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Updating expected survival of biodiversity indicators

Implementation report supporting the NSW biodiversity outlook report 2024

Department of Climate Change, Energy, the Environment and Water

Acknowledgement of Country

Department of Climate Change, Energy, the Environment and Water acknowledges the Traditional Custodians of the lands where we work and live.

We pay our respects to Elders past, present and emerging.

This resource may contain images or names of deceased persons in photographs or historical content.

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About this report

This report includes the workflow, data sources and methods used to calculate indicators for the **expected survival of biodiversity** theme, reported by the NSW Biodiversity Indicator Program.

The NSW Biodiversity Indicator Program

The Biodiversity Indicator Program reports on the state and trends of biodiversity and ecological integrity in New South Wales. We have developed a framework of indicators (Figure 1) to help scientists, managers and policymakers understand the current state of biodiversity and how it is likely to change in the future.

The indicator framework uses the best available science for measuring biodiversity and ecological integrity. It reflects how we manage our landscapes and protect natural areas. The framework is arranged hierarchically by class, theme and family (Figure 1).

The expected survival of biodiversity theme

The **expected survival of biodiversity** theme comprises 2 indicator families (Figure 1): **listed threatened species and ecological communities** (3 indicators reported here) and **all known and undiscovered species** (1 indicator reported here). These indicators report on the likely long-term survival of species and ecological communities, including those that have been formally assessed for risk of extinction and listed as threatened.

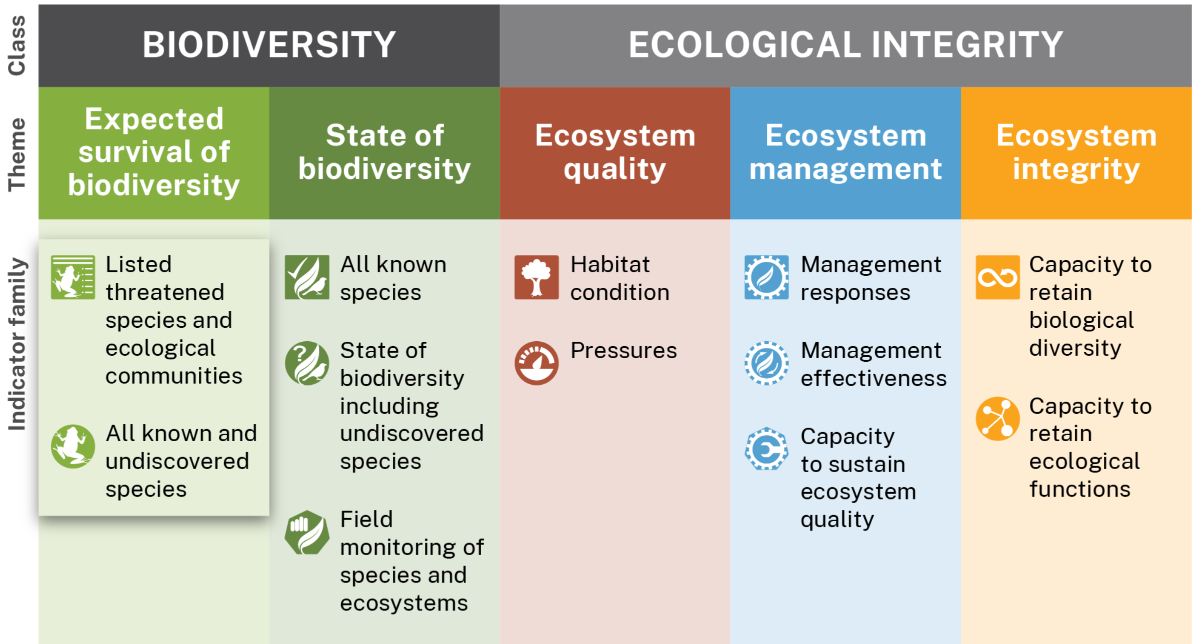

Figure 1 Hierarchy of classes, themes and indicator families in the NSW Biodiversity Indicator Program. Indicator families for the expected survival of biodiversity theme are highlighted

1. Introduction

1.1 Expected survival of biodiversity indicators

The **expected survival of biodiversity** theme is a set of related indicators reported by the Biodiversity Indicator Program. This indicator theme measures the rate of loss of biodiversity by predicting the amount or proportion of diversity expected to become extinct over a given time period. Remaining diversity at the end of the period, after predicted losses, is therefore the expected survival. The measurement framework is applicable to many facets of biodiversity (Jarzyna and Jetz 2016), including the count of species (that is, species richness) and phylogenetic diversity (Faith 1992).

Based on the expected diversity model (Weitzman 1992), expected survival of the diversity of a set of species or ecological communities is inferred using standard categories of extinction risk (Mace et al. 2008), for example, endangered and vulnerable. Those extinction risk categories are equated with a probability of survival in 100 years and the probabilities are aggregated into measures of diversity expected to survive, depending on the indicator. The general model is broadly applicable to conservation decision science, such as assessment of the relative benefit of alternative conservation scenarios (Brazill-Boast et al. 2018).

The technical method (OEH and CSIRO 2019) for the Biodiversity Indicator Program divides the expected survival of biodiversity theme into 5 indicators grouped into 2 indicator families. The indicator families and **indicators** can be briefly described as follows:

- Expected survival of listed threatened species and ecological communities:
  - **Expected survival of listed threatened species:** the number or percentage of species listed as threatened or extinct in New South Wales expected to survive in 100 years.
  - **Expected existence of listed threatened ecological communities:** the number or percentage of ecological communities listed as threatened in New South Wales expected to exist in 100 years.
  - **Expected survival of phylogenetic diversity for listed threatened species:** the sum of branch lengths of the phylogenetic tree of a biological group expected to survive in New South Wales in 100 years. Alternatively expressed as the percentage of the original sum of branch lengths (including extinct species and lineages) expected to survive. In practice, the indicator is reported for all species, not just threatened species, because all species need to be included in the relevant phylogenetic tree.
- Expected survival of all known and undiscovered species:
  - **Expected survival of all known species:** the number or percentage of all known species (listed and unlisted) in a biological group originally occurring in New South Wales expected to survive in 100 years.

– **Expected survival of all known and undiscovered species:** the number or percentage of all species (known and undiscovered) originally occurring in New South Wales expected to survive in 100 years.

1.2 Updating the expected survival indicators

The first *NSW biodiversity outlook report* (DPIE 2020a) included results for 4 of these indicators; and in some cases indicators were reported for only specific biological groups (Table 1). Details of the method design and implementation of these indicators are found in 2 separate implementation reports (Nipperess et al. 2020a; Nipperess et al. 2020b), each corresponding to an indicator family.

The Biodiversity Indicator Program continues to refine workflows and indicator results as methods, data and technology improve. Where changes are made to inputs and data processing, results are hindcast to previous years, including those years previously reported on. This may result in small discrepancies from previously reported results. Nevertheless, continual improvement of indicators is necessary to ensure accuracy, confidence and repeatability.

This report describes changes made to data processing and analysis for the expected survival of biodiversity theme and presents results for a range of years between 1997 and 2022 (depending on the indicator), as a 'second assessment' of these indicators (Table 1). These indicators are presented together in this report because they share the same measurement framework and share some data inputs and data processing steps. This report updates methods previously reported for this suite of indicators in 2 separate reports (Nipperess et al. 2020a; Nipperess et al. 2020b). For clarity, all components of the workflows for these indicators will be briefly described here, but they are described more fully in the original reports. Where methods or inputs have changed, these changes are fully described in this report, including the reasoning for these changes.

Table 1 Indicators in the expected survival of biodiversity theme and their reporting in the first *NSW biodiversity outlook report* (DPIE 2020a) and in this second assessment report

Indicator family	Indicator	First outlook report	Second assessment
Expected survival of listed threatened species and ecological communities	Expected survival of listed threatened species	Reported for 1997, 2002, 2007, 2012 and 2017 for all NSW threatened species	Reported for 1997, 2002, 2007, 2012, 2017, 2020 and 2022 for all NSW threatened species
	Expected existence of listed threatened ecological communities	Reported for 1997, 2002, 2007, 2012 and 2017 for all NSW threatened ecological communities	Reported for 1997, 2002, 2007, 2012, 2017, 2020 and 2022 for all NSW threatened ecological communities
	Expected survival of phylogenetic diversity for listed threatened species	Reported for 2017 for all known NSW species of birds, frogs and mammals	Reported for 2017, 2020 and 2022 for all known NSW species of tetrapods (birds, frogs, reptiles and mammals) Reported for 2020 and 2022 for all known species of gymnosperms and Proteaceae
Expected survival of all known and undiscovered species	Expected survival of all known species	Reported for 2013 for all known NSW species of vascular plants	Reported for 2007, 2013, 2017 and 2020 for all known NSW species of vascular plants Reported for 2020 for all known NSW species of tetrapods, gymnosperms and Proteaceae, and 2017 and 2020 for tetrapods
	Expected survival of all known and undiscovered species	Not reported	Not reported

2. Updated method and implementation

2.1 Mathematical framework

The method described in this section applies to **all indicators** reported here.

Expected diversity is the number of biodiversity features expected to still exist in the future (for example, 100 years from now), where 'features' are units of biodiversity such as genes, species or ecological communities, and for these features to 'exist' in the future, they must be represented by one or more surviving examples. The expectation of the number of features ($\mathrm{E}[D]$) at some point in the future (Equation 1) is the sum of the probability (q_i) of survival of each feature (i) across a set of features (F) where $i \in F$ (that is, where i belongs to F) (Weitzman 1992).

Equation 1 $\mathrm{E}[D] = \sum_{i \in F} q_i$

This core concept can be extended to phylogenetic diversity by interpreting the lengths of branches on a phylogenetic tree as being proportional to the number of unique features possessed by taxa descendant from that branch (Faith 1992). The features being counted can be interpreted literally as a count of traits (morphological or molecular) that descendent taxa share, or, more generally, as the length of time that these taxa shared a common ancestor. Summing the branches of a tree therefore gives either the count of unique features or the total unique evolutionary heritage (Mooers and Atkins 2003). Expected phylogenetic diversity ($\mathrm{E}[PD]$) is then the sum of the length (L_j) of each branch (j) in a phylogenetic tree ($T, j \in T$) multiplied by its probability (q_j) of survival (Equation 2). The probability of survival of internal branches is the probability that at least one species (i) in the set ($S_j, i \in S_j$) of species descendent from that branch survives.

Equation 2 $\mathrm{E}[PD] = \sum_{j \in T} \left[L_j * \left(1 - \prod_{i \in S_j} (1 - q_i)\right)\right]$

The complement to expected survival is expected loss and is the difference between total diversity (such as the count of species) and expected diversity. To be explicit, expected loss is defined as $D - \mathrm{E}[D]$, where D is the count of features and $\mathrm{E}[D]$ is the expected number of features surviving into the future. Alternatively, loss can be calculated as the sum of extinction probabilities ($\sum_{i \in F}(1 - q_i)$). The phylogenetic equivalent is $PD - \mathrm{E}[PD]$, where PD is the sum of the lengths of branches in a phylogenetic tree and $\mathrm{E}[PD]$ is the sum of branch lengths expected to survive into the future.

Expected loss can be further partitioned into that subcomponent that is considered 'already lost' due to recorded historical extinctions and the remainder, referred to here as 'potential loss'. Species listed as extinct are included in expected loss when those species are given a non-zero probability of survival, due to the possibility of rediscovery (see section 2.2). The contribution to expected loss of species presumed to be extinct can be determined as the difference between expected diversity if these species were truly extant ($q_i = 1$) and expected diversity if they are assigned a small but non-zero probability of survival. For species diversity, the ‘already lost’ subcomponent is the equivalent of summing extinction probabilities $(1-q_i)$ for only presumed extinct species. For phylogenetic diversity, the subcomponent can only be determined by subtraction as described above.

This basic framework for calculating the expected count of species or ecological communities or expected phylogenetic diversity has not changed from the first assessment and is provided here for context and clarity. The following are 2 extensions of the framework, conducted as part of the second assessment, to accommodate some methodological refinements of the expected survival indicators.

When there is a mix of species and subspecific taxa (subspecies, varieties, populations), it is prudent to first standardise the unit of measurement to the species level. This can be done by aggregating the survival probabilities of subspecific taxa to generate a single probability for each parent species-level taxon. This is achieved similarly to the approach for phylogenetic diversity, that is, the probability of survival (q_k) of a parent species (k) is the probability that at least one subspecific taxon (i) in the set of subspecific taxa $(S_k, i \in S_k)$ belonging to that species survives.

Equation 3 $$q_k = \left(1 - \prod_{i \in S_k}(1-q_i)\right)$$

These newly derived species-level probabilities can then be substituted back into Equation 1 to derive a count of species (in the strict sense) expected to survive.

The expected diversity framework can also be extended to allow for analysis of conservation scenarios by assigning a target probability of survival (q_T). The notional benefit of conservation actions (improvement in probability of survival) for a single species is therefore the difference between the probability of survival (with no conservation) and the target. Realistically, the benefit accorded by conservation for a species should be weighted by feasibility (f_i), that is, the probability of achieving the benefit for species i, given the proposed or actual conservation actions. This follows the same procedure as the project prioritisation protocol of the Saving our Species program (Brazill-Boast et al. 2018). The change in expected diversity due to conservation $(\Delta[D])$ is therefore the sum of species benefits weighted by their respective feasibilities, as per Equation 4.

Equation 4 $$\Delta[D] = \sum_{i \in F}(q_T - q_i) * f_i$$

To calculate change in expected phylogenetic diversity $(\Delta[PD])$, the most straightforward method is to calculate a realised probability of survival $(\acute{q}_\iota)$, which is the probability of survival from conservation weighted by feasibility. The change from conservation is then the difference between expected phylogenetic diversity with original survival probabilities and that with realised survival probabilities (Equations 5 and 6).

Equation 5 $$\Delta[PD] = \sum_{j \in T}\left[L_j * \left(1 - \prod_{i \in S_j}(1-\acute{q}_\iota)\right)\right] - \sum_{j \in T}\left[L_j * \left(1 - \prod_{i \in S_j}(1-q_i)\right)\right]$$

Equation 6 $$\acute{q}_\iota = q_i + (q_T - q_i) * f_i$$

Change in expected phylogenetic diversity due to conservation is not assessed in this report but is included for completeness.

2.2 Probabilities of survival for threatened entities

The method described in this section applies to **all indicators** reported here.

