). Slow-reproducing species had the most habitat contraction in the no-dispersal scenario (Appendix S7).

## DISCUSSION

Our results showed that our framework can be used to estimate the impact of climate change on species under different mod-

eling approaches, climate adaptability scenarios, and emission scenarios. This can be adapted to provide a widely applicable framework for assessors to use species distribution modeling outputs in a formal red-list assessment. Although we conducted a generic test with a large number of species, actual red-list assessments must use actual species occurrence points as presences (instead of points randomly sampled across the species range as we did) and species-specific information to select predictor variables (IUCN Standards & Petitions Committee, 2022).

We predicted that most species will not lose a major portion of habitat due to climate change in the next 10 years or 3 generations, yet multiple species may lose more than 30% of their habitat and could therefore be classified as threatened under criterion A3. The species predicted to lose more habitat due to climate change often did not have climate change documented as a threat in the IUCN Threats Classification Scheme, and several of the species with climate change documented as a threat had limited predicted exposure. Inconsistent identification of threats to species might result in climate change being under-



**FIGURE 3** Amphibian, mammal, and reptile species predicted to have their International Union for Conservation of Nature Red List category worsen based on averaged climate change impact under no-dispersal and dispersal scenarios (current category, above bars; predicted category, colors; numbers in bars, absolute number of species in each predicted category; categories defined in Figure 2's legend).

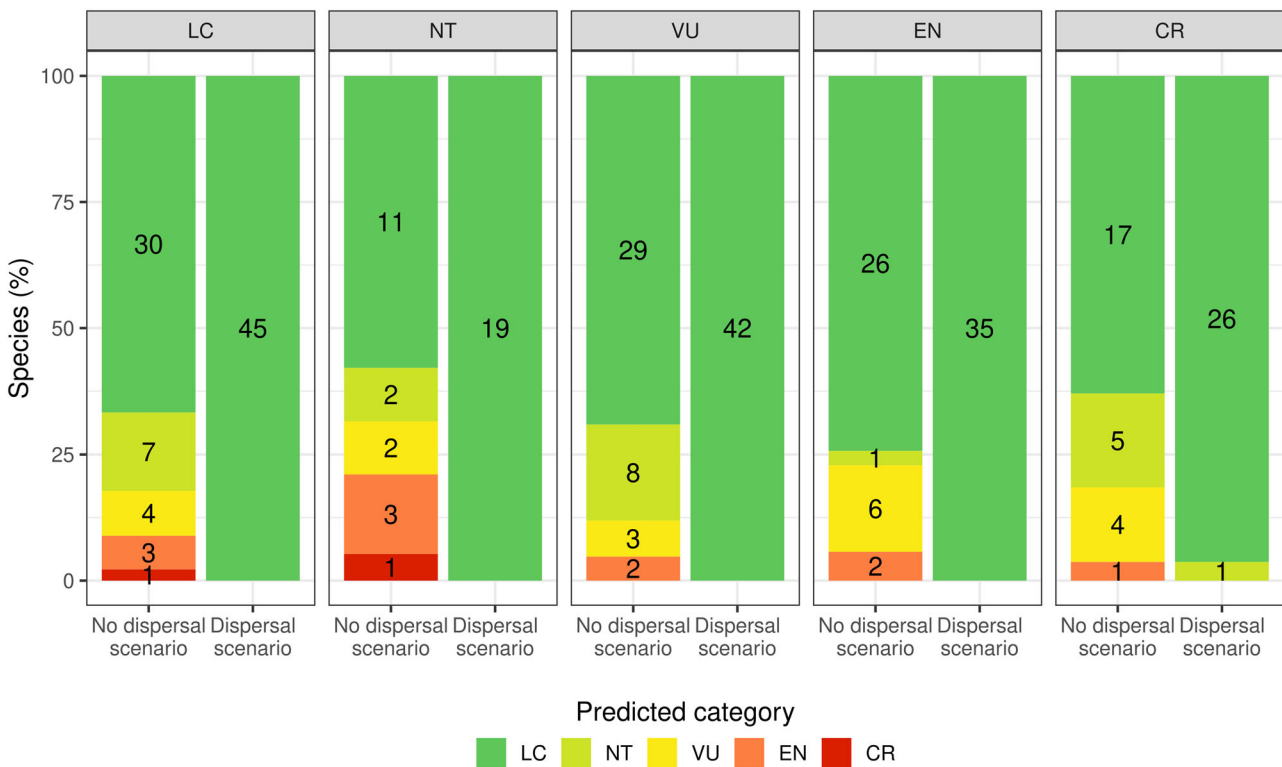
documented, and not listed for species potentially facing high climatic vulnerability. However, we did not provide a full evaluation of vulnerability, and it is possible that species facing high climate exposure have low climate sensitivity and do not have climate listed as a threat for legitimate reasons. Expert assessment is therefore key in evaluating our results in the broader red-list context. We also found small-ranged, long-generation, and short-dispersal species were predicted to lose the most habitat.

