High-resolution modelling of biodiversity under the shared socio-economic scenarios

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Abstract

Impacts on biodiversity from global climate and land use change manifest through changes in habitat availability and suitability for species. We currently lack fine grain predictions about how species and their habitats respond at the local level to global drivers of change, particularly under future scenarios of coupled climate and land use change. Policies for biodiversity management often place an emphasis on management and protection of threatened and socially important species and their habitat. This requires modelling many species individually to inform national policy design and decisions. However, most multi-species modelling systems focus on the role of bioclimatic drivers of species distribution and abundance to the exclusion of the land use variables needed to understand and predict outcomes of socio-economic drivers of biodiversity change. We provide high-quality predictive species distribution models that capture the impacts of change in land use and other environmental drivers, and a comprehensive biodiversity dataset for Australia for thousands of species at high spatial resolution. We model the response of 1,488 species, including 592 birds, 254 mammals and 642 reptiles under coupled land-use (Shared Socioeconomic Pathways) and climate (Representative Concentration Pathways) scenarios. Our analyses present new possibilities for developing bespoke species-specific models when analysing many species at large spatial scales, that combine disciplinary ideas from data-science, high performance computing and species distribution modelling. Our assessment provides a new understanding of how projected socio-economic and climate scenarios play out for biodiversity.

Introduction

Scenarios and model predictions are useful for helping map pathways and shape policy. Making robust predictions of biodiversity response to climate and land use, drivers that operate at the global scale yet their impacts manifest at the local/regional scale, is a step towards developing realistic strategies for achieving national targets such as the 30 by 30 target of the Global Biodiversity Framework (GBF)[1]. Though many studies map global pathways to achieving GBF targets[2–4], they fail to inform decisions at the national scale. This is because these analyses do not comprehensively capture the biodiversity of any specific country, nor do they provide a nuanced understanding of the local level dynamics and impacts of drivers of change on biodiversity. We need nationally relevant analyses that consider scenarios and constraints suited to the national context to inform policy decisions and articulate the trade-offs of competing environmental or biodiversity targets[5].

The Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) recognises the need to understand biodiversity impacts under future environmental and anthropogenic conditions[6]. Governments are developing national plans to align with internationally agreed sustainability goals and biodiversity targets and the private sector's appetite to integrate biodiversity impacts into project design is growing[7,8]. However, biodiversity detail in current approaches for mapping or evaluating policy or planning pathways are either taxonomically incomplete or overlook local-level dynamics in biodiversity impacts. State and regional policies for biodiversity management often emphasise management and protection of individual, threatened or locally significant, species and their habitats. As such, species are a critically important attribute for conservation planning but very few continental or global-scale analyses model individual species responses to future scenarios[9,10]. We need better approaches to (i) accurately assess individual species' outcomes under future change scenarios and (ii) aggregate predicted outcomes for many species into indices of biodiversity change to enable more reliable guidance for national and continental scale environmental policy design and evaluation.

Most national-scale biodiversity assessments for Australia model aggregated biodiversity, e.g. dissimilarity, richness, or mean species abundance[11,12]. Top-down approaches that rely on modelling macro-ecological relationships between the whole of biodiversity and land use/climate cannot reveal individual species responses, their vulnerability to changing conditions or the predicted future spatial distribution of their habitats. Few studies have evaluated spatial biodiversity patterns under coupled global climate and land use change scenarios for large numbers of species using species distribution models that explicitly models individual species responses to individual climate and land use change variables[13–15]. The absence of species-level (bottom up *sensu*[16]) model inference in national or continental analyses of biodiversity change under land use futures limits our ability to understand species-level response to new and emerging drivers of change, to infer which elements of biodiversity are declining or improving, or to identify the winners and losers and future land use and climate scenarios. Ignoring the intimate link between land use change and species response downplays the influence of a direct driver of biodiversity change, both for habitat and species persistence. It also hampers the kind of understanding and communication of change that most people can connect with, which tends to individual species or ecosystem-level connections[17].

Scenario analyses that describe future outcomes for biodiversity based on shared socio-economic pathways (SSP)[18] often model biodiversity at the global scale using proxies[19], coarse range maps for species[20] or macro-ecological models such as PREDICTS that rely on correlations between land use and biodiversity intactness[14,21]. In Australia, where significant effort has been made to develop biodiversity data repositories for use in conservation planning and climate change impact analysis at the state and federal levels, a high spatial resolution and taxonomically rich analysis of biodiversity under SSP scenarios is currently lacking. Building a picture of biodiversity outcomes under coupled climate and land use change scenarios from the bottom up, starting with species and aggregating to biodiversity, should arguably provide a more accurate and interrogable picture of future biodiversity trends because individual species responses to environmental change is accommodated, rather than assuming all elements of biodiversity will respond in approximately similar ways to environmental change.

Individual species responses to environmental change can be modelled using species distribution models (SDMs) to assess likely habitats and for use within conservation decision making[22,23]. Using SDMs within scenario modelling requires high resolution spatial information on the environment and biodiversity. With the aid of cutting-edge, high-performance computing and data storage solutions, we conduct a comprehensive national scale biodiversity assessment for Australia under global climate and land use change projections, for a suite of coupled Shared Socioeconomic Pathways (SSPs) and Representative Concentration Pathways (RCPs), focussing on outcomes for species. We model current and future predicted distributions of 1,488 species at a high spatial resolution (250m) to help tease apart individual species response and whole-of-biodiversity outcomes under the scenarios. Our assessment encompasses all known, recorded and valid species of birds, mammals and reptiles for Australia. We highlight differential response across scenarios and taxonomic groups as well as emphasize the likely impacts for threatened species. Furthermore, the SDMs developed are operationalised for reproducibility and computational efficiency with respect to data and compute requirements. We provide our high-quality, open-source biodiversity modelling workflow and comprehensive data to allow users to model many species at once and at high spatial resolution to represent whole-of-biodiversity outcomes of scenarios and policies.