In the first assessment, following the Saving our Species program, probabilities of survival for threatened species and ecological communities are derived from Criterion E of the *IUCN Red List of Threatened Species* (IUCN 2012a) (IUCN Red List of Species) and the *IUCN Red List of Ecosystems* (Bland et al. 2017) (IUCN Red List of Ecosystems). Values have been estimated for probability of survival over 100 years (Table 2) for each threatened category (vulnerable, endangered, critically endangered) by interpolation from the stipulated IUCN thresholds (Kindvall and Gärdenfors 2003). Note that these categories and criteria for threatened species, while defined by the IUCN, are also used for species assessments and listings in New South Wales and nationally. A small probability was also derived for the 'extinct' category for species from a sighting model, which estimates probability of survival of a hypothetical species not seen for more than 50 years (Nipperess et al. 2020a). Species and ecological communities not listed as threatened were assumed to be 'secure' and given a conservative probability of survival, again following Saving our Species (Brazill-Boast et al. 2018).

This basic approach for inferring probabilities of survival has not changed in the second assessment, except for the substitution of the 'secure' category with the non-threatened categories of 'near threatened' and 'least concern' used by the IUCN (Table 2). This adjustment was done as part of the revised list unification process (see section 2.4) to ensure compatibility with IUCN assessments. The 'near threatened' category has assumed the 0.95 probability previously assigned to 'secure' and is a conservative estimate (see Mooers et al. 2008 for a range of possible higher values). A notional and conservative probability of 0.95 was also assigned to species considered 'data deficient' that is equivalent to assuming they are 'near threatened'. This follows previous practice, where species not listed as threatened or extinct in New South Wales were assumed to be 'secure'. The 0.99 probability value for the 'least concern' category is interpolated, assuming an approximately logistic model, while remaining conservative relative to other estimates (Mooers et al. 2008).

Table 2 Survival probabilities (over 100 years) of species and ecological communities for each IUCN category

First outlook report category	Second assessment category	Species	Ecological communities
Secure	Least concern	0.99	*
Secure	Near threatened	0.95	*
Vulnerable	Vulnerable	0.90	0.90
Endangered	Endangered	0.30	0.65
Critically endangered	Critically endangered	0.05	0.25
Extinct/Collapsed	Extinct/Collapsed	0.01	*
N/A	Data deficient	0.95	*

Notes:
Categories with * were not used in analyses and so probabilities were not derived.
IUCN = International Union for Conservation of Nature (see IUCN 2012a; Bland et al. 2017).

Species with one or more listed subspecific taxa were assigned a probability of survival by aggregating the survival probabilities of all known subspecific taxa in New South Wales (see section 2.1). When subspecific taxa were not listed, they were categorised as 'data deficient'. However, aggregated probabilities were capped to 0.95, that is, species-level values could not be greater than 0.95. This approach was considered suitably conservative in that any species with at least one threatened subspecific taxon had to be considered at least as much at risk as a 'near threatened' species.

Any species or subspecies with one or more populations listed as endangered was categorised as 'near threatened', but only if it was not itself listed as a threatened species. The reasoning was similar to that for species with threatened subspecies. While there is evidence for the decline of specific populations, there is currently not yet sufficient evidence to qualify the species or subspecies as a whole as threatened. An approach that aggregates survival probabilities for individual populations was not adopted because populations are poorly defined and available data are currently insufficient.

2.3 Lists of species and ecological communities

The method described in this section applies to **all indicators** reported here.

The expected survival indicators require a number of inputs: lists of entities (species or ecological communities), their names and corresponding risk categories (if known). For expected survival of listed threatened species and ecological communities, inputs were the lists of threatened and extinct entities provided as Schedules 1, 2 and 3 of the *Biodiversity Conservation Act 2016*. For expected survival of phylogenetic diversity and expected survival of all known species, comprehensive lists of **all species** (within a biological group) known to occur in New South Wales were used. A summary of source data for lists for each indicator for both the first outlook report and this second assessment is provided in Table 3, and a description of each data source is provided in Table 4.

Table 3 **Source data for lists of entities used as inputs in the first and second assessments of the expected survival indicators**

Indicator	First outlook report	Second assessment
Expected survival of listed threatened species	• NSW Threatened Species Scientific Committee final determinations	• NSW Threatened Species Scientific Committee final determinations • Species Profile and Threats Database • IUCN Red List of Threatened Species
Expected existence of listed threatened ecological communities	• NSW Threatened Species Scientific Committee final determinations	• NSW Threatened Species Scientific Committee final determinations
Expected survival of phylogenetic diversity for listed threatened species	• NSW Threatened Species Scientific Committee final determinations • Australian Faunal Directory	• NSW Threatened Species Scientific Committee final determinations • Australian Faunal Directory • Species Profile and Threats Database • IUCN Red List of Threatened Species • Australian Plant Census • PlantNET
Expected survival of all known species	• PlantNET	• PlantNET • NSW Threatened Species Scientific Committee final determinations • Species Profile and Threats Database • IUCN Red List of Threatened Species • Australian Faunal Directory • Australian Plant Census

Note: All data sources for the second assessment were accessed at the end of 2022.

Table 4 **Description of source data for lists of entities used as inputs in the first and second assessments of the expected survival indicators**

Source[1]	Description
NSW Threatened Species Scientific Committee final determinations	Database of final determinations of the NSW Scientific Committee, indicating risk category assigned and date of listing under the *Biodiversity Conservation Act 2016*
Species Profile and Threats Database	Database summarising listings of species and ecological communities under the *Environment Protection and Biodiversity Conservation Act 1999*, including risk category and date of listing
IUCN Red List of Threatened Species	Database of species assessed for risk of extinction, including risk category assigned and date of assessment
Australian Faunal Directory	Database of all known animal species known to occur in Australia, including accepted scientific name and geographic distribution
Australian Plant Census	Database of all known vascular plant species known to occur in Australia, including accepted scientific name and geographic distribution
PlantNET	Database of all known vascular plant species known to occur in New South Wales, including accepted scientific name and geographic distribution

1. See 'More information' section for links to these online data sources.

As shown in Table 3, the second assessment of the indicators involved a significant expansion of the number of data sources used. This was for 2 reasons:

1. an expansion of the number of biological groups reported for some indicators, requiring additional taxonomic sources
2. an integration of all reasonable sources of data informing extinction risk category for threatened and non-threatened entities.

Comprehensive lists of all known native NSW species in a biological group were sourced from national species lists: the *Australian Faunal Directory* (for animals) and the *Australian Plant Census* (for vascular plants). In the case of plants, *PlantNET* (NSW Flora Online) was also used, particularly for confirmation of known natural distribution in New South Wales, and for lists of known NSW subspecies of threatened species. Comprehensive species lists were generated for tetrapods, gymnosperms and the Proteaceae family of flowering plants.

Lists of species with assigned risk category were integrated to interpolate extinction risk of each species over time. The final determinations of the NSW Threatened Species Scientific Committee, which describe the risk assessment of each entity, were compiled to recreate the NSW threatened entities list (Schedules 1, 2 and 3 of the Biodiversity Conservation Act) at selected points in time. The national threatened species list (in the *Species Profile and Threats Database*, or SPRAT) and the global *IUCN Red List of*

Threatened Species were also sourced for more recent risk assessments than those of the NSW Scientific Committee. Some species not listed as threatened in New South Wales still required a plausible risk category (for the phylogenetic diversity and 'all known species' indicators) and these were sourced from the national or global lists, if available. Integration and unification of these data sources is described in section 2.4.

2.4 List unification

The method described in this section applies to **all indicators** reported here.

List unification is the process of merging lists across multiple sources and across multiple points in time. This includes resolution of taxonomic names and their corresponding risk categories. Lists evolve as species are added or removed, taxonomic names are revised, and risk categories are reassessed. Tracking change in expected survival over time requires careful consideration of these changes and whether they represent true changes in the overall pattern of extinction risk.

The expected survival indicators require as inputs lists of species that have been standardised taxonomically. Taxonomic assignments can be different across authorities (such as state and national species lists, and the IUCN Red List of Species) and can also change over time as species delineations and corresponding taxonomic names are revised. In addition, calculation of expected survival of phylogenetic diversity requires matching of taxonomic names in threatened species lists with those used in source phylogenetic trees.

For species, the resolution of taxonomic conflicts followed previous practice (Nipperess et al. 2020a). The names of threatened and extinct species as currently listed in Schedules 1 and 3 of the Biodiversity Conservation Act are used as given and are treated as the standard against which other taxonomies must be reconciled. This is because the risk category of a species in New South Wales is inextricably associated with the name as listed in the Act and therefore that name must take precedence. For species that are not listed as threatened or extinct in New South Wales, taxonomic names were standardised to the *Australian National Species List* (National Species List). In practice, names were used as listed in the *Australian Faunal Directory* or the *Australian Plant Census* for animals and vascular plants, respectively.

Threatened ecological communities are defined as part of the assessment process by the NSW Threatened Species Scientific Committee and those names were used exclusively in analyses described here. Ecological communities are also listed under the Commonwealth *Environment Protection and Biodiversity Conservation Act 1999*, while ecosystems are listed in the IUCN Red List of Ecosystems (Bland et al. 2017). However, there is no simple means of resolving equivalency of these entities across lists, nor is there is a nomenclatural standard of practice equivalent to that for species names. However, a very basic level of mapping to the recently established *IUCN Global Ecosystem Typology* (Keith et al. 2020) was done by assigning listed ecological communities to functional realms (terrestrial, marine, freshwater, or transitional between realms) to be able to report the relevant indicator (expected survival of listed threatened ecological communities) against the highest level in the classification.

The risk category assigned to an entity (species, subspecies or ecological community) was inferred for multiple points in time by applying decision rules to the final determinations of the NSW Threatened Species Scientific Committee. Final determinations are formal risk assessments of the committee which indicate the risk category assigned and the date of listing for each entity. Where entities have been assessed more than once, multiple determinations are given. Following previous practice, entities were assumed to have the same risk category as that of the determination **before** being formally listed, and until such time as a new determination assigns that entity a new risk category. This is a conservative approach that means that any entity assessed only once will have the same risk category (and probability of survival) over the entire reporting period. A change in an expected survival indicator can therefore only occur when entities are assessed multiple times. Additionally, any entity that was listed as endangered prior to 2006 and subsequently listed as critically endangered in 2006 or later was assumed to be critically endangered for the entire period. This is because the scientific committee did not adopt the critically endangered category until 2006 and thus subsequent changes in category are conservatively assumed to reflect procedural revisions of previous determinations rather than genuine further declines in populations.

Where species have changed listed category in New South Wales over time (including delisting), the final determinations were carefully assessed for any indication that this change in category was either: a) a revision in the light of better information, or b) due to an observed or inferred recovery or decline. In the former case, the revised category was assumed to also be in effect prior to the determination. In the latter case, the change in risk category was interpreted as a genuine change in extinction risk.

Information on changes over time in risk category for NSW entities was also sourced from national and global lists. This is a change in method used in the first assessment that was motivated by the need for:

1. better assessments of overall extinction risk for entire biological groups (by also considering species that are not currently listed as threatened in New South Wales)
2. more reliable interpolation of risk over time from more frequent assessments (from all sources).

The NSW threatened species list and the national threatened species list (under the Environment Protection and Biodiversity Conservation Act) both use the same categories and criteria as the IUCN Red List of Species (IUCN 2012a) making all 3 lists (NSW, national and global) directly comparable in assessment of extinction risk. Again, decision rules were applied when integrating this information. Where a species was not listed in New South Wales, its risk category was inferred to be that of the national list or, if not listed nationally, to be that of the IUCN Red List of Species. If not assessed anywhere, a species was categorised as 'data deficient'. When a species was listed in New South Wales, it was assumed to have the risk category assigned by the scientific committee unless a more recent assessment had been made at a national or global scale **and** the extinction risk assigned was higher than that assigned for New South Wales. The reasoning for this approach is that a species could have a much smaller range in New South Wales than at a national or global scale, and therefore must be at least as much at risk in New South Wales as nationally or globally. Therefore, a more recent national or global assessment should only be integrated when it assigns a higher risk category, implying a recent decline that has not yet been formally recognised in New South Wales. This approach is consistent with the IUCN regional assessment guidelines when translating assessments from global or national to regional scales (IUCN 2012b).

The list unification process resulted in compiled lists of **accepted names** for species and ecological communities. Accepted names of species were mapped to names used by the Biodiversity Conservation Act, the Environment Protection and Biodiversity Conservation Act, the IUCN Red List of Species, the National Species List, and phylogenetic sources (see section 2.5). Entries were made for:

- each species or subspecies listed under the Biodiversity Conservation Act
- any species or subspecies with one or more populations listed as endangered under the Biodiversity Conservation Act, but only if the species or subspecies itself is not listed as threatened
- every species known to occur in New South Wales for selected biological groups (tetrapods, gymnosperms and Proteaceae)
- every known NSW subspecies for species which have at least one subspecies listed as threatened in New South Wales.

For ecological communities, the list of accepted names corresponded to those used under the Biodiversity Conservation Act without mapping to names used by other authorities.

Resolution of **threat category** over time was compiled into an assessments database for species and ecological communities. Accepted names were matched to listed threat category and year of listing for the Biodiversity Conservation Act or the preceding *Threatened Species Conservation Act 1995*, Environment Protection and Biodiversity Conservation Act, and IUCN Red Lists. From this information, the inferred threat category was recorded for selected years (1997, 2002, 2007, 2012, 2017, 2020 and 2022) including notes for the basis of the decision. Entries were made for every accepted name in the compiled lists of species and ecological communities for which there was at least one threat category listing for at least one authority (NSW, national or global).

2.5 Resolving evolutionary relationships

The method described in this section applies to the **expected survival of phylogenetic diversity** indicator.

Summary of first assessment

In the first assessment of the expected survival of phylogenetic diversity indicator, phylogenetic trees (depicting evolutionary relationships) were developed for all known

NSW species of frogs, mammals and birds. These trees were adapted from existing compiled phylogenies of the world's amphibians, mammals and birds, respectively. Names of species in the source trees were matched to accepted names for all known NSW species (see section 2.4). Where NSW species were missing from the source tree, these were inserted at random into the subtree defined by the known closest relatives of the missing species. This set of closest relatives was typically defined as all members of the same genus as the missing species. To reflect uncertainty of phylogenetic relationships, especially with respect to inserted species, 100 versions of the tree for each biological group were generated. Versions differed in the branching pattern (topology) and lengths of branches, representing a range of plausible hypotheses of evolutionary relationships. Missing species were randomly and independently inserted into each of the 100 versions of a tree to capture a suitable range of possible placements. After inserting missing species, trees were then trimmed to only include all known NSW species. This process is more fully described in Nipperess et al. (2020a) and follows the method outlined by Rangel et al. (2015).