Among the 989 species in our final subset, 171 (13%) may qualify for uplisting under criterion A3 based on predictions of habitat reduction due to future climate change; 159 of these may qualify for uplisting from least concern or near threatened to threatened. Although these results do not represent actual red-list assessments, they can be combined with assessors' knowledge of species biology and threats. For example, the blue ridge dusky salamander (*Desmognathus orestes*) is currently least concern, and climate change was not listed as a threat in the last assessment. However, our model predicted that it might lose habitat in both averaged adaptability scenarios (20% under the dispersal scenario and 30% under no-dispersal scenario), and it may thus qualify for vulnerable under criterion A3 if assessors consider it unlikely to disperse in currently

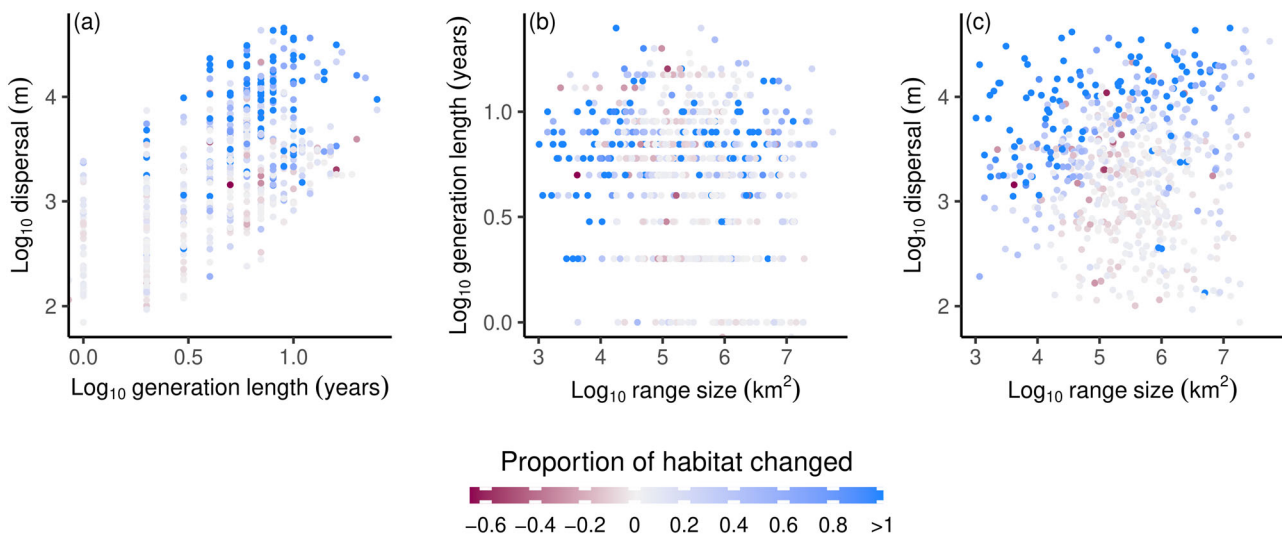
unoccupied sites, based on their knowledge on the species and region. Our method also provides important information on many species predicted to lose a relatively small proportion of habitat, which can be combined with information on the effects of other threats. For example, we predicted that the red-eyed green treefrog (*Litoria chloris*), a least concern Australian amphibian, may lose 2–8% of its habitat. This is insufficient to reassess the species as threatened under criterion A3, but it has lost habitat in the range due to megafires that recently burned western Australia (Ward et al., 2020). Such a threat might lead to declines that can add to, or even exacerbate, declines induced by climate change (Di Marco et al., 2019; Guo et al., 2018; Jetz et al., 2007). Thus, our method might help in the categorization of many species facing climate change and land-use change (e.g., mammals [Baisero et al., 2020]) or climate change and disease (e.g., amphibians and chytridiomycosis [Sopniewski et al., 2022]).