Results

Mean relative likelihood of occurrence for the current time step (2020) for each taxonomic group and across all species for the entire study region highlights clear geographic variation in biodiversity patterns across Australia (Figure 1). Areas of high mean relative likelihood of occurrence are concentrated primarily along the east coast with additional pockets around Perth and Darwin for birds and mammals, with a stronger coastal preference for mammals. Reptile species have approximately equivalent preferences for arid and semi-arid areas as they do for coastal areas. All three taxa groups have a very high mean likelihood of occurrence values for Tasmania.

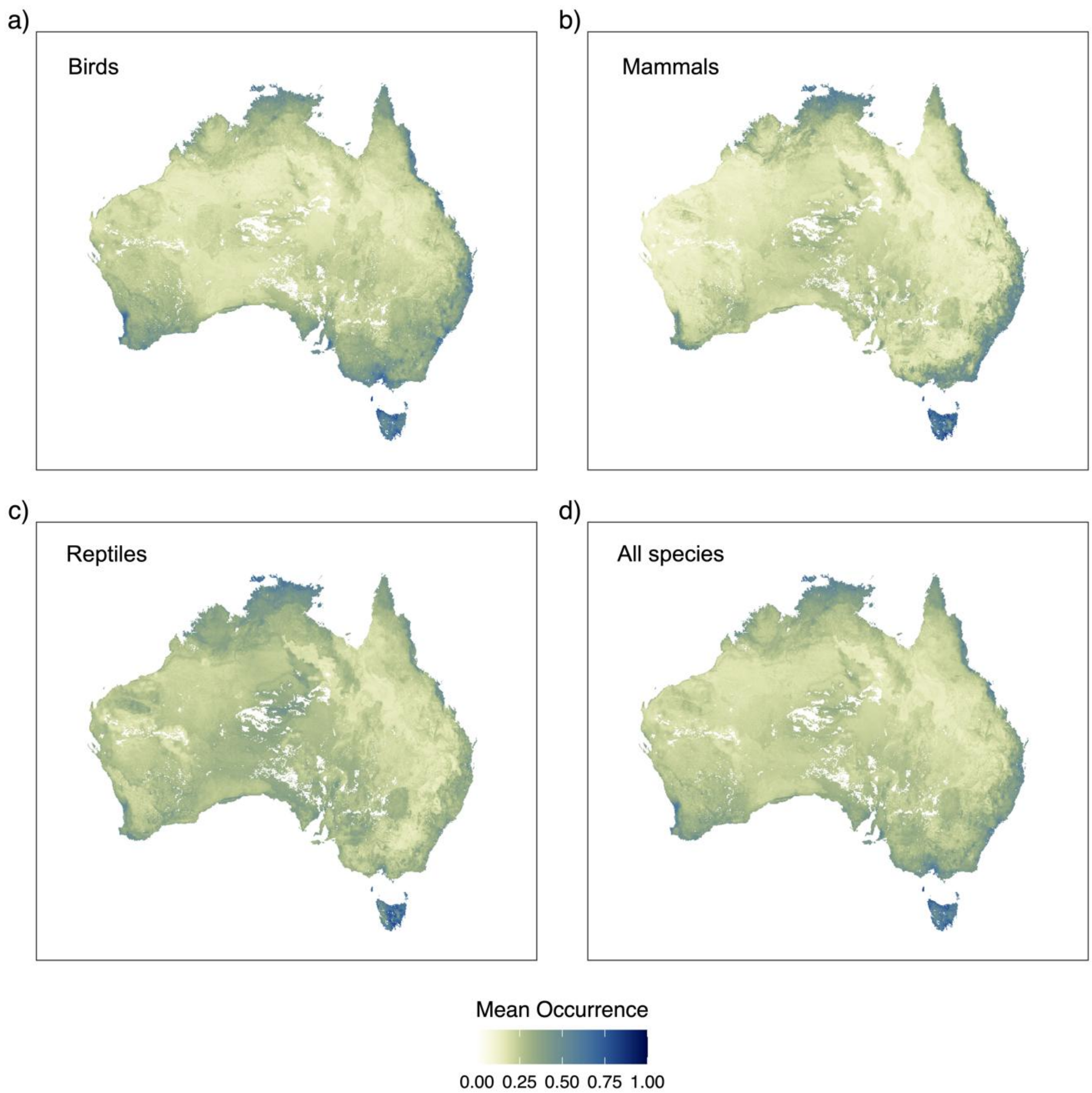

Figure 1: Mean relative likelihood of occurrences for each taxonomic group, including a) birds, b) mammals, c) reptiles and d) all species for the current time period. d) Performance metric summaries (additional metrics provided in the supplementary information).

Model performance is typically high across most species. Mean Boyce Index (BI) values across all species, taxa groups and EPBC listed species is greater than 0.8 indicating good model performance overall (Figure 2, extended data Table E2.1). Only 5.8% of the models (n = 86 including 5 birds, 21 mammals and 60 reptiles) performed poorly with a BI value equal to or less than 0.5 (Table E2.2). Notably, birds performed consistently well: 99% of species with BI values greater than 0.5. 99% of the models (n = 1472) had an AUC value greater than 0.7. 16 out of the 201 EPBC listed species models had a BI value of less than 0.5. Model outputs from the three GCMs exhibit similar predicted patterns (Figures E2.1 a-c), though the projected values vary (Figure E2.1 d-f). A similar trend was observed when comparing individual GCM projections to the averaged projections from all three models (Figures E2.1 g-h). This variation reflects model uncertainty in future climate projections.