Second assessment

Since the first outlook report, new and improved phylogenetic and risk assessment data have become available, allowing expansion of the indicator to encompass more biological groups. Expected survival of phylogenetic diversity is now reported for 3 biological groups: tetrapods (with frogs, reptiles, mammals and birds reported together in a single indicator), gymnosperms, and Proteaceae. These groups were chosen because they had comprehensive phylogenetic and risk assessment data (see section 2.3). Both of these inputs are necessary to reliably assess the degree to which phylogenetic diversity is threatened with extinction. This is an improvement on the first assessment, where all species not formally listed as threatened or extinct in New South Wales were assumed to be 'secure'.

A tree of tetrapods was constructed by joining separate trees of birds (Aves), mammals (Mammalia), frogs (Anura), squamate reptiles (Squamata) and turtles (Testudines) together via a 'backbone' tree. The backbone tree (Figure 2) shows current understanding of the evolutionary relationships of major groups of tetrapods and is based on the phylogeny of Crawford et al. (2015). Divergence dates were derived from the TimeTree of Life database (Hedges et al. 2015). Crocodiles (Crocodylia) and Tuatara (Rhynchocephalia) were included in the backbone tree, despite having no representatives in New South Wales, so that divergence dates of internal nodes would be correct prior to joining to other trees. Comprehensive, fully resolved and dated phylogenetic trees for all major groups (frogs, mammals, squamates, turtles and birds) were sourced from the scientific literature (Table 5). In each case, trees consisted of 10,000 versions from which 100 versions were randomly sampled to reflect phylogenetic uncertainty. To each of 100 copies of the backbone, one version of each of the bird, mammal, frog, squamate and turtle trees were attached to the appropriate tip on the backbone tree. The length of the tip on the backbone was shortened to ensure that the resulting join would result in an ultrametric tree (that is, a tree where all paths from root to tip are equal in length). Once all trees were joined together, the tips Crocodylia and Rhynchocephalia were removed.

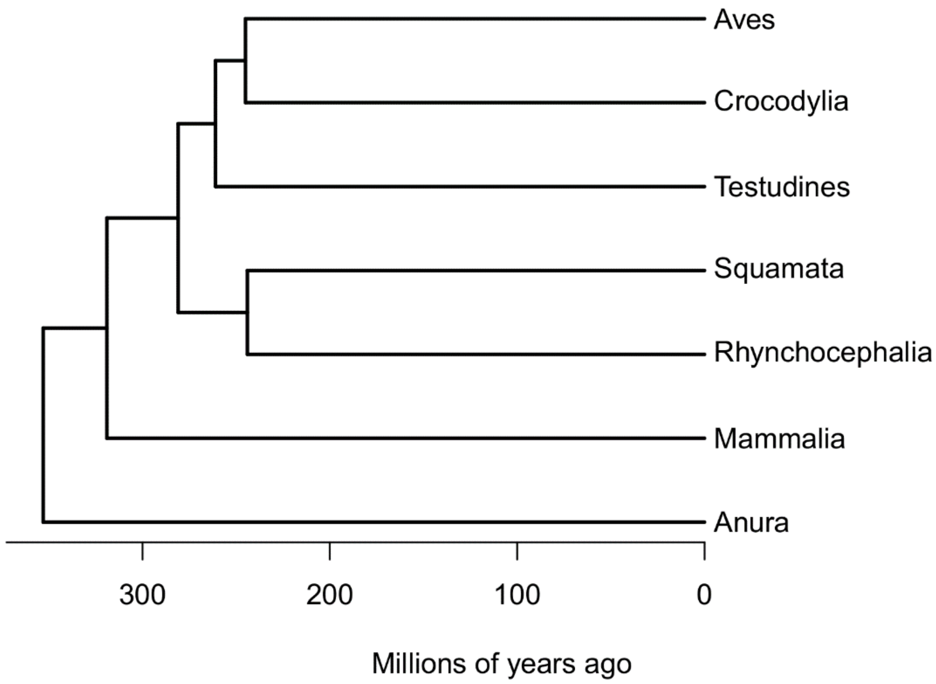

Figure 2 **Phylogenetic tree of major groups of tetrapod vertebrates used as a 'backbone' for joining together phylogenetic trees of frogs (Anura), mammals (Mammalia), squamate reptiles (Squamata), turtles (Testudines) and birds (Aves)**

Table 5 **Phylogenetic trees sourced to compile a composite tree of all known species of tetrapod vertebrates in New South Wales**

Group	No. of species	No. of versions	Source
Frogs (Anura)	7,238	10,000	Jetz and Pyron (2018)
Mammals (Mammalia)	5,911	10,000	Upham et al. (2019)
Squamate reptiles (Squamata)	9,574	10,000	Tonini et al. (2016)
Turtles (Testudines)	357	10,000	Colston et al. (2020)
Birds (Aves)	9,993	10,000	Jetz et al. (2012)

Trees for gymnosperms and the flowering plant family, Proteaceae, were extracted from an existing tree of all vascular plant species known to occur in New South Wales. The vascular plant tree was generated using the automated 'V.PhyloMaker' tool (Jin and Qian 2019) from a list of NSW species sourced from the *Australian Plant Census*. To reflect phylogenetic uncertainty, the source tree had 100 versions differing in topology and branch length. Lists of all known NSW species of gymnosperms and Proteaceae were created from the *Australian Plant Census*, supplemented with data from NSW

PlantNET, and used to trim back the vascular plant tree to the relevant group. In the case of the Proteaceae tree, some polytomies (where an internal node has more than 2 descendent branches) were present. These were resolved randomly and independently for each version of the tree, following the procedure described by Rangel et al. (2015), with the 'bifurcatr' function in the 'PDcalc' package (Nipperess and Wilson 2023) for the R programming language.

For tetrapods and Proteaceae, some species and subspecies known to occur in New South Wales were not present in the source trees and had to be inserted. Insertions of missing species (23 tetrapods and 1 Proteaceae) were done using the same method as the first assessment, that is, inserting at random (and independently for each version of the tree) into the subtree defined by the closest known relatives of the missing species (Rangel et al. 2015). In all cases of missing species, this group of close relatives was defined as members of the same genus. In the case of missing subspecies (48 tetrapods and 23 Proteaceae), these were inserted only if they were either listed as threatened at the subspecies level or were sister subspecies of a threatened subspecies. This was done to accurately reflect the potential loss of biodiversity of threatened subspecies, which is generally less than that expected for threatened species (see sections 2.1 and 2.2). Subspecies were attached at a random position along the length of the terminal branch for the parent species or a sister subspecies (if already present in the tree). This again followed the same procedure as used in the first assessment, with the exception that the terminal branch leading to a subspecies was constrained to be no more than 1 million years in length. This additional constraint was applied to prevent sister subspecies of distinct species from being more divergent from each other than could be expected of full species. The choice of 1 million years is based on estimated divergence times observed for sister species in a rapidly speciating taxon (Rowe et al. 2011).

To facilitate some additional computationally intensive analysis (see section 2.7), a single version was selected from each set of 100 versions for each biological group. The selected version was that with maximum clade credibility. Each version of the tree is given a score based on the frequency with which the clades in that version appear in other versions of the tree (Heled and Bouckaert 2013). The version with the highest score has maximum clade credibility because the clades defined in that version occur frequently in the sample and are therefore well supported by the evidence. The maximum clade credibility tree version for each biological group was chosen using the 'MaxCladeCred' function in the 'phangorn' package (Schliep 2011) for the R programming language. Maximum clade credibility trees are shown in Figure 3 (tetrapods), Figure 4 (gymnosperms) and Figure 5 (Proteaceae).

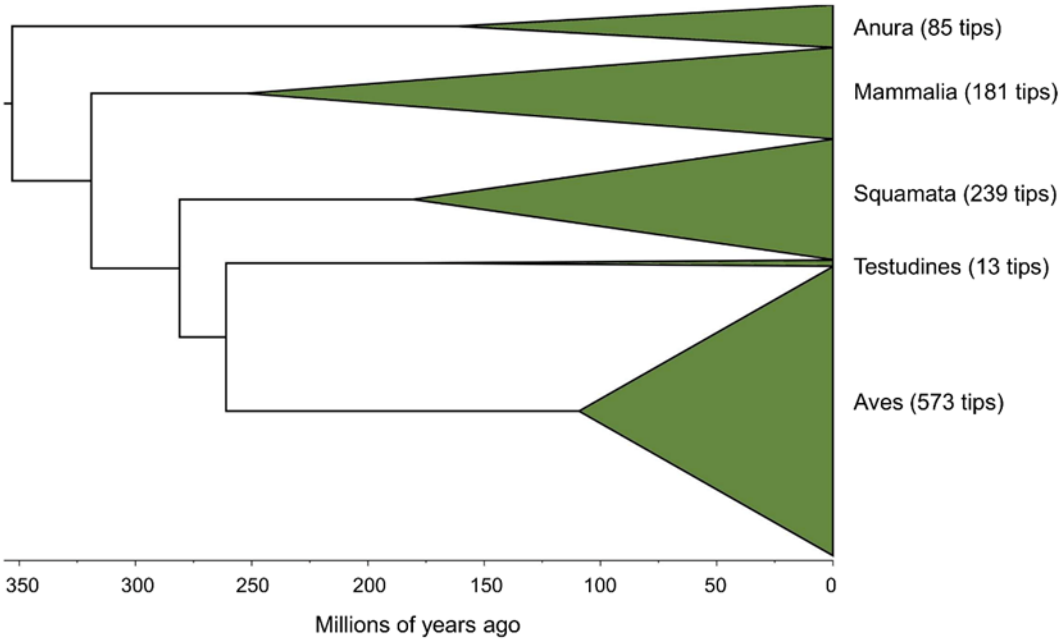

Figure 3 **Phylogenetic tree (maximum clade credibility) of NSW tetrapods with 1,091 tips (1,041 species and 50 subspecies). Tree is simplified to show major clades as triangles, with dimensions proportional to the age (horizontal) and diversity (vertical) of each clade**

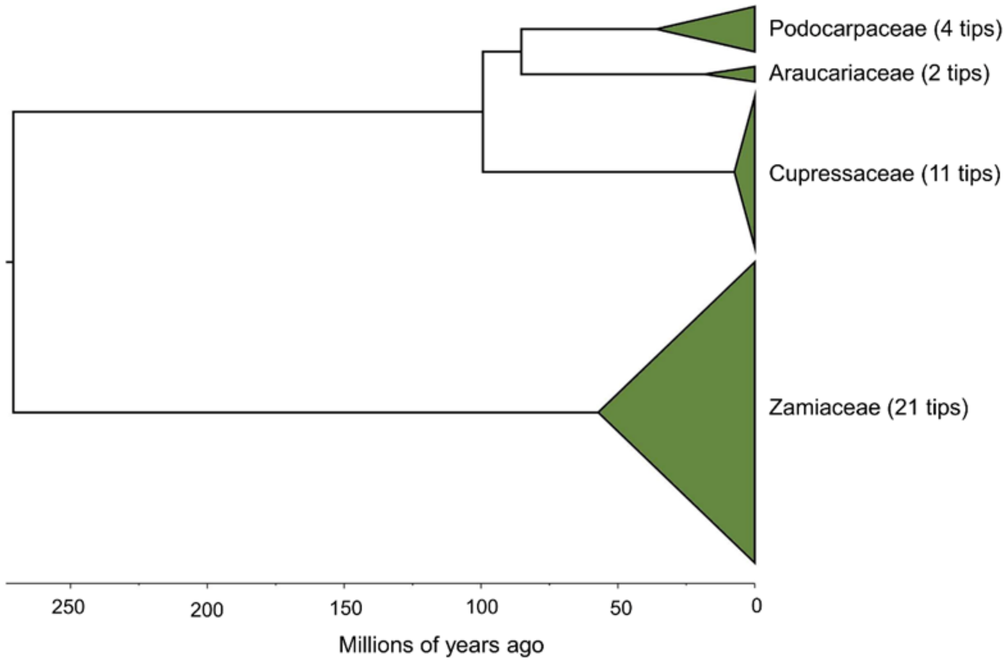

Figure 4 **Phylogenetic tree (maximum clade credibility) of NSW gymnosperms with 38 tips (38 species). Tree is simplified to only show major clades (families) as triangles, with dimensions proportional to the age (horizontal) and diversity (vertical) of each clade**

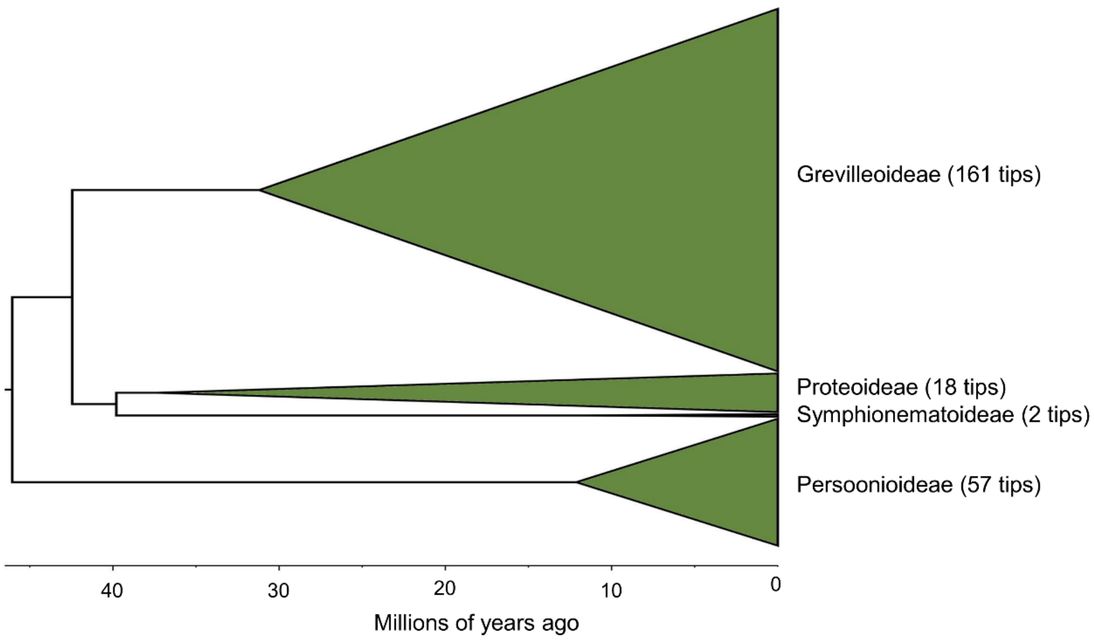

Figure 5 **Phylogenetic tree (maximum clade credibility) of NSW Proteaceae with 238 tips (215 species and 23 subspecies). Tree is simplified to only show major clades (subfamilies) as triangles, with dimensions proportional to the age (horizontal) and diversity (vertical) of each clade**

2.6 Threatened species conservation scenario analysis

The method described in this section applies to the **expected survival of listed threatened species** indicator.