For most of the species, we predicted a possible expansion of habitat when the potential adaptive capacity of the species to track climate was considered (dispersal scenario). A predicted positive effect of climate change does not imply species will be moved to a lower risk category. In case of contrasting categories, the guidelines clarify that the highest category is retained (IUCN





**FIGURE 4** Predicted category of amphibian, mammal, and reptile species currently with climate change documented as a threat in application of the of the International Union for Conservation of Nature Threats Classification Scheme based on averaged climate change impact under no-dispersal and dispersal scenarios (current category, above bars; predicted category, colors; numbers in bars, absolute number of species in each predicted category; categories defined in Figure 2's legend).



**FIGURE 5** Relationship between habitat change and species' traits for the dispersal scenarios (species traits  $\log_{10}$  transformed) (values  $>1$  were aggregated).

Standard & Petition Committee, 2022). Species with limited dispersal were more prone to proportional habitat contraction, consistent with studies that showed the dispersal capacity of species is an important feature for predicting future impact of climate change (Pacifi et al., 2015; Santini et al., 2016, 2017). This result is critical for many amphibians because this group

generally lacks adaptive capacity due to their short dispersal ability (Smith & Green, 2005).

Predictions of new habitat do not mean the species will be able to disperse to these areas. For example, we predicted the long-eared hedgehog (*Hemiechinus auritus*), currently classified as least concern, would lose 24% of its habitat in the no-dispersal

scenario and gain 26% under the dispersal scenario. Red-list assessors, with their knowledge of the species, the region where it occurs, and the threats it faces, should be able to evaluate the real accessibility of dispersal areas to the species, depending on the habitat, population conditions, and tolerance. Species with highly specific habitat requirements and sensitivity to fragmentation may be unable to colonize new areas outside their current range. In this case, assessors may rely on the more precautionary prediction (no-dispersal scenario). For example, assessors may combine species land-use preferences with the climate suitability maps produced using our framework (Figure 1) to exclude areas predicted to be climatically suitable but not accessible to the species (Visconti et al., 2016). This way they could better estimate population change from change in available habitat. In our analyses, for simplicity, we assumed that any range loss is equivalent over the entire species range, but an expert of the species would know whether losing a portion of the range in a certain area (e.g., north of the range) would be more severe than losing the same portion in another area (e.g., south of the range). If red-list assessors apply our framework, they can estimate the population loss nonlinearly based on the spatial distribution of where the habitat is predicted to be lost and where it is predicted to increase.

Overall, species with slow reproductive cycles and small ranges were predicted to lose relatively more habitat, supporting the importance of range size in assessing species' extinction risk (Böhm et al., 2016; Lucas et al., 2019, 2023 [preprint]). We were not able to evaluate the impact of climate change on very range-restricted species because the resolution of the bioclimatic raster we used to extract climate information was too coarse (5 km at the equator) and because we included species with available traits, which are less threatened (Gonzalez-Suarez et al., 2012). Most likely narrow-range and less-studied species will be the most affected by climate change. However, narrow-range species can be evaluated based on other criteria, such as criterion B, which addresses restricted geographic range, and criteria C and D, which address small population size. Most likely those species are already considered threatened under these criteria. Additionally, our approach might overestimate the risk for those species. They will likely be species with major habitat gain in the dispersal scenario. In fact, availability of new habitat was higher when range was small and dispersal was large. Our results are consistent with results from previous comparative extinction risk analyses (Cardillo et al., 2005; Purvis et al., 2000) in that species with slow reproduction cycles were generally more threatened. This suggests that the application of criterion A3 based on climate change information may be particularly relevant for long-generation species. These species are expected to be more sensitive to climate change (Pacifiçi et al., 2015; Pacifiçi et al., 2017).