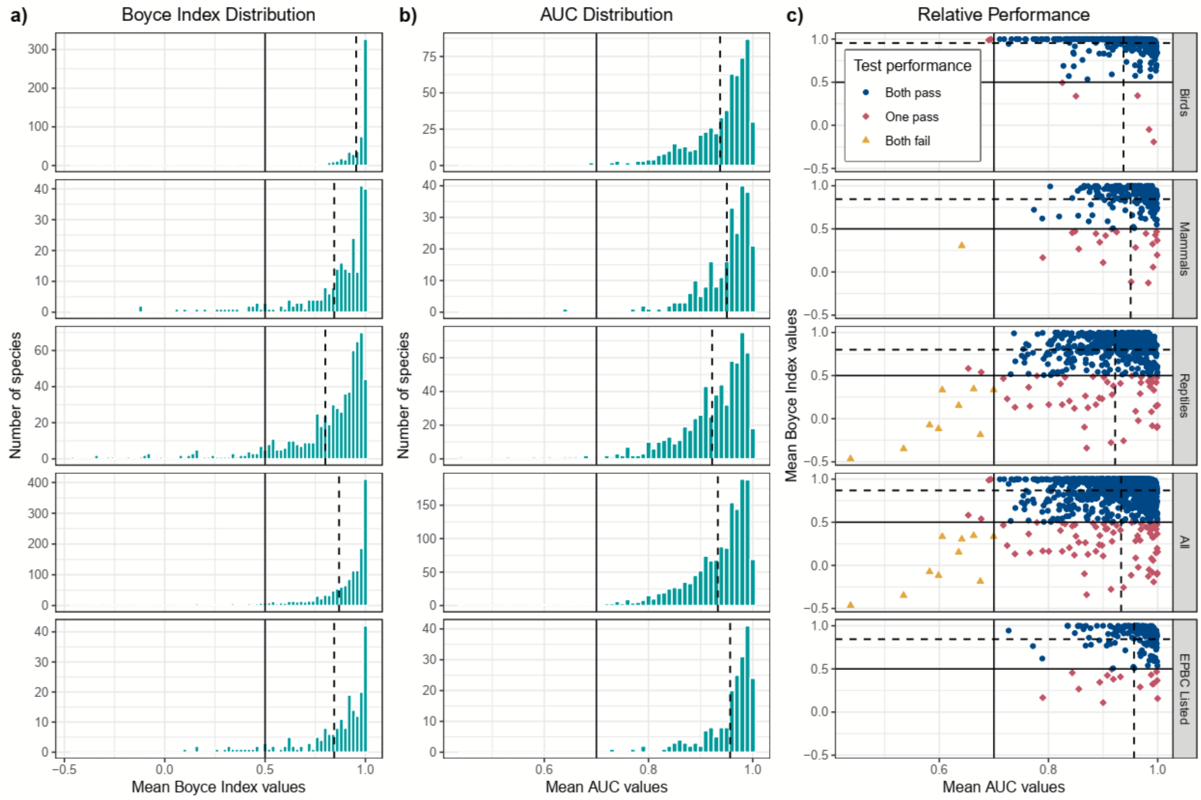

Figure 2: Distribution plots of model performance metrics (a) Boyce Index (BI) and (b) the Area Under the Curve (AUC) across species for birds, mammals, reptiles, all species, and for EPBC listed species (indicated in rows). Dotted lines are mean performance values and solid lines indicate the 0.5 and 0.7 minimum thresholds for good model performance for BI and AUC, respectively. The scatter plots (c) indicate overall performance showing that very few models performed poorly with respect to both metrics examined here.

Predictions under each coupled land use and climate scenarios (SSP-RCPs) for 2030, 2050 and 2070 show spatial patterns of increase or decrease in habitat suitability across the landscape and we can explore these variations for individual species (Figure 3) and across taxon groups (Figures 4, 5, extended data Figure E2.2). For instance, some species showed divergent responses under alternate climate and land-use scenarios. The mean relative likelihood of occurrence of the green ringtail possum (*Pseudochirops archeri*) declined under all future scenarios, but declines were most severe for SSP5 (Figure 3a). By contrast, the spotted-tailed quoll (*Dasyurus maculatus*) showed both increases and decreases in the relative likelihood of occurrence across its range under the future scenarios modelled (Figure 3b). Most species in our analysis, on average, are expected to decline in both mean relative likelihood of occurrence and range extent under all SSPs (Figure 6).