For the second assessment, a basic conservation scenario analysis was conducted for species managed for conservation under selected programs. Gains in expected diversity (species count) from conservation action were estimated using Equation 4 (see section 2.1). A target survival probability was set to 0.95 (that is, 95% over 100 years) matching that of the project prioritisation protocol of the Saving our Species program (Brazill-Boast et al. 2018). This analysis is very limited because it depends on the reporting of overall project-level outcomes, rather than the direct outcomes of population monitoring, and is intended here as a proof of concept.

The outcomes of 2 conservation scenarios for expected survival were estimated. To model the scenarios, feasibility was set to either 0 (zero) or 1 (one), depending on the scenario. The assignment of feasibility scores for these scenarios is not realistic, but instead it partitions projects into those assumed to be successful and those assumed to be not successful. This is done for the purposes of demonstrating how conservation outcomes might be incorporated into expected survival indicators, and in the absence of better data on project feasibility.

In the first scenario, species that were actively managed under the Saving our Species program during the 2021–22 reporting period, and whose projects were reported at the species level to be ‘on track’ or ‘on track (inferred)’, were assigned a feasibility of 1 for reaching their targets within 100 years. All other species, that is species that were not ‘on track’, not reported at the species level or without active projects, were assigned a feasibility of 0. In the second scenario, species listed as extinct in New South Wales but with either active or planned reintroduction projects under the feral predator–free areas project in 2022 were assigned a target survival of 0.95 with a feasibility of 1.

By estimating the hypothetical gains in expected diversity under each scenario, it was then possible to partition the ‘potential loss’ and ‘already lost’ components of expected survival into further subcomponents along a spectrum of plausibility for conservation outcomes. The ‘potential loss’ component was partitioned into 2 subcomponents: the fraction ‘less likely’ to be lost due to active projects reaching their targets (gains under scenario 1); and the fraction ‘more likely’ to be lost due to active projects not reaching or not reporting species-level targets or without active projects (the remainder). The ‘already lost’ component was partitioned into 2 subcomponents: the fraction of diversity achieving ‘potential recovery’ through reintroduction of locally extinct species (scenario 2); and the fraction of diversity achieving ‘no recovery’ because no reintroduction project is planned or is possible (the remainder). The latter fraction includes those species for which no living populations are known to occur, in the wild or in captivity, anywhere in the world.

2.7 Permutation analysis of phylogenetic diversity

The method described in this section applies to **expected survival phylogenetic diversity** indicator.

To test for phylogenetic bias of extinction risk, permutation analysis was conducted to compare expected phylogenetic diversity against a null model of random allocation of survival probabilities. A significant result would indicate that threatened species are clustered in clades in the tree, resulting in greater or lesser loss of phylogenetic diversity than would otherwise be the case. For one version of the tree for each biological group, the order of survival probabilities assigned to the tips (species or subspecies) of the tree were permuted 1,000 times (including the actual order) and expected survival was calculated for each permutation. The tree version used was that identified as having maximum clade credibility (see section 2.5). If the observed expected phylogenetic diversity was significantly higher or lower than the mean of permuted values (2-tailed test), then the distribution of risk was phylogenetically biased.

2.8 Range area estimation for vascular plants

The methods described in this section applies to the **expected survival of all known species** indicator.

As described previously, in order to assess the expected survival of a species, we need to estimate the risk of that species going extinct. Given extinction risk assessments have not been conducted for every species, surrogate methods of assigning extinction risk are needed. The IUCN Red List of Species categories and criteria for listing have formed the basis for making these assessments for this indicator. The IUCN criteria require an estimation of the original and current range area (that is, distribution) of a species.

First assessment

The first assessment of expected survival of all known species was based on estimates of the area of the original and current geographic distributions for as many NSW species of vascular plants as possible. Following IUCN guidelines (IUCN 2012a), original range area was measured as the extent of occurrence and the area of occupancy.

- Extent of occurrence (EOO) is the area of a convex polygon covering all reliable records of the species' presence.
- Area of occupancy (AOO) is the summed area of 2 km × 2 km grid cells containing reliable records of that species.

Occurrence records of species were downloaded from the *Atlas of Living Australia* and filtered for those that were preserved specimens collected in 1950 or later and with coordinate uncertainty of less than 3 km (Nipperess et al. 2020b).

Estimates of original range areas were intersected with high-resolution maps of habitat intactness to estimate what proportion of original range area might be currently effective in supporting species' survival (Nipperess et al. 2020b). This was done by multiplying area of EOO or AOO by the mean habitat intactness index (scaled 0 to 1) within the defined area to estimate 'effective EOO' and 'effective AOO' (referred to collectively as 'effective range area'). Habitat intactness was measured by the 'ecological condition' and 'ecological carrying capacity' indicators (referred to collectively in this report as 'habitat condition'). These indicators estimated the relative intactness of original habitat in 2013 (compared to a 1750 baseline), with the latter also factoring in the relative connectivity of intact habitat (Love et al. 2020). This transformation of original range areas assumes a linear relationship between the habitat intactness index and the effective area of available habitat.

Second assessment

Methods for estimating original and current range area remain largely unchanged in the second assessment, with the exception that rules for filtering occurrence records were somewhat relaxed. Filtering for the first assessment was deemed too conservative and likely to underestimate range area. For the second assessment, we used the 'galah' R package (Westgate et al. 2023) to filter for all records of vascular plants occurring in New South Wales that were not fossil specimens and were collected in 1950 or later and with coordinate uncertainty of less than 3 km. Observation records (without preserved specimens) were thus also included in estimating range area. If a species had 3 or fewer records in total in New South Wales after filtering, then a range area was not calculated. For species listed as extinct in New South Wales, filtering rules were relaxed further to include all historical NSW records (including those prior to 1950) that were not flagged as spatially suspect in the Atlas of Living Australia.

For the second assessment, new maps of habitat intactness were available for the years 2007, 2013, 2017 and 2020 (DCCEEW 2025). The new maps were generated using updated methods and data. Range areas were intersected with these maps to calculate remaining effective habitat for each species for each of the reporting years. To match the 2-km grid resolution of the range areas, maps of habitat intactness were rescaled from their original 90-m resolution (Figure 6). This was done by resampling values from the 90-m raster to a new 2-km empty raster by bilinear interpolation using the 'resample' function of the 'raster' package (Hijmans 2021). This is a departure from the first assessment where raster cells were aggregated from 90 m to 1.98 km (ratio of 1:22) by averaging values in the aggregated cells. The resampling method produced very similar results to aggregation (spatial correlation of 0.994) while also producing rasters of precisely 2-km resolution (thus matching range area estimates exactly) while retaining the same origin and projection (Australian Albers EPSG: 3577) as the new habitat intactness maps.

Due to some missing source data, the new habitat intactness maps were missing a small area of the south-east corner of New South Wales (Figure 6). The size of this missing area was approximately 585 km^2 and was deemed to be insignificant for the purposes of calculating the ecological condition and ecological carrying capacity indicators at regional and statewide scales (DCCEEW 2025). However, this missing area might represent a significant proportion of the range area of any plant species with a restricted range in south-east New South Wales. To correct this problem, the missing area was patched with data from the 2013 ecological condition and ecological carrying capacity rasters produced for the first assessment. This was done to produce complete maps for 2007, 2013 and 2017. For the 2020 reporting year, the missing area was patched with data from the rasters produced for the *Fire and the environment 2019–20 summary* report (DPIE 2020b). The latter analysis intersected the habitat intactness maps from the first assessment with the fire extent and severity mapping spatial layer (Gibson et al. 2020) to model the impact of the 2019–20 bushfires on ecological condition and ecological carrying capacity (DCCEEW 2025).

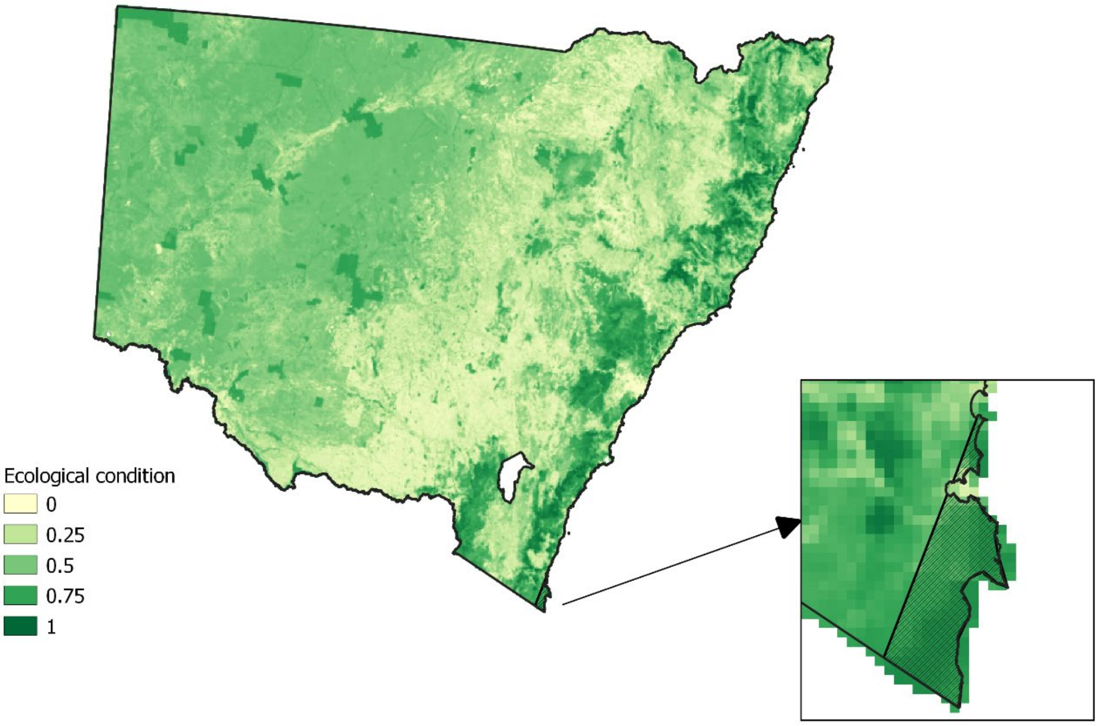

Figure 6 Map of ecological condition for 2017 rescaled from an original 90-m resolution to a 2-km resolution. Inset shows a close-up of the area (hatched) that was patched with 2013 data from the first assessment

2.9 Assessing extinction risk for all known species

The method described in this section applies to the **expected survival of all known species** indicator.

Summary of first assessment

The first assessment of the expected survival of all known species indicator used survival probabilities inferred from original and current range area by applying a modification of the IUCN criteria (IUCN 2012a). This approach was adopted to estimate extinction risk for a representative sample of species for a biological group (vascular plants) for which relatively few species have been formally assessed and listed. A species was considered to have an extinction risk equivalent to that of an IUCN risk category if the current AOO of that species, after down-weighting by ecological condition, was less than the relevant threshold value stipulated under Criterion B2 for that category (Nipperess et al. 2020b). Given that the criterion also required evidence of recent decline in range area, critical thresholds in proportional loss of AOO were also adopted from Criterion A of the IUCN Red List of Ecosystems (Bland et al. 2017) for the corresponding risk category. Thus, a species would have an extinction risk equivalent to an IUCN category if it qualified for critical thresholds for both remaining habitat (Criterion B2 of IUCN Red List of Species) and loss of habitat (Criterion A of IUCN Red List of Ecosystems). This provisional risk assessment process was applied to a **representative set of species** to infer the likely distribution of extinction risk across all known species of vascular plants. The representative set of species was selected such that they evenly and adequately covered the full range of environmental conditions (for example, climate, soil) present in New South Wales. See Nipperess et al. (2020b) for a description of how a representative set was generated.

Second assessment

The second assessment of the expected survival of all known species indicator adopted new approaches for assessing extinction risk. Firstly, there are some groups of species for which extinction risk has been **comprehensively assessed** at a global level by IUCN. There are 3 biological groups for which all (or almost all) species in New South Wales have been assessed by the IUCN: tetrapods, gymnosperms and plants in the family Proteaceae. This allowed us to use the IUCN categories (threatened and non-threatened) to assign an extinction risk category to all species in these groups.

Secondly, following on from the first assessment, we assessed the extinction risk of non-threatened vascular plants in New South Wales. Improved **statistical modelling** of a training set of 939 NSW vascular plant species was used to classify species into IUCN extinction risk categories based on threshold values of range area, loss of range area and phylogenetic position.

Comprehensively assessed biological groups

For selected biological groups that have been comprehensively assessed for extinction risk by the IUCN Red List of Species, risk categories for all known NSW species were compiled from multiple sources. Three comprehensively assessed groups were identified for New South Wales – tetrapods, gymnosperms and Proteaceae – allowing for the assignment of risk categories to all (or almost all) known species in those groups.

Adopting the list unification process described in section 2.4, species in these groups were preferentially assigned a risk category corresponding to their NSW threatened species listing. If not listed in New South Wales, a national or global listing was substituted instead. This included the threatened and non-threatened categories from the IUCN assessments (see Table 2). In the rare case where a species was not assessed by any authority (5 tetrapod spp., 10 Proteaceae spp.), it was considered 'data deficient'.

Statistical modelling of extinction risk

For vascular plant species **not formally listed**, extinction risk was predicted from a statistical model. A statistical approach was adopted for the second assessment because it doesn't rely on assumptions of the critical thresholds for assigning a species to a risk category which were made in the first assessment. It is, for example, not known what the exact relationship is between occupied habitat for a species and the habitat intactness indices. Therefore, the exact thresholds of range areas (AOO and EOO) used by IUCN to assign a species to a risk category may not be suitable when range area is adjusted by a habitat intactness index. Statistical modelling allows these thresholds to be informed by the data such that predictive error is minimised.