One of the difficulties of predicting the impact of climate change for assessors is the uncertainty of climate predictions (Murphy et al., 2004). To address this, we considered the uncertainty of the predictions providing a range of results based on RCPs, GCMs, and algorithms (Appendix S9). Incorporating uncertainty in climate models through different global emissions scenarios and multiple statistical models is critical to

having a range of plausible predictions (Thuiller et al., 2019). The predictive ability of species distribution models is low on average (Santini et al., 2021). Thus, examining different predictions, instead of a single prediction, helps one cope with their high variability (Araújo & New, 2007). Another difficulty stems from the potential to underestimate risk from climate change in the future dispersal scenario associated with consideration of species adaptive capacity. The measure of dispersal we used may exceed the actual ability of a species to disperse.

Cazalis et al. (2022) highlighted a major gap between methods used to address extinction risk and their effective use by the red-list assessors that is associated primarily with poor communication between researchers and practitioners. For example, the methods proposed by researchers, usually a category-predictive framework based on a set of biological or environmental variables (Darrah et al., 2017; de Oliveira Caetano et al., 2022), do not align with the assessors' need for methods that explicitly address the parameters used to apply red-list criteria (e.g., population trends). These methods might also fail to extrapolate predictions to newly assessed species (Di Marco, 2022). Our method provides a protocol for estimating species population trends that can be adapted for use in red-list assessments based on criterion A3 and can guide the measure of climate change impact. This may help address the uneven distribution of IUCN climate change assessments and provide a helpful tool with which to evaluate taxa less adaptive to changes in climatic conditions (e.g., herptiles [Bickford et al., 2010; Winter et al., 2016]). Moreover, our framework can be implemented in an interactive platform (e.g., ShinyApp [Bachman et al., 2020]) that can be easily accessed by all assessors. Although this framework is not strictly compliant with the IUCN Red List guidelines, it can be easily adapted for use in formal assessments. Assessors can use actual species occurrence points, rather than ranges, as presence points and their knowledge to identify important climatic variables for the species assessed and species' dispersal ability.

Our framework is a compromise between the needs of red-list assessors and the complexity of species distribution modeling, and its results should be used in combination with other information on species biology and threats. Our method is not as complex as others (e.g., machine learning), and the output it provides is a range of potential extremes in habitat loss and gain. However, our framework is easy to understand and is based on well-established methods. Even though our application of the framework does not fully align with IUCN Red List guidelines (i.e., selection of species occurrences, selection of explanatory variables, and use of land-use data [see "Methods"]), it can be adapted to assessors' needs and potentially applied directly in formal extinction risk assessments. However, the framework is not exempt from future challenges. For example, uncertainty in the dispersal scenario may be reduced with new estimates of the variables we used to define the dispersion buffer of the species: species dispersal ability, generation length, and maturity (especially for herptiles). Similarly, the climate variables we used were the only high-resolution monthly projections available. If new data become available, they should be used in the framework. Because our framework was conceptualized to

help assessors, if IUCN Red List guidelines change, the framework would need modification as well. Moreover, as a result of the application of this framework, nongenuine changes in red-list categories could be generated (see section 2.2.1 “Transfer between Categories” in IUCN Red List guidelines [IUCN Standards & Petitions Committee, 2022]), which we did not originally consider. If assessors identify a more appropriate category based on information provided by our framework, an additional future challenge is to determine whether the species was already threatened by climate change before the assessment.

The IUCN Red List is severely underfunded (Juffe-Bignoli et al., 2016; Rondinini et al., 2014), despite its crucial role in biodiversity conservation (Betts et al., 2020). Thus, low-budget solutions to improve accuracy of assessments are needed. Our method provides a standardized way to estimate future climate change impacts that can be adapted for use in red-list assessments. Assessors can use such estimates to consider the single effect of climate change or the combined effects of climate change and other threats to provide a comprehensive overview of the extinction risk of the species.

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## SUPPORTING INFORMATION

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