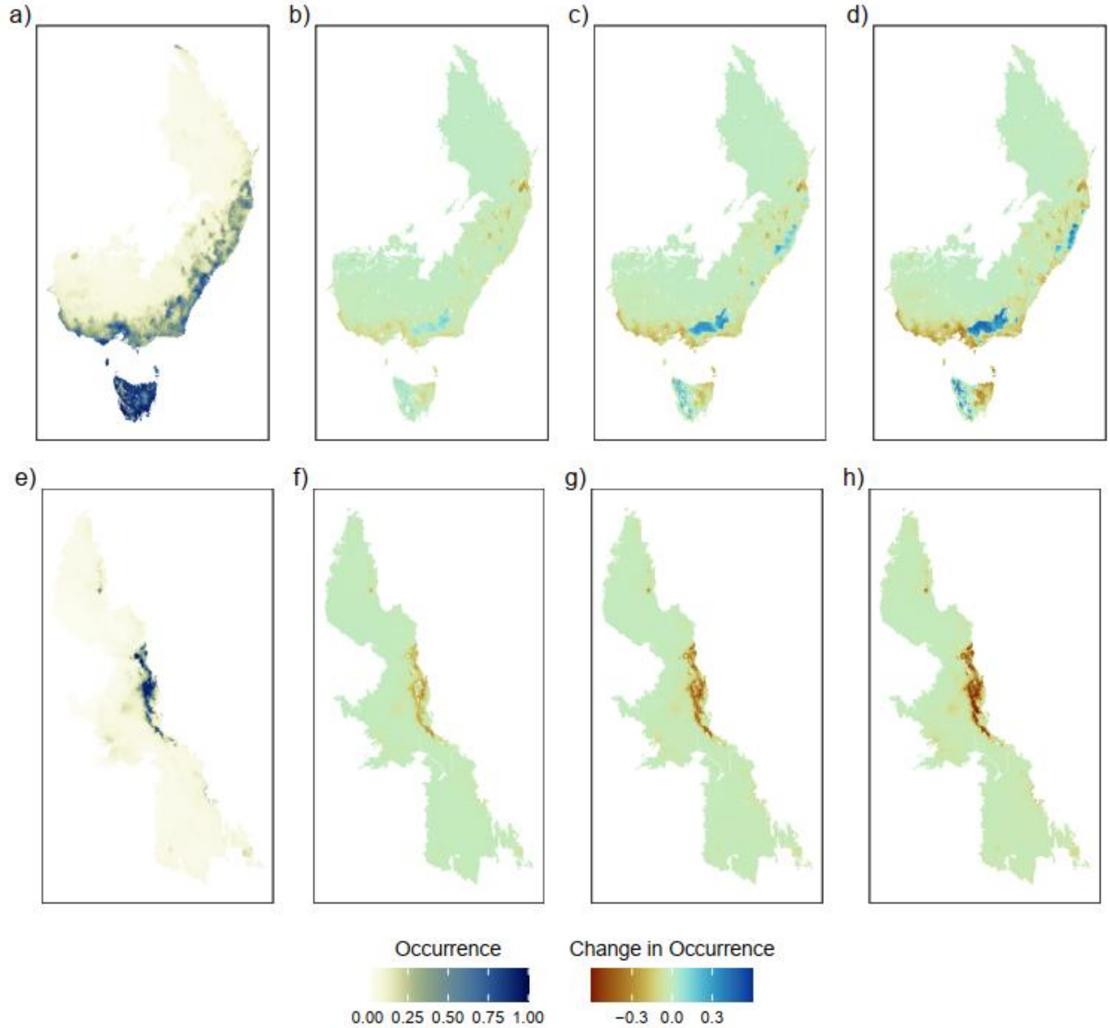

Figure 3: The current estimated relative likelihood of occurrence (a) and expected change in relative likelihood of occurrence under the SSP 5 - RCP 8.5 climate scenario in the years b) 2030, c) 2050 and d) 2070 for the spot-tailed quoll (Dasyurus maculatus), and the current estimated relative likelihood of occurrence (e) and expected change in relative likelihood of occurrence under the SSP5 (RCP 8.5) climate scenario in the years f) 2030, g) 2050 and h) 2070 for the green ringtail possum (Pseudochirops archeri).

When looking across taxonomic groups in their entirety, we found that on average the relative likelihood of occurrence of all species declined under the future scenarios, and these declines were most severe for SSP 5 - RCP 8.5(Figure 4). Across the species in our study, at least 75% are predicted to decline in their average likelihood of occurrence by 2070 under the SSP 5 -

RCP 8.5 scenario (Figure 4). On average, the relative likelihood of occurrence for all taxon groups in our study is expected to decline by 5-10% by 2070 under SSP 5 - RCP 8.5 (Figure 4). However, these declines were not ubiquitous across Australia. Rather, declines in the relative likelihood of occurrence for all species were centred in central Australia in the arid and semi-arid regions, as well as localised declines in western Tasmania, mountain regions of far-north Queensland and parts of coastal Western Australia (Figure 5g,i). By contrast, our models predict increases in the mean relative likelihood of occurrence of all taxa in the eastern foothills and coast of south-eastern Australia, especially under the most severe future scenarios (SSP 5 - RCP 8.5) (Figure 5g,h). More specifically, locations with the highest richness of species expected to decline under SSP 5 - RCP 8.5 were in southern Queensland and the western Australian coast (Figure 5i). Most of the high elevation parts of Australia's eastern coast also had >100 species expected to decline (Figure 5i). Locations with the highest richness of species expected to increase under SSP 5 - RCP 8.5 were on the eastern coast of Australia, as well as central Victoria (Figure 5h).