A statistical model was fitted to a training set of 939 species of NSW vascular plants. This training set consisted of 425 species formally listed as threatened in New South Wales and a further 514 species that have been assessed by the IUCN Red List of Species as non-threatened ('least concern' or 'near threatened' categories). The non-threatened species were added to the training set to enable parameterisation of the full range of extinction risk (as captured by IUCN categories). Non-threatened species were only included in the training set if they had a range entirely within New South Wales (that is, endemic to the state) **or** they had an EOO within New South Wales of more than 20,000 km^2. This restriction was imposed to ensure that species listed as non-threatened at a global scale were likely to also be non-threatened in New South Wales and would exclude, for example, species with large ranges globally but only marginal distributions in New South Wales. The resulting training set comprised 5 extinct, 22 critically endangered, 216 endangered, 182 vulnerable, 63 near threatened and 451 least concern species.

Current effective range area (see section 2.8) and loss of original range area were used as the primary predictors of extinction risk category in the fitted model. This essentially follows the previous practice of adapting Criterion B of the IUCN Red List of Species. Effective range area was calculated as EOO and AOO adjusted by ecological condition or ecological carrying capacity (see section 2.8). Loss of range area was calculated as the difference between original range area and effective range area, as a proportion of original range area. Adjustment for habitat intactness was done from the raster spatial layers for the 2017 reporting year, rather than from the latest available (2020), because 2017 was considered more representative of the longer term pattern of habitat intactness affecting occupancy and therefore range area. The 2020 layers were adapted from the 2017 layers by adjusting habitat intactness by fire severity values from the fire extent and severity mapping spatial layer (Gibson et al. 2020), to reflect the impact of the 2019–20 bushfires, but are not otherwise based on more recent data than the 2017 layers (DCCEEW 2025).

Phylogenetic position (that is, clade membership) was also included as a predictor of extinction risk category in the second assessment. Clades are known to vary in their extinction risk (Lughadha et al. 2020) and phylogeny is a useful surrogate for traits known to be factors predicting extinction risk (Ripple et al. 2017). Phylogenetic predictor variables were generated as phylogenetic eigenvectors (Diniz-Filho et al. 1998) of the vascular plant phylogenetic tree. The eigenvectors are the dimensions of an ordination where distances between species in the ordination space are scaled relative to their phylogenetic relatedness. First, a phylogenetic distance matrix was calculated, where phylogenetic distance is the total path length (millions of years of branch length) between each pair of species on the tree. Thus, if a pair of species last shared a common ancestor 5 million years ago, then the phylogenetic distance would be 10 million years. A principal coordinates analysis was then performed on the distance matrix to generate ordination dimensions (phylogenetic eigenvectors). The first 3 eigenvectors were retained as predictors for the model and cumulatively explained 33%, 42% and 49% of the variance in phylogenetic distance between species (Figure 7).

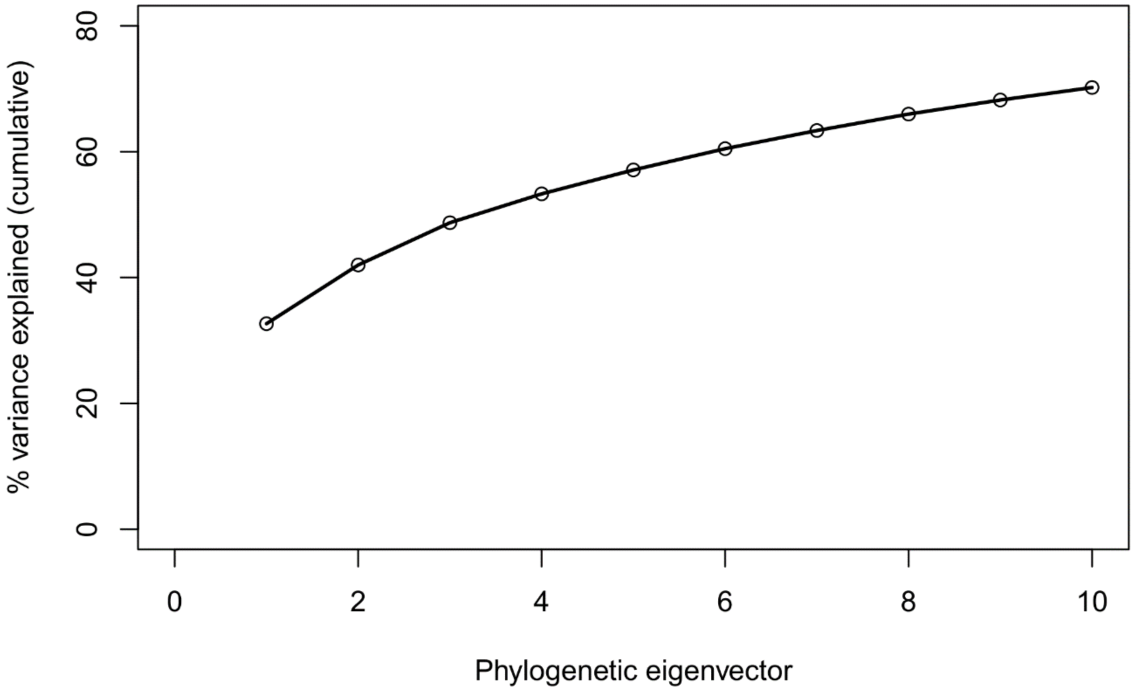

Figure 7 **Cumulative variance explained by the first 10 eigenvectors of an ordination of phylogenetic distances between species of NSW vascular plants**

A boosted regression tree algorithm was used to model extinction risk category of the species of the training set from the predictor variables. This is a very similar approach to that recently used to predict extinction risk for the world's flowering plants (Bachman et al. 2024). The algorithm classifies objects by recursively partitioning the data to produce progressively smaller groups based on threshold values of the predictor variables (De'ath 2007). The threshold values are chosen to minimise error in assigning an object (species) to a category (extinction risk category). To avoid overfitting, the algorithm can be constrained to limit the complexity of the resulting tree and thus the number and size of groups into which objects are classified. The initial tree was generated by running the 'rpart' algorithm in the 'rpart' package (Therneau and Atkinson 2019), using default settings for classification trees. Cross-validation was then used to assess the complexity of a range of simpler trees versus their relative error rate in predicting risk category (Figure 8). Cross-validation used a jack-knife procedure which repeatedly split the data into 10 equal segments, left one segment out when fitting the tree, and measured relative predictive error for the left-out segment. The 'best' tree is one that balances model simplicity with relatively low error (De'ath 2007). Thus, while the tree with the lowest relative error classified the training set into 11 groups, we instead chose the simpler 7-group tree which had very similar error rates (within 1 standard error of the 11-group tree – dashed line in Figure 8).

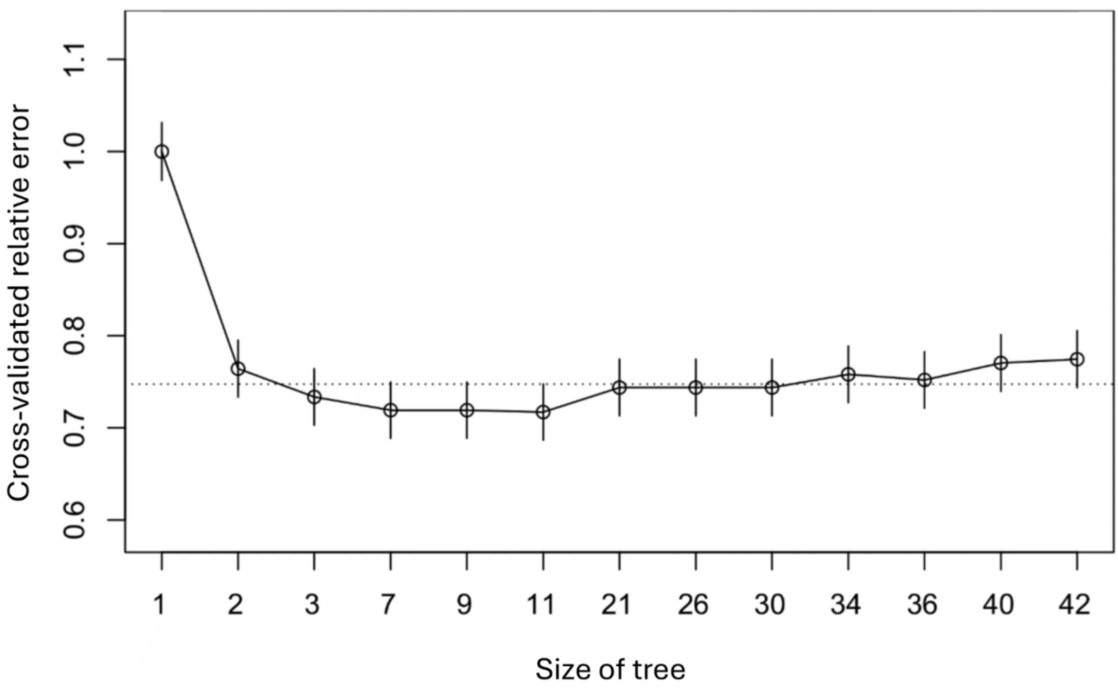

Figure 8 **Cross-validated relative error (mean ± 1 standard error) of regression trees compared to their size (number of groups in classification) classifying NSW vascular plant species into extinction risk categories**

The resulting decision tree (Figure 9) classified the 939 species in the training set into risk categories via a series of binary splits based on threshold values of the predictor variables. The risk category assigned to each species was the most likely, given the effective range area, loss of range area and phylogenetic position of that species. However, the model also assigned, for each species, probabilities of membership for all risk categories. The most important factor in the model, separating out most non-threatened species, was the effective extent of occurrence (EOO), where effective area was determined by down-weighting by habitat condition. The next most important factor was effective area of occupancy (AOO), as weighted by habitat condition. Proportional loss of range area and phylogenetic position were less important factors but allowed for some discrimination between categories.

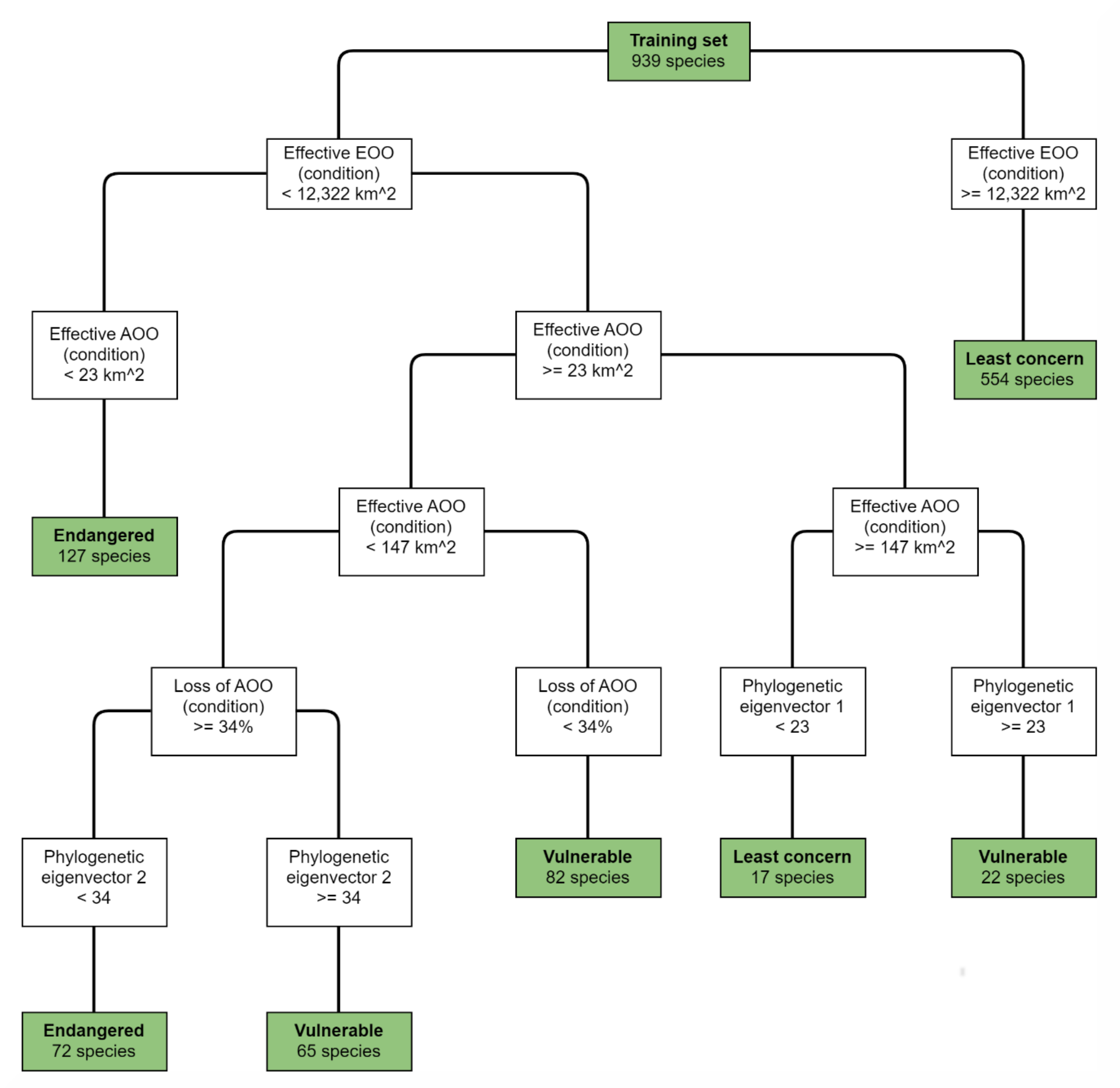

Figure 9 **Decision tree classifying a training set of 939 NSW vascular plant species into IUCN extinction risk categories based on threshold values of range size, loss of range size and phylogenetic position**

The decision tree was used to predict probabilities of survival for all species in the training set. The decision tree was also used for 4,683 species of vascular plants in New South Wales that have adequate predictive data. For each species (i), the predicted probability of survival ($\hat{q}_i$) is the probability of membership (p_{ic}) in the risk category (c) multiplied by the probability of survival (q_c) of category c, summed for the set (R) of all risk categories (Equation 7). These predicted probabilities were then summed to calculate a predicted overall expected survival.