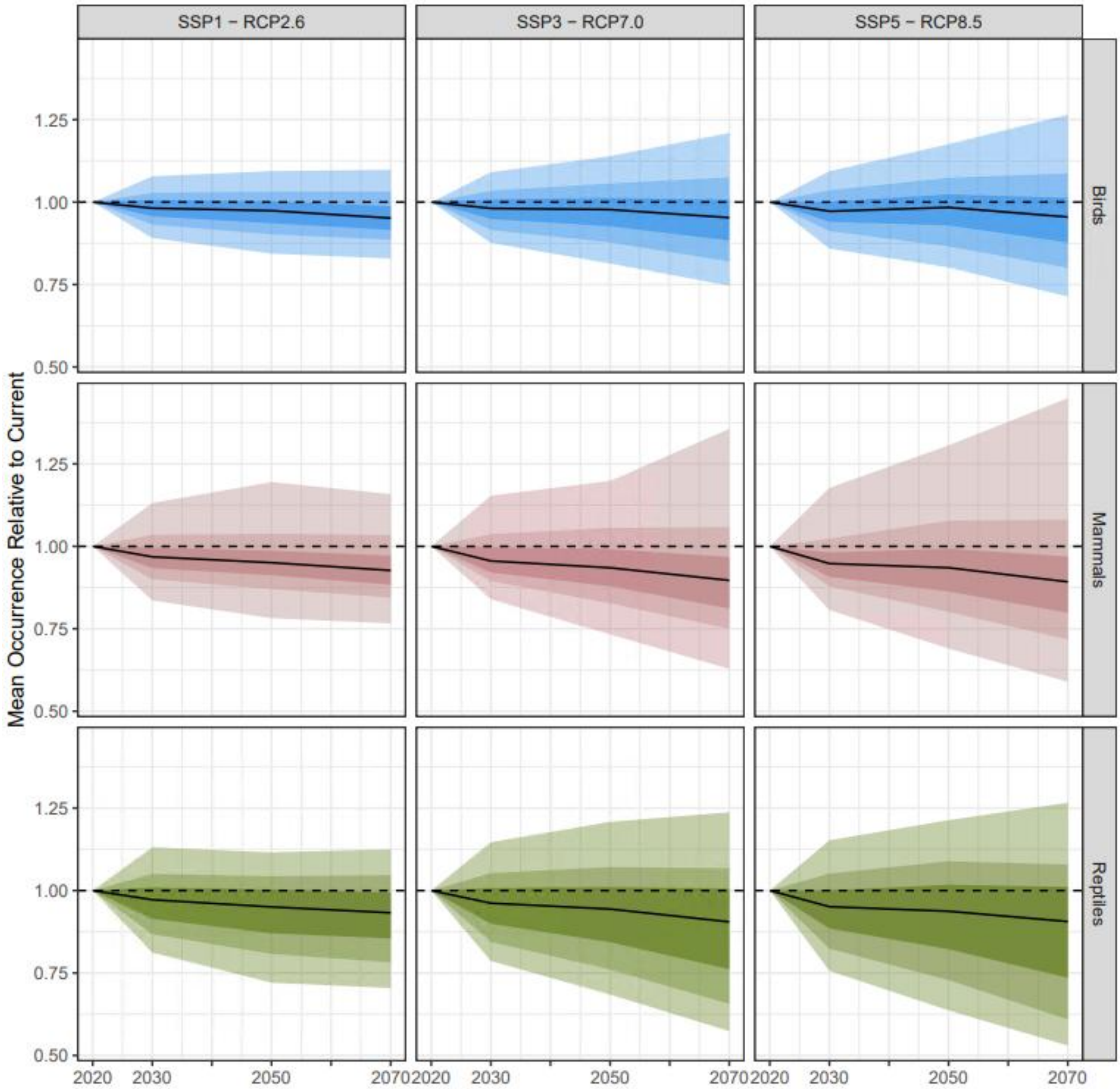

Figure 4: Change in the relative likelihood of occurrence for each taxonomic group in 2030, 2050 and 2070 compared to current time step (2020) under each SSP scenario. Dotted line indicates no change and the solid black line indicates the median change in the likelihood of occurrence for each taxonomic group under each scenario and the ribbons indicate the 50%, 75% and 90% quantiles of individual species trajectories under averaged projections from the three GCMs.

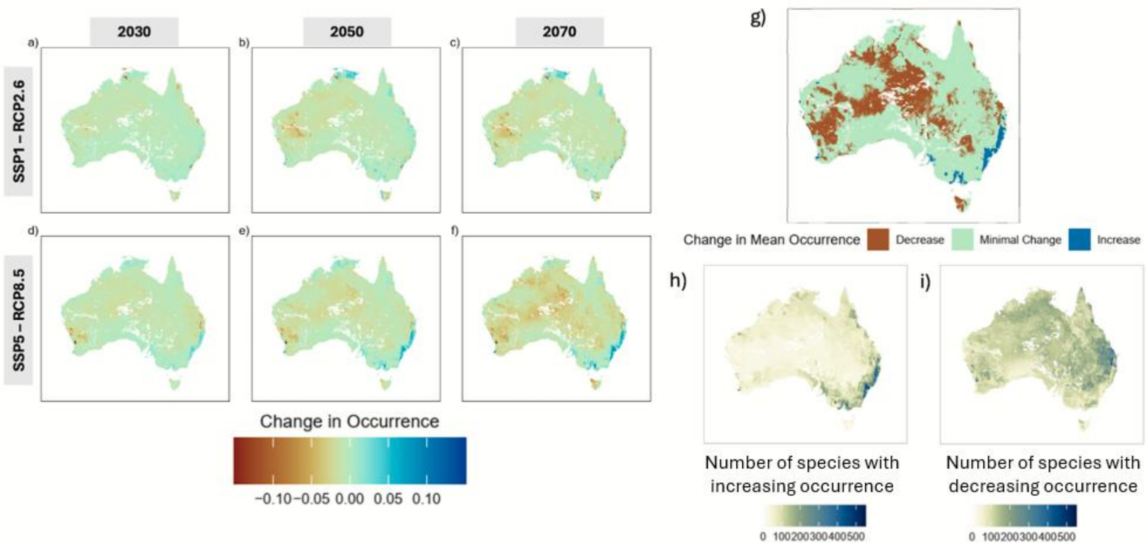

Figure 5: Projections under the RCP-SSP scenarios for all species showing (a) change in mean relative likelihood of occurrence in 2030, 2050 and 2070) relative to mean relative likelihood of occurrence in 2020 for SSP1 - RCP2.5 (a-c) and for SSP5-RCP8.5 (d-f). Predicted increase versus decrease and areas of minimal change in the mean relative likelihood of occurrence under the RCP8.5-SSP5 scenario (g). Number of species with a predicted increase in relative likelihood of occurrence under the RCP8.5-SSP5 scenario (h). Number of species with a predicted decrease in relative likelihood of occurrence under the RCP8.5-SSP5 scenario (i). Projections for SSP3 can be seen in supplementary Figure E2.2.

We also related the change in habitat suitability and extent of suitable habitat across taxonomic groups to identify types of biodiversity response under future scenarios. As expected, most species show decreased habitat suitability and range contraction while some show increase in habitat suitability and range (Figure 6b). Examples of species showing range contraction despite increased habitat suitability and vice versa were few (e.g. *Amaurornis cinerea* and *Motacilla tschutschensis*). Under SSP 5 - RCP 8.5, 39 species are predicted to experience range declines by between 30-50% (consistent with a vulnerable EPBC listing), 26 species between 50-80% (consistent with an endangered EPBC listing) and three species, including the green ringtail possum (*Pseudochirops archeri*) and chameleon gecko (*Carphodactylus laevis*) by >80% (consistent with a critically endangered EPBC listing, Figure 6b). When looking at EPBC listed species, we find that the impacts on certain species under SSP 5 - RCP 8.5 in 2070 are likely to be severe. For example, the Adelaide pygmy blue-tongue skink (*Tiliqua adelaidensis*), northern greater glider (*Petaurus minor*) and lesser sooty owl (*Tyto multipunctata*) are all predicted to have a reduction in their range (number of pixels >0.05) of at least 70% under SSP 5 - RCP 8.5 (Figure 6b).

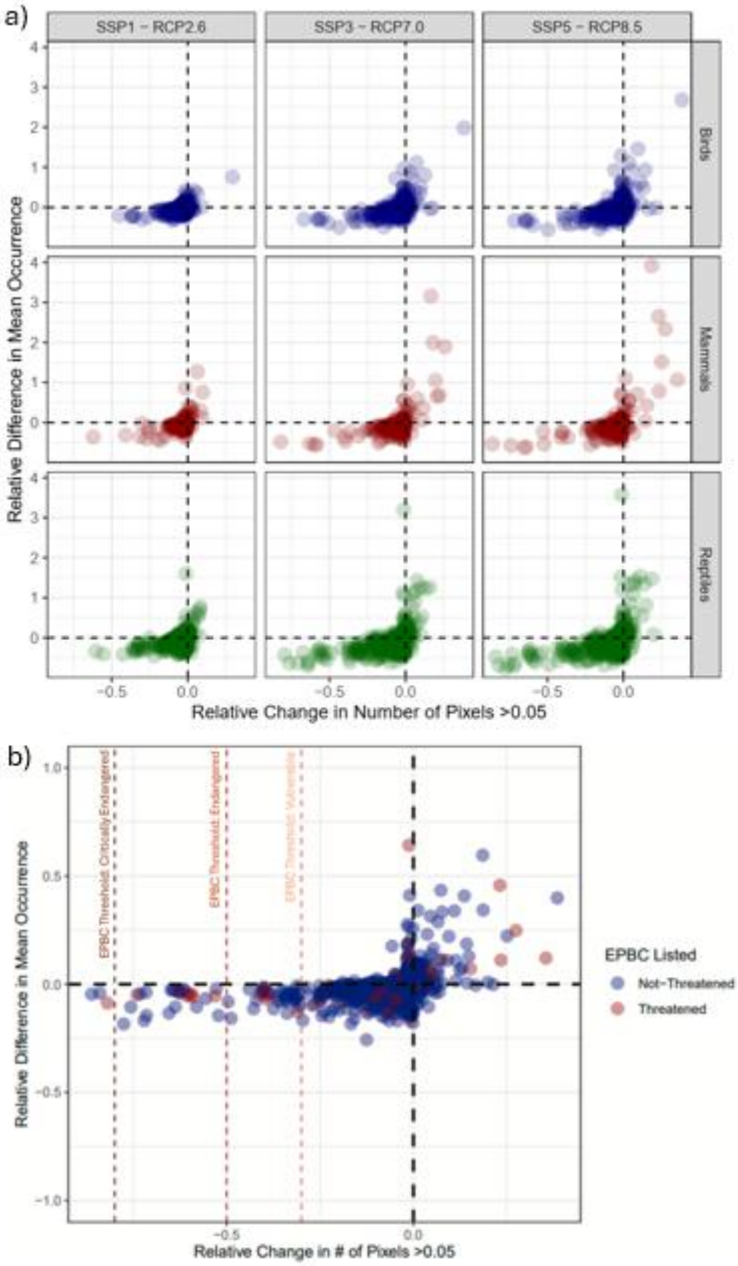

Figure 6: Scatter plots showing the spread of change in species geographic range (on the x axis – proportional change in range size, positive values indicating expansion and negative values indicating contraction) as impacted by change in the species' habitat suitability (on the y axis – proportional change in probability of occurrence, positive values indicating increase in suitability and vice versa) for across taxa groups. In a) Change is estimated from the current time step to 2070 under each climate scenario. Relative change indicates the change as a proportion of overall probability of occurrence and range size of a species within its species mask. Each point indicates a species, colour coded according to the corresponding taxon group. In b) Change is estimated from the current time step to 2070 under RCP8.5-SSP5. Relative change indicates the change as a proportion of overall probability of occurrence and range size of a species within its species mask. Each point indicates a species, colour coded according to the current EPBC status of the species. Vertical coloured dashed lines represent EPBC Act threat status range reduction thresholds at 30% (light red), 50% (red) and 80% (dark red) for vulnerable, endangered and critically endangered, respectively.

Discussion

Our modelling results highlight spatial and taxonomic variation in biodiversity responses under future climate and land-use scenarios. When assessing cumulative effects on biodiversity – whether across all species or within taxonomic groups – predicted patterns remain consistent across scenarios, though impact severity generally increases with increasing climate change intensity, with SSP 5 - RCP 8.5 showing the most adverse outcomes for species. Future projections indicate overall declines in biodiversity across taxonomic groups, with expected declines of 5-10% on average in the worst-case scenario and reduced habitat suitability and range contractions for most (approximately 75%) of the species. Impacts on EPBC-listed species were particularly concerning, with several species projected to experience severe declines. These results give further warning of likely extinctions for Australia given current economic growth trajectories if adequate environmental and sustainability targets are not recognised and legislated.

At the species level, responses varied, with some, like the green ringtail possum, experiencing widespread declines, while others, such as the spotted-tailed quoll, exhibited mixed responses depending on the scenario and section of their range (Figure 3). Under the most severe climate scenario (SSP 5 - RCP 8.5), we predict that 69 mammal, bird and reptile species will experience range declines of at least 30%. Many of these species are not currently listed under the EPBC Act, highlighting the conservation implications of future climate and land-use change. Further, many of these species co-occur in hotspots of decline. For example, our models suggest that far north Queensland and central Australia are likely to experience significant declines in species occurrence (e.g. green ringtail possum, spot-tailed quoll and northern greater glider) under future climate. Indeed, many species in these locations are already experiencing declines. For example, arboreal mammals in far North Queensland have declined in abundance over the past two decades mostly due to increasing temperatures[24,25].These insights strengthen the rationale for developing individual species SDMs in scenario modelling as it reveals underlying dynamics in species responses that contribute to the emergent trends in aggregated biodiversity metrics (e.g. overall suitability, richness). Additionally, the ability to identify likely risks and the severity of land use and climate change pressures for vulnerable species or those of national interest (Figure 6b) is crucial for targeted management and threatened species conservation.