Equation 7 $\hat{q}_i = \sum_{c \in R} p_{ic} * q_c$

Predictions of survival probabilities for each species and overall expected survival showed good agreement with the values calculated directly from the listed categories of species of the training set. There was a reasonably strong linear relationship (Pearson correlation of 0.760) between probability of survival inferred from a listing versus that predicted from the model (Figure 10). Variability in prediction for species listed in a category was relatively high, however, and the model tended to overpredict survival for species listed as extinct, critically endangered or endangered; and underpredict survival for vulnerable and non-threatened species. Despite variability in prediction at the species level, the ratio of 'predicted' expected survival (calculated from predicted probabilities) to 'inferred' (calculated directly from the listed categories) was very close to 1 (Figure 11). Bootstrap testing, by randomly sampling (with replacement) the species of the training set, showed that the ratio varied only a small amount when species membership was altered. This indicates that 'outlier' species, that is those species with the greatest discrepancy between predicted and inferred probabilities of survival, have little influence on the prediction of overall expected survival.

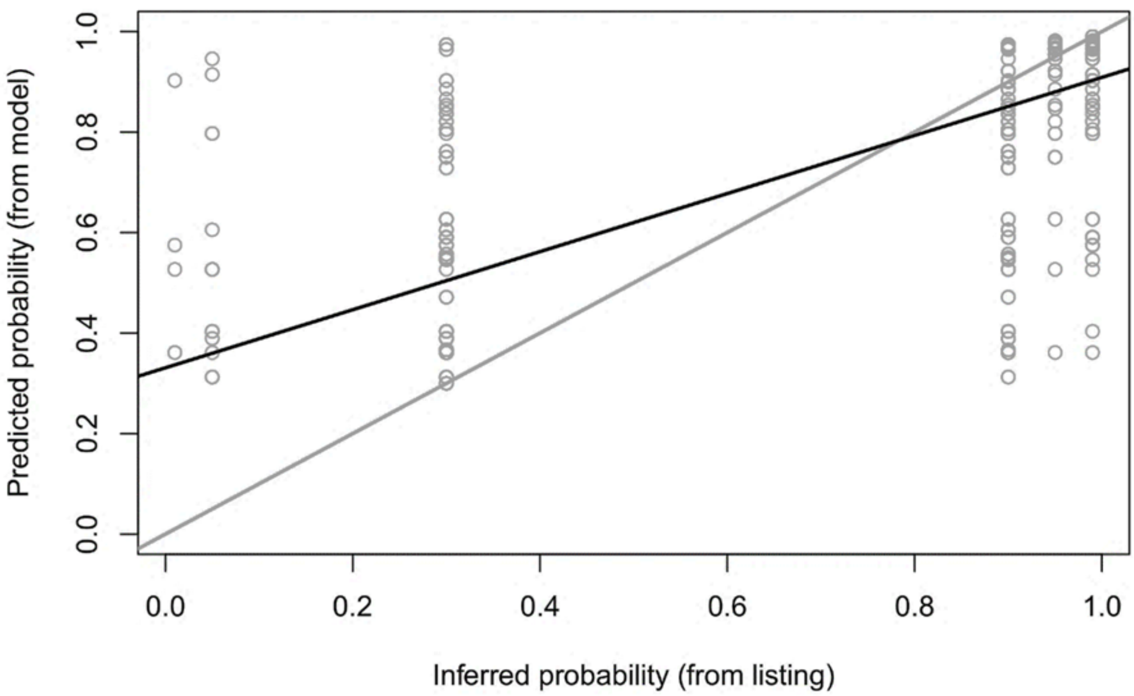

Figure 10 **Scatter plot of probability of survival for NSW vascular plant species as inferred from formal listings versus predicted from a decision-tree model. Black line is a linear fit (illustrative purposes only) and grey line indicates the ideal one-to-one relationship**

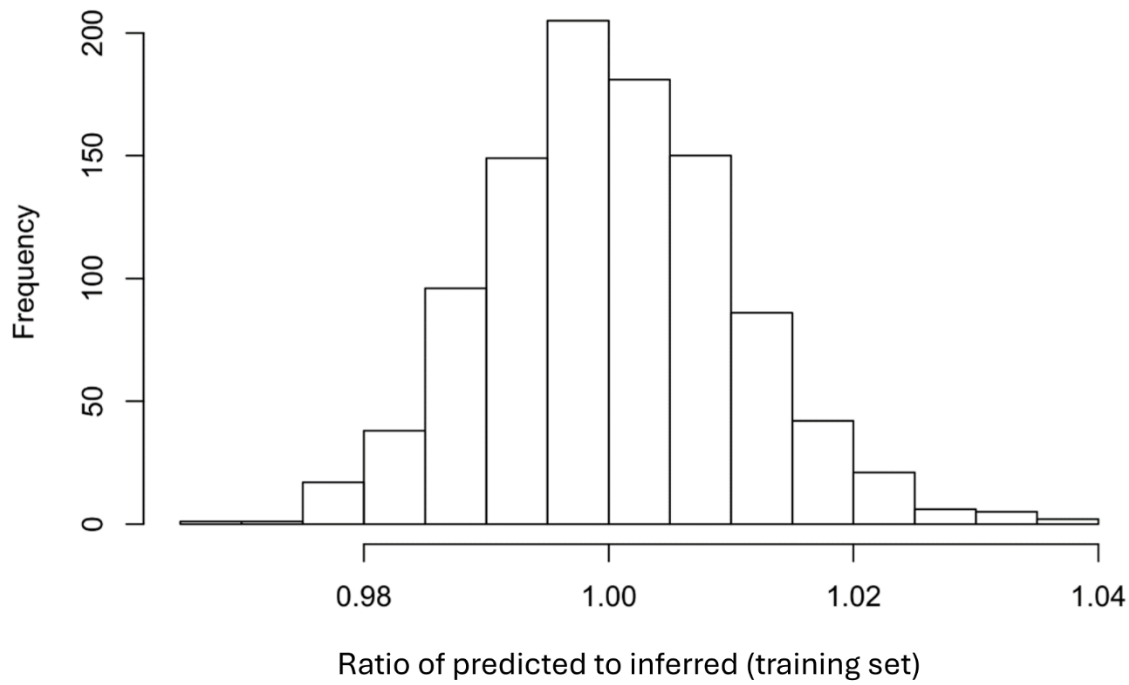

Figure 11 **Frequency histogram of the ratio of expected survival predicted from a decision-tree model to that 'inferred' (calculated directly from listed categories) across 1,000 bootstrap replicates**

The **expected survival of all known species indicator** for vascular plants was calculated by predicting survival probabilities of unlisted species in a representative species set. For the first assessment, 9 representative species sets were generated. The species in these sets were chosen such that they collectively and evenly represented the full range of environmental conditions encountered in New South Wales (see Nipperess et al. 2020b for a full description of the selection method). These sets were used again without alteration in the second assessment.

For each set, the survival probabilities of species with no formal listing in New South Wales were estimated from the decision tree. Species that were formally listed were assigned a survival probability corresponding to their listed category. Once all species were assigned a probability of survival, these values were summed for all species in the set to obtain an estimate of expected survival. This summation was divided by the number of species in the set to calculate the proportion of species expected to survive. Because there were 9 sets, varying in species membership, these results were averaged across sets to get the final value for the indicator. Under the assumption that the species in the sets were representative of all known species in New South Wales, then the indicator, as a proportion, is a viable estimate of expected survival for all known species. With somewhat less certainty, the proportion is also a viable estimate of expected survival of all known and undiscovered species, so long as undiscovered species are relatively few and are not strongly biased towards higher or lower survival relative to known species. However, the latter may be a weak assumption as there is evidence that recently discovered species are more likely to be threatened (Bachman et al. 2024).

2.10 Indicator workflows

This section refers to the workflow diagrams for each indicator, which are included in Appendix A. Object identifiers listed below (for example, 'SD2501') relate directly to parts of the workflow. Where a workflow object occurs in multiple workflows, it is defined only once at first appearance in a workflow.

Expected survival of listed threatened species

This indicator is the number or percentage of species listed as threatened in New South Wales expected to survive in 100 years. The workflow (Appendix A, Figure 20) takes lists of threatened species as input, resolves differences with a list unification process, and then assigns probability of survival based on assigned risk category. Expected survival is then calculated as the sum of probabilities. Targets for conservation, and the feasibility of those targets, are optional inputs used to calculate potential change in the indicator under conservation scenarios.

Threatened species lists (SD2501, SD2502)

Lists of species and subspecies formally assessed as threatened in New South Wales or a larger jurisdiction, along with their assigned extinction risk category. Includes species or subspecies with one or more populations listed as endangered under the Biodiversity Conservation Act, but only if the species itself is not listed as a threatened species.

The foundational list is that comprising species and subspecies listed under Schedule 1, Parts 1, 2 and 3, and Schedule 3, Part 1 of the Biodiversity Conservation Act. These data are supplemented by additional assessments under the Environment Protection and Biodiversity Conservation Act and the IUCN Red List of Species.

List unification process (P02501)

The decision process by which data are integrated across lists (see section 2.4) to produce a list of threatened species and their assumed risk categories over time. This includes resolution of taxonomic names and risk categories over time and across authorities.

Standardised threatened species list (DD02501, DD02502)

List of all species and subspecies listed as threatened in New South Wales, and any species with one or more populations listed as endangered under the Biodiversity Conservation Act, but only if the species itself is not listed as a threatened species.

Taxonomic names are as given in the Schedules of the Biodiversity Conservation Act. Risk category at time t for a listed taxon is as resolved by the list unification process.

Probabilities of survival (SD02504)

Probabilities of survival in 100 years for species for each risk category (see Table 3).

Targets and feasibility (SD02505, SD02506)

Targets (probabilities of survival) and feasibility (per species) for conservation scenario analysis (see section 2.6). For the second assessment, the target for all species managed under the Saving our Species program was set to a survival probability of 0.95 (that is, 95% surviving over 100 years). Feasibility was set to either 0 (if species not 'on track' to recovery) or 1 (if species 'on track' to recovery).

Expected diversity calculator (P02502)

Mathematical process by which expected survival for species is calculated from risk category (see section 2.1) and corresponding probability of survival (see section 2.2). Expected survival for subspecies is aggregated to species level.

Expected existence of listed threatened ecological communities

This indicator is the number or percentage of ecological communities listed as threatened in New South Wales expected to exist in 100 years. The workflow (Appendix A, Figure 21) takes lists of threatened ecological communities as input, resolves differences with a list unification process, and then assigns probability of survival based on assigned risk category. Expected survival is then calculated as the sum of probabilities.

Threatened ecological communities (SD03001, SD03002)

Lists of ecological communities formally assessed as threatened in New South Wales. The list is that comprising ecological communities listed under Schedule 2, Parts 1, 2 and 3, and Schedule 3, Part 3 of the Biodiversity Conservation Act.

List unification process (P03001)

The decision process by which data are integrated across lists (see section 2.4) to produce a list of ecological communities and their assumed risk categories over time. Involves resolution of names and risk categories if they have changed over time. Matching of entities across authorities was not attempted for the second assessment.

Standardised threatened ecological communities (DD3001, DD3002)

List of all ecological communities listed as threatened in New South Wales. Names are as given in the Schedules of the Biodiversity Conservation Act. Risk category at time t for a listed community is as resolved by the list unification process.

Probabilities of viability (SD03004)

Probabilities of existence in 100 years for ecological communities for each risk category (see Table 3).

Targets and feasibility (SD03005, SD03006)

Targets (probabilities of existence) and feasibility (per community) for conservation scenario analysis. Not attempted for the second assessment.

Expected diversity calculator (P03002)

Mathematical process by which expected existence for ecological communities is calculated from risk category (see section 2.1) and corresponding probability of viability (see section 2.1).

Expected survival of phylogenetic diversity for listed threatened species

This indicator is the percentage of phylogenetic diversity in a biological group expected to survive in New South Wales in 100 years. The workflow (Appendix A, Figure 22) takes a list and phylogenetic tree of all known species in a biological group and lists of threatened species as input, resolves differences with a list unification process, and then assigns probability of survival for each branch in the tree based on the risk categories of descendent species. Expected survival is then calculated as the sum of probabilities, weighted by branch length. Targets for conservation, and the feasibility of those targets, are optional inputs used to calculate potential change in the indicator under conservation scenarios.

Official census (SD03503)

A list of all known species in a biological group occurring naturally in New South Wales. The list is sourced from the relevant taxonomic authority for the biological group (see section 2.3), with taxonomic nomenclature aligned to the National Species List.

List unification process (P03501)

The decision process by which data are integrated across lists (see section 2.4) to produce a list of all known species and their assumed risk categories over time. This includes resolution of taxonomic names and risk categories over time and across authorities.

Standardised official census (DD03501, DD03502)

List of all species in a biological group known to occur in New South Wales. Subspecies listed as threatened in New South Wales, and any known sister subspecies, are also included. Taxonomic names are as given in the National Species List, except where this conflicts with the Schedules of the Biodiversity Conservation Act. Risk category at time t for a listed taxon is as resolved by the list unification process.

Phylogenetic tree structure (SD03504)

Set of 100 versions of phylogenetic tree of species of a biological group. Lengths of branches connecting species together are scaled in millions of years of evolutionary history. Produced by editing published source phylogenetic trees (see section 2.5). Names match those of the standardised official census.

Expected diversity calculator (P03502)

Mathematical process by which expected survival of phylogenetic diversity is calculated from risk category (see section 2.1), phylogenetic structure (see section 2.5) and probability of survival (see section 2.2).

Expected survival of all known species

This indicator is the number or percentage of all known species of a biological group in New South Wales expected to survive in 100 years. The indicator has 2 separate workflows, one for the comprehensively assessed biological group (Appendix A, Figure 23) and one for the representative species set (Appendix A, Figure 24). For a comprehensively assessed group, the workflow takes lists of threatened species as input, resolves differences with a list unification process, and then assigns probability of survival based on assumed risk category. For a group that is not comprehensively assessed, the workflow takes a list of species that is thought to be representative of the group (in this assessment, vascular plants) and assigns survival probabilities through a statistical modelling process. In either case, expected survival is then calculated as the sum of probabilities.

Species occurrence records (DD00001)

Table of known occurrence records for the set of species identified in the representative species sets. Each record includes the species name, higher taxonomy, spatial coordinates and date of collection or observation. Data were downloaded from the *Atlas of Living Australia* and filtered by the process described in section 2.8.

NSW mask (DD01002)

A spatial mask defining the area of jurisdiction for New South Wales. Used to constrain range area estimates to that within the defined jurisdiction.

Habitat condition (DD09014, DD09015)

Spatial layers of the habitat condition indicators rescaled to a 2-km resolution on an Australian Albers equal-area projection (EPSG:3577). One layer for each year (2007, 2013, 2017, 2020) for each of ecological condition and ecological carrying capacity. Each pixel is scored 0 to 1.

Range area calculator (P04501)

Process by which estimates of effective range area (area of occupancy [AOO] and extent of occurrence [EOO]) are calculated by intersecting habitat condition layers with species occurrence records (see section 2.8).

Training species set (DD04509)

List of species names selected to parameterise the extinction risk model, including their risk category as assigned by either the NSW Threatened Species Scientific Committee or the IUCN Red List of Species (see section 2.9).

Extinction risk categorisation (P04502)

Process by which species are assigned by the model to predicted risk categories based on their range area (original and current) and phylogenetic position (see section 2.9). Output from the model is probability of assignment to each risk category.

Representative species sets (DD00009)

Stack of 9 lists (sets) of species names used to create samples for which expected survival was calculated. Each set consists of species selected to evenly represent the full range of environmental conditions in New South Wales (Nipperess et al. 2020b).

Expected diversity calculator (P04503)

Mathematical process by which expected survival for species is calculated from probability of assignment to risk category and corresponding probability of survival (see sections 2.1 and 2.9).

3. Updated reporting

3.1 Expected survival of listed threatened species

The expected survival of listed threatened species has been updated for the 2022 reporting year for all 1,050 species listed as threatened in New South Wales. The 'all groups' category here relates to all listed species. A breakdown into biological groups (vascular plants, tetrapods and other) is also included. See Figure 12 and Table 6. The indicator is now reported as a strict species count, with subspecific taxa being aggregated into species-level units (see section 2.1). Species with endangered populations are also now included (see section 2.2), even if the species as a whole is not currently listed as threatened.

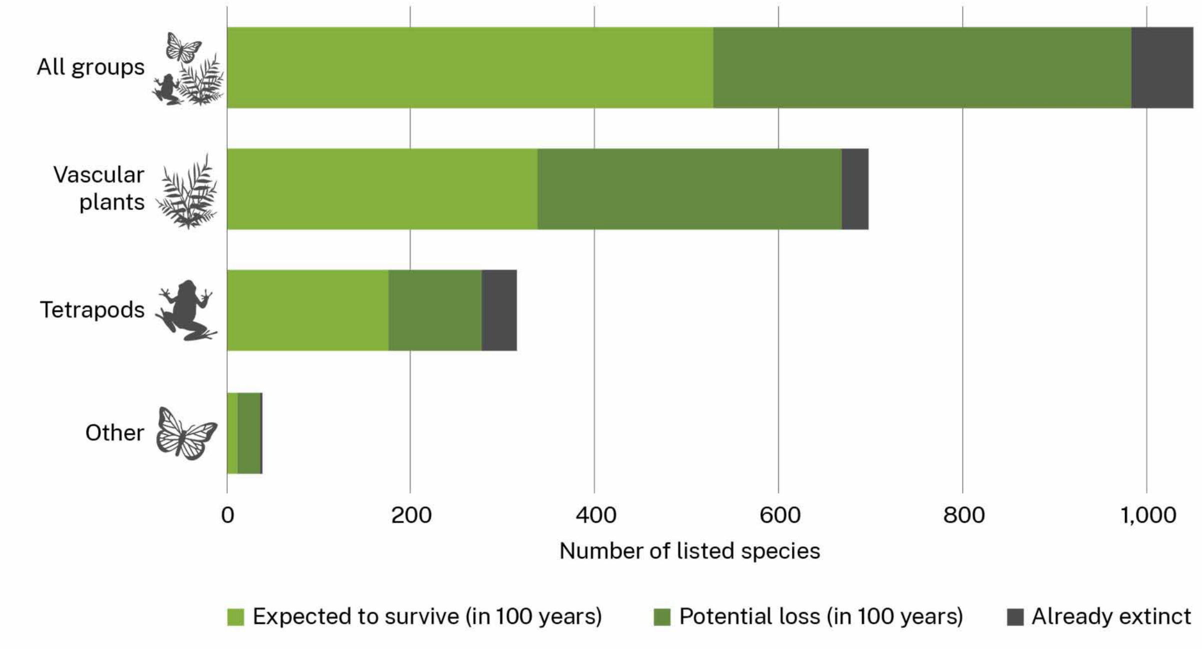

Figure 12 Count of listed threatened species in 2022 expected to survive in 100 years, by biological group

Total species count is partitioned into 3 components: expected survival (count of species expected to survive), potential loss (count of species expected to be lost), and already extinct (count of species presumed to be extinct in New South Wales). This follows previous practice, although with a change in language from 'expected loss' to 'potential loss' to better reflect the uncertainty regarding the true probabilities of extinction associated with IUCN risk categories. Also, 'already lost' is referred to as 'already extinct' in the corresponding report card in this specific case.

The historical trajectory in expected survival, potential loss and already lost species counts has been updated for the reporting years 1997, 2002, 2007, 2012, 2017, 2020 and 2022 (Figure 13, Table 7). The trend is updated from previous reporting to make better of use of available data by integrating the latest information on threatened species listings across authorities. The total count of species is standardised to the 2022 reporting year, with species being generally assumed to be threatened prior to listing (see section 2.4).

Table 6 **Count (and percentage) of listed threatened species in 2022 expected to survive in 100 years, by biological group**

Group	Expected survival in 100 years	Potential loss in 100 years	Already lost	Total
All groups	**528 (50%)**	**455 (43%)**	**67 (7%)**	**1,050**
Vascular plants	**338 (49%)**	**330 (47%)**	**29 (4%)**	**696**
Flowering plants	330 (49%)	315 (47%)	28 (4%)	673
Ferns	5 (31%)	10 (63%)	1 (6%)	16
Gymnosperms	3 (43%)	4 (57%)	0 (0%)	7
Tetrapods	**177 (56%)**	**100 (32%)**	**38 (12%)**	**315**
Birds	92 (65%)	38 (27%)	12 (8%)	142
Mammals	46 (49%)	22 (24%)	25 (27%)	93
Reptiles	29 (59%)	19 (39%)	1 (2%)	49
Frogs	13 (42%)	18 (58%)	0 (0%)	31
Other	**13 (33%)**	**25 (64%)**	**1 (3%)**	**39**
Invertebrates	7 (26%)	19 (70%)	1 (4%)	27
Fungi	5 (56%)	4 (44%)	0 (0%)	9
Algae and moss	1 (33%)	2 (67%)	0 (0%)	3

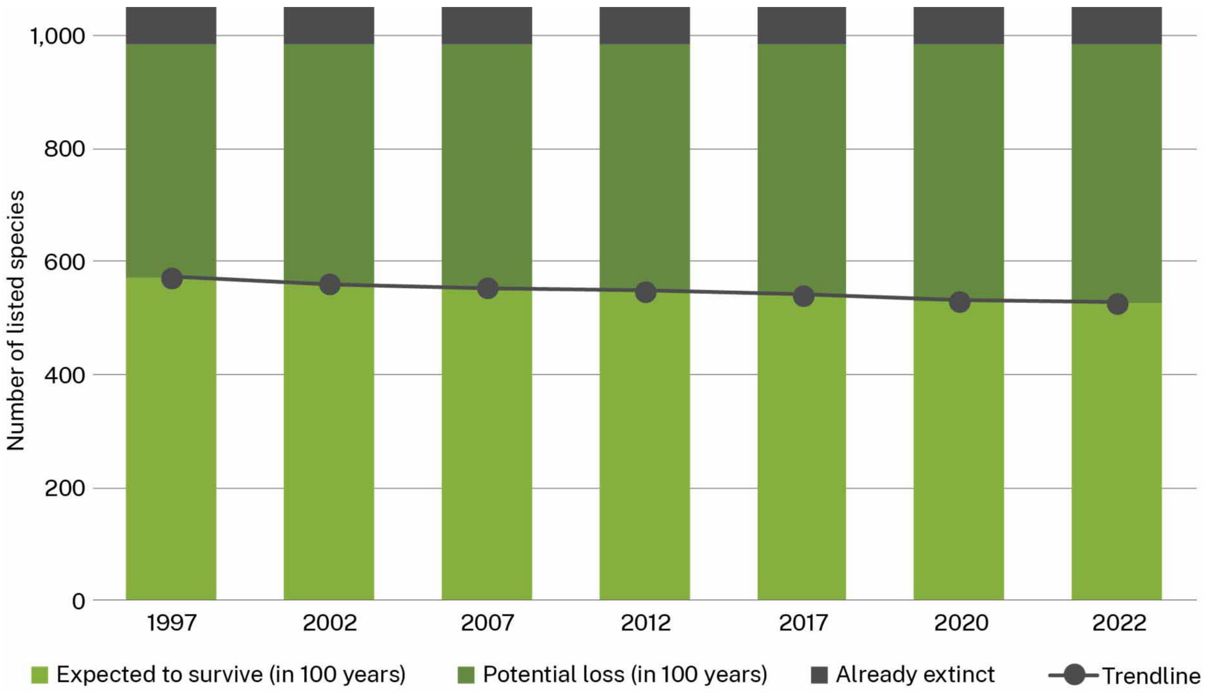

Figure 13 **Historical trend in the count of listed threatened species expected to survive in 100 years**

Table 7 **Count (and percentage) of listed threatened species expected to survive in 100 years, by reporting year**

Year	Expected survival in 100 years	Potential loss in 100 years	Already lost
1997	572 (55%)	412 (39%)	65 (6%)
2002	560 (53%)	424 (41%)	65 (6%)
2007	554 (53%)	431 (41%)	65 (6%)
2012	548 (52%)	436 (42%)	66 (6%)
2017	541 (51%)	442 (42%)	67 (7%)
2020	531 (51%)	452 (43%)	67 (7%)
2022	528 (50%)	455 (43%)	67 (7%)

A basic conservation scenario analysis divided the potential loss and already lost components into subcomponents based on the qualitative likelihood of either avoiding loss or recovering lost populations (Table 8). In this simple demonstration, loss was assumed to be less likely for those species actively managed in 2021–22 in conservation projects reported to be on track to reaching targets. Loss was assumed to be more likely for those species that were actively managed in 2021–22 in projects that were either not on track or where species-level outcomes are unknown or without active projects (see section 2.6). Potential recovery of locally extinct species was considered possible for those species with active or planned reintroduction projects in 2022, under the feral predator–free areas project.

Table 8 **Count (and percentage) of listed threatened species as of 2022 expected to survive in 100 years, including potential offsets of loss through conservation actions**

Component	Subcomponent	Species count (%)
Expected survival	–	528 (50%)
Potential loss	Less likely to be lost – on track to recovery	113 (11%)
	More likely to be lost – limited or no evidence of recovery	342 (33%)
Already lost	Potential recovery through reintroduction	11 (1%)
	Locally or globally extinct	56 (5%)
Total	**–**	**1,050 (100%)**

3.2 Expected existence of listed threatened ecological communities

The expected existence of listed threatened ecological communities has been updated for the 2022 reporting year (Figure 14 and Table 9). Ecological communities were classified into realms, following the *IUCN Global Ecosystem Typology* (Keith et al. 2020), and expected existence reported all threatened ecological communities ('all realms') and separately for each realm group. Because the Biodiversity Conservation Act does not list entities that are the purview of the *Fisheries Management Act 1994*, those communities listed under the Biodiversity Conservation Act are predominately terrestrial. A small number of listed communities are transitional between the terrestrial and marine or freshwater realms, or habitats (Table 9).

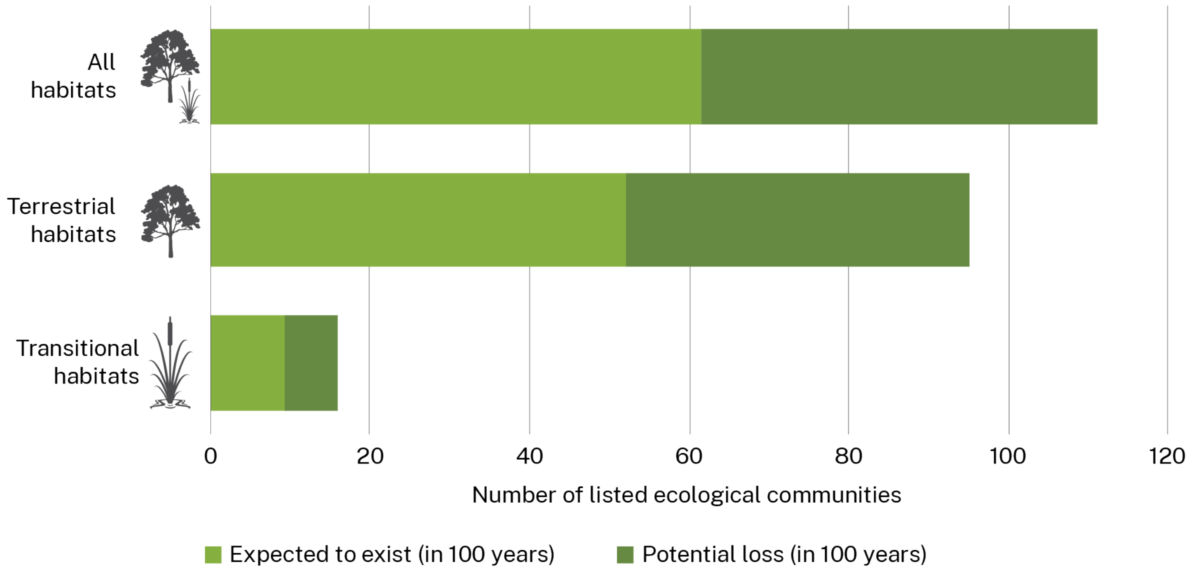

Figure 14 **Count of listed threatened ecological communities in 2022 expected to exist in 100 years, by realm**

Table 9 **Count and percentage of listed threatened ecological communities as of 2022 expected to exist in 100 years, by realm**

Group	Expected survival in 100 years	Potential loss in 100 years	Already lost	Total
All realms	62 (55%)	49 (45%)	0 (0%)	111
Terrestrial	52 (55%)	43 (45%)	0 (0%)	95
Terrestrial-Freshwater[1]	8 (57%)	6 (43%)	0 (0%)	14
Terrestrial-Marine[1]	1 (50%)	1 (50%)	0 (0%)	2

1. Terrestrial-Freshwater and Terrestrial-Marine are collectively referred to as 'Transitional habitats' in Figure 14.

The historical trajectory in the expected count of listed threatened ecological communities is not displayed as a graph in the second assessment because there is no change in the indicator from 1997 to 2022. This is a result of the conservative approach taken where entities are considered the same risk category prior to listing and where critically endangered entities that were previously listed as endangered prior to 2006 are considered to have been critically endangered for the whole period (see section 2.4).