Understanding the role of land use and land use change in shaping species response is vital for shaping biodiversity policy and targets under future scenarios of change. Our models provide the first step towards achieving this in national biodiversity assessments.
In response to coupled climate and land-use change, we identify locations across Australia that are likely to face the biggest biodiversity declines and therefore are of immediate conservation concern (e.g., central Australia, parts of Tasmania and coastal Western Australia) as well as biodiversity hotspots in the future (e.g., mountainous regions of southeastern Australia). Our results suggest that the coastal regions of eastern Australia and

parts of southern Australia may experience a net increase in the relative likelihood of occurrence of species, indicating the potential of these locations as biodiversity refuges under a changing climate and landscape and warrant recognition in priority planning for habitat protection measures. The locations identified in our results generally mirror previous studies that aim to identify Australian climate refugia[26]. However, previous studies focus only on climate change, rather than the joint drivers of both climate change and land-use change[26]. By incorporating land use change variables explicitly in the SDMs coupled with other climate and environmental drivers, we allow for more accurate prediction of likely risks to species habitats as countries move through future stages of economic, social and demographic change.

The national-scale SDM workflows developed in our study provide three *key* improvements to existing approaches because we: (1) incorporate land use variables from global SSP projections[27] explicitly in the SDMs, (2) model the response of individual species under coupled climate-land use scenarios, and (3) provide a reproducible integrated data and analysis pipeline. We also provide technical innovations in national scale biodiversity modelling by developing automated workflows for data processing, allowing expert input into model variable selection[28], creating dynamic vegetation layers that vary in response to predicted land use change to use in the SDMs for future predictions, and make explicit modelling decisions to achieve computation efficiency (e.g. use of species masks, hierarchical variable multicollinearity checks) without losing model robustness. Our framework is modular to enable complete transparency and reproducibility for users to review and improve iteratively[28]. Each step in the workflow is sequential, can be set up for parallel processing if resources allow, and generates standalone outputs that can be examined enroute to final predictions. Moreover, our outputs can be summarised in various ways to address at-scale policy objectives[29].

The challenges of conducting large scale assessments at high spatial resolution, such as the one presented in this study, cannot be understated. Such analyses can often be discouraging due to their considerable data and computation requirements, need for detailed deliberation on modelling assumptions to capture the appropriate response of many species, and the lack of expertise in high performance computing within ecological research. While we overcome many of these challenges, our study presents some limitations that give way to suggestions to help improve biodiversity assessments for national environmental policy. Achieving the best possible model for individual species requires species-specific tailored approaches that are infeasible when modelling large quantities of species at scale. Instead, our priority was to develop a robust modelling workflow to generate predictions for many species at once. Therefore, trade-offs needed to be made between ecological accuracy and computational efficiency while retaining model robustness. This includes the automation of species mask generation, outlier detection, and data cleaning following a set of rules that apply consistently across all species and may miss species-specific nuance. Our modular workflow design does allow fine-tuning of individual species models, if required, without having to re-run the full analyses, albeit with some advice from the authors.

The exclusion of marine species potentially underestimates overall impacts on Australian biodiversity. While the majority of mammalian and reptilian marine species are entirely marine bound there are several species that are partially terrestrial. These are limited to the coast or around inland rivers and are likely driven by the marine conditions not captured by our existing environmental variables. Extending the analysis to marine species presents significant computational challenges due to the larger spatial extents required for the analysis, however, collaboration with existing marine modelling research provides some opportunities for such assessments[30]. Marine avian species, on the other hand, especially migratory species, can be found further inland as they are potentially selecting breeding grounds based on terrestrial conditions and thus can be more easily included using our workflow. It is important to note that such areas are often highly productive for agriculture (e.g. the southern Australia riverina) and therefore likely to be in potential conflict between biodiversity and land use change; as such it is important they be included. Our approach can also easily be adapted to include other taxa such as plants, invertebrates or freshwater species where data is available[31,32], and with the inclusion of appropriate environmental variables and modelling decisions[33,34].

While we use SSP land use predictions from the global LUH2 project[27] to align with global scenario modelling efforts worldwide, using more accurate land use predictions for Australia[35] can greatly improve our predictions. For example, some spatial artefacts do appear in our maps of net biodiversity change (e.g. straight-line borders around locations with a net increase in the relative likelihood of occurrence) that could be refined with more precise land use predictions. Alternatively, coupling a land use change model with our SDMs can help better capture land use dynamics and its effect on species distributions[15]. This will overcome the shortcomings of current integrated approaches that consider biodiversity simplistically from static range maps (e.g. IUCN range maps[16]), aggregated metrics (e.g. mean species abundance[20]), or proxies (e.g. biodiversity services via environmental plantings[5]), thereby obscuring differential species' response to threats. Used within integrated assessment approaches, our SDMs can represent biodiversity in a more appropriate and meaningful way for policy and impact evaluation, as well as provide the necessary biodiversity detail sought after in footprint analyses[8].

Planning towards environmentally sustainable targets and economic activity requires at scale biodiversity assessments that translate the impacts of global socio-economic drivers to local level land use. At the same time, we need to model many species at sufficient spatial and thematic resolution to capture patterns in biodiversity response across the landscape. Our study presents insights on likely future impacts on targeted species and locations across Australia under coupled climate and land use scenarios. By providing individual species models and aggregated whole-of-biodiversity patterns through metrics such as average habitat suitability and species richness, we illustrate the versatility of our approach in informing species-focussed versus habitat-focussed national policy design. The key strength of our approach is the provision of reproducible and adaptable workflows, while drawing on advances in data science and high-performance computing to enable modelling thousands of species at the national scale.

Methods

Species data

We collated all records of terrestrial birds, mammals and reptiles from the Atlas of Living Australia for the years 1970 – 2023 (Atlas of Living Australia website at http://www.ala.org.au. Accessed 5 December 2023) using the *galah* package in R (version 2.0.2[36]). Data was screened for geographic and taxonomic quality, resulting in a clean dataset with 15,173,393 records from 1,488 species (Supplementary Table S1.1).

Species masks

Cleaned species occurrence records were overlaid on the IBRA 7 regions and a mask was created for each species by including the IBRA regions with known presences for that species and their adjoining regions. Models were trained using species-specific raster masks and likely distributions were predicted within the mask for a species.

Environmental variables

We considered three coupled socio-economic (Shared Socioeconomic Pathways, SSP) and climate (Representative Concentration Pathways, RCP) scenarios at 2030, 2050 and 2070 for modelling: SSP 1 – RCP 2.6, SSP 3 – RCP 7.0 and SSP 5 – RCP 8.5. To use a consistent set of global climate models (GCMs) across our scenarios, we considered three out of the 14 GCMs from WorldClim that had data for all scenarios (i.e., INM-CM5-0, MIROC6, MRI-ESM2-0) for 2021-2040, 2041-2060 and 2061-2080 (referred to as 2030, 2050 and 2070 in our analysis, respectively). We ran all nine GCM-RCP combinations instead of averaging across GCMs. This is because species respond to a combination of rainfall and temperature, and the other variables in SDMs, and pre-averaging GCMs smooths out this important interaction. Vegetation classes in the National Vegetation Information System (NVIS) dataset[37] were reclassified to six vegetation classes: rainforests, eucalyptus forests, woodlands, shrublands, grasslands and wetlands, based on expert advice. Future projections of the vegetation variables considered in this study (i.e., tree cover, NDVI, NVIS variables, native neighbourhood and canopy height) were not available. To account for future change in vegetation and non-vegetation classes (i.e., cropland and urban) under future scenarios, we estimated the change based on predicted land use (see supplementary information for details).

All spatial datasets for environmental variables were obtained from publicly accessible repositories (Table S1.2). Layers were resampled to 250m resolution, reprojected in GDA2020/Australian Albers (EPSG 9473) and clipped using a land/water mask of the Australian coastline.

Bias layers

A unique sampling bias layer was created for each taxon group by combining a kernel density estimate layer and the inverse-distance to features layers (roads, protected areas and water bodies). Each source of bias was normalised to be 0-1 before summing all bias sources together to give each source equal weighting, before a final normalisation 0-1 to serve as the bias layer for background point generation. For each species, the appropriate taxon group bias layer was clipped using the species mask such that the values within the mask were indicative of the sampling bias in the data for that species.

Background points

We generated 50,000 weighted-random background points[38] for each species using the ppmData package in R[39] (version 1.0.0) using the species-specific bias layer. Range-restricted species, with less than 50,000 non-NA pixels within their species mask, generated background points up to the number of available pixels.

Variable multicollinearity checks

We set up a hierarchical multicollinearity testing method for each species individually to account for expert advice. Variables were split into land use variables, variables considered informative in species distribution modelling as per experts and published literature, and all other remaining variables (Table S1.3). Our hierarchical testing method involved running three multicollinearity tests per species. First, we evaluated multicollinearity within just the land use variables set, then those passing the first stage combined with the expert set (retaining all variables that passed the preceding test), and then a final evaluation using the variables that passed the preceding test with all remaining variables (again retaining all variables that passed the preceding test). All multicollinearity evaluations consisted of 10,000 random samples of the environmental variables within the species' mask using Pearson correlation ($<|0.7|$) and Variance Inflation Factor (<10) tests using the usdm R package[40] (version 2.1-7) and removing all variables that failed one or both tests.

Species distribution models

We used a Poisson point process-based approach to fit species distribution models to species with ≥20 presence records after data cleaning (592 birds, 254 mammals and 642 reptiles, 1488 total) using the *glmnet* R package[41] (version 4.1-8). We fit Infinitely Weighted Logistic Regression models with a logit link function and penalised maximum likelihood, which is equivalent to an inhomogeneous Poisson point process[42]. In this approach the data points are weighted such that a presence point carries a weight of 1 and the weight of a background point is equal to the ratio of presences to background points. We also utilise lasso regularisation to penalise complex model structures and reduce the risk of overfitting the data. Model formulae were constrained by the number of data points available for a species: 20-89 presence records used linear terms only and could select up to one variable per five presence records and ≥90 presence records used linear and quadratic terms and could select one variable per ten presence records (as each variable has two model terms). Variables were randomly selected up to this limit from the variables that passed the multicollinearity tests for each species in order from: 1) random selection from land use set variables up to a maximum of 50% of the total allowed variables; 2) random selection from the expert set variables; and 3) random selection from the remaining variables. Distributions were modelled and predicted at 250m resolution and predictions were made for the current time period as well as the 27 permutations of the three time periods, three SSP-RCP scenarios, and three GCMs.

Model cross validation

We used "p-thinning" to implement cross-validation for model evaluation of point-process based SDMs[43]. We implement "five-fold cross-validation" using five simulations of "p-thinning" to randomly generate 75:25 splits of training and testing data. Model performance of the underlying models is evaluated using the Boyce Index (BI) representing deviation of predictions from randomness such that positive values away from zero indicate a good model. Corresponding AUC values are also reported, with values closer to 1 indicating a good model, however these are less informative than the Boyce Index for presence-only based predictions[44].

Estimating biodiversity response

Predictions under each coupled land use and climate scenarios generated 27 outputs per species at the three time points (2030, 2050, 2070) under the three SSPs and for the three GCM per SSP. For each species-scenario-time period combination, we estimated the mean, minimum and maximum predicted occurrence per pixel across the three GCMs. Then, to summarise across species, we calculated and mapped the relative likelihood of occurrence of a species within each 250m pixel. Mean relative likelihood of occurrence was calculated for all species, each taxonomic group (birds, mammals, reptiles) and for EPBC-listed species.

Model uncertainty

We examine the influence of uncertainty in the climate scenarios on our SDM outputs. We compare the mean predicted occurrence (relative likelihood of occurrence) for all species averaged across the three GCMs to the minimum and maximum predicted values across the three GCM), and to the predicted values obtained under each individual GCM. This provides us with a range of biodiversity response maps under alternate climate scenarios.

Further details on methods can be found in the supplementary information.

Data availability

Accompanying scripts in R[45,46] (versions 4.4.0 and 4.4.1) and python (version 3.10.12) and the sequence in which they are implemented can be accessed at <pending-zenodo-link>. All data used in the study is available at <pending-figshare-link>.

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Author contributions

Conceptualisation: PB, BW. Methodology: PB, DW. Formal analysis: PB, DW, DAR, WLG Computation: PB, DW, DAR, RV, UN. Writing – original draft: PB, DW. Writing – review and editing: all.

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