3.3 Expected survival of phylogenetic diversity

The expected survival of phylogenetic diversity of listed threatened species has been updated for the 2022 reporting year (Figure 15, Table 10) and is reported separately for selected biological groups. Tetrapods are reported as a single group (combining frogs, mammals, reptiles and birds), and 2 evolutionarily significant vascular plant groups (gymnosperms, Proteaceae) have been added. The selection of biological groups is constrained by data availability but better represents the diversity of species listed as threatened in New South Wales. For comparison over time, tetrapod phylogenetic diversity is reported for 2017, 2020 and 2022 (Table 10). The indicator for the 2017 reporting year has been updated from that of the first outlook report due to changes in method and input data (see section 2.5). Indicator values are reported as percentages (proportion of original phylogenetic tree expected to survive), and in millions of years of summed branch length, averaged across 100 plausible trees.

The reported indicator values are means across 100 plausible trees for each biological group, reflecting uncertainty in evolutionary relationships. The distribution of values around the mean was relatively small, with the largest proportional variation seen in gymnosperms (Figure 16). Generally, smaller biological groups (gymnosperms and Proteaceae) showed more proportional variation across plausible trees.

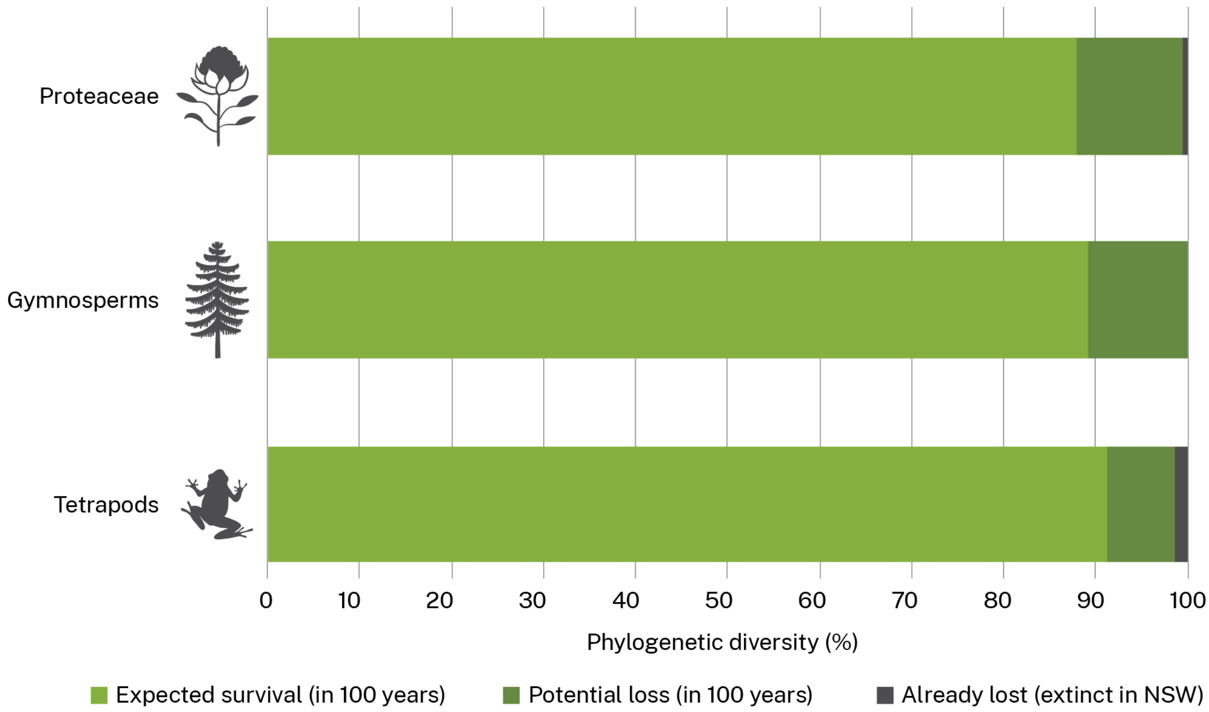

Figure 15 Mean percentage of phylogenetic diversity in 2022 expected to survive in 100 years, by biological group

Table 10 Mean phylogenetic diversity in millions of years (Ma) (and percentage of total tree length) expected to survive in 100 years, by biological group

Group	Year	Expected survival in 100 years	Potential loss in 100 years	Already lost	Total
Tetrapods	2017	21,086 Ma (92%)	1,635 Ma (7%)	318 Ma (1%)	23,038 Ma
	2020	21,063 Ma (91%)	1,647 Ma (7%)	329 Ma (1%)	23,038 Ma
	2022	21,011 Ma (91%)	1,698 Ma (7%)	329 Ma (1%)	23,038 Ma
Gymnosperms	2020	1,052 Ma (89%)	125 Ma (11%)	0 Ma (0%)	1,177 Ma
	2022	1,049 Ma (89%)	128 Ma (11%)	0 Ma (0%)	1,177 Ma
Proteaceae	2020	1,254 Ma (88%)	164 Ma (12%)	8 Ma (1%)	1,426 Ma
	2022	1,254 Ma (88%)	164 Ma (12%)	8 Ma (1%)	1,426 Ma

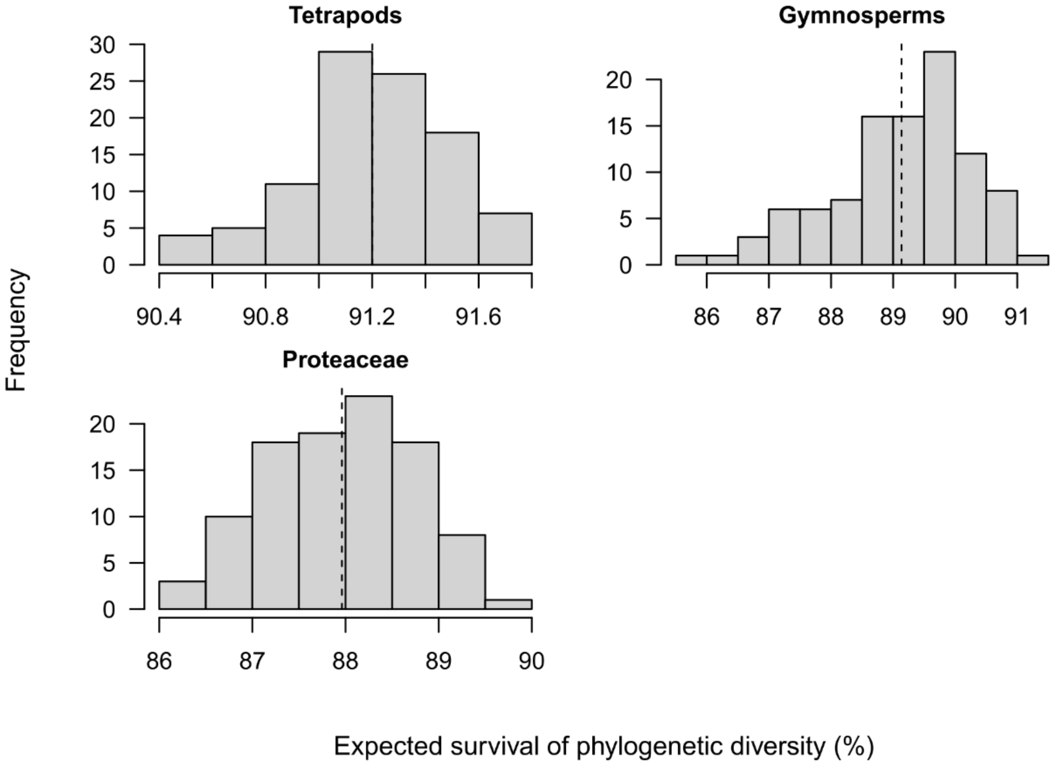

Figure 16 **Frequency distribution, for each biological group, of percentage phylogenetic diversity as of 2022 expected to survive in 100 years across plausible trees. The mean percentage is indicated by a vertical dashed line**

A permutation test of phylogenetic bias in survival probabilities for each biological group indicated that the observed pattern was generally not significantly different from the randomisations (Figure 17). The exception was gymnosperms in which the observed expected survival of phylogenetic diversity was lower than most randomisations. This indicates that extinction risk was somewhat biased towards more evolutionarily distinctive species and clades in gymnosperms (2022 data, $p = 0.073$, 2-tailed test).

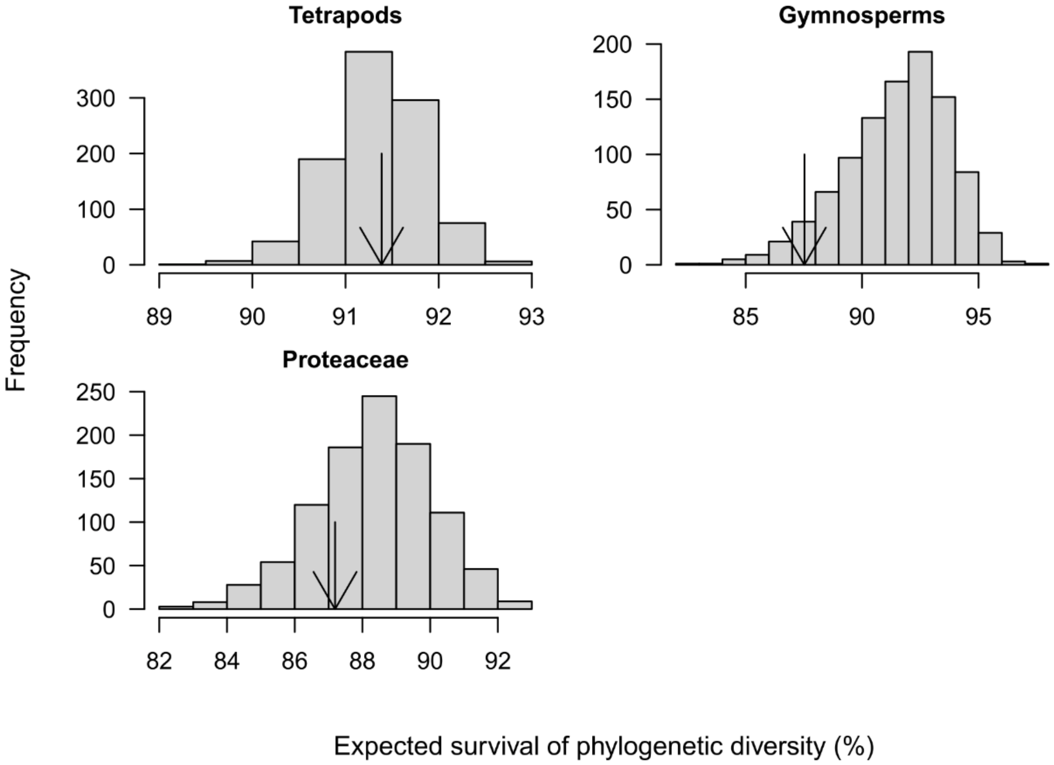

Figure 17 **Frequency distribution, for each biological group, of percentage phylogenetic diversity as of 2022 expected to survive in 100 years for 1,000 random permutations of survival probabilities. The expected phylogenetic diversity for the observed pattern of survival probabilities is indicated by an arrow**

3.4 Expected survival of all known species

The expected survival of all known species has been updated for the 2020 reporting year for selected biological groups and all vascular plants.

Comprehensively assessed biological groups

Three biological groups are reported for the first time: tetrapods (reported as a single group combining frogs, mammals, reptiles and birds), gymnosperms and Proteaceae (Figure 18, Figure 19 and Table 11). Expected survival for all known NSW species in these biological groups is reported from the compilation and unification of state, national and global threatened species lists. For comparison over time, expected survival of all known tetrapods is also reported for 2017 (Table 11). Choice of biological groups and reporting years is constrained by available data.

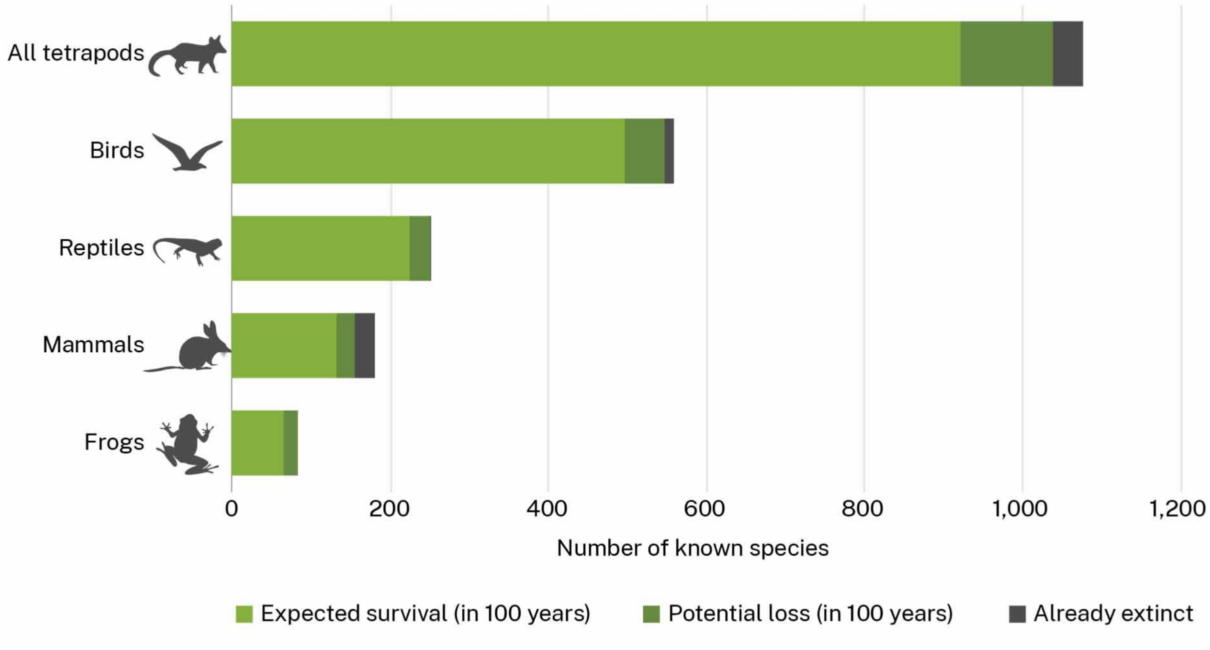

Figure 18 **Count of all known NSW species of tetrapods in 2020 expected to survive in 100 years, by biological group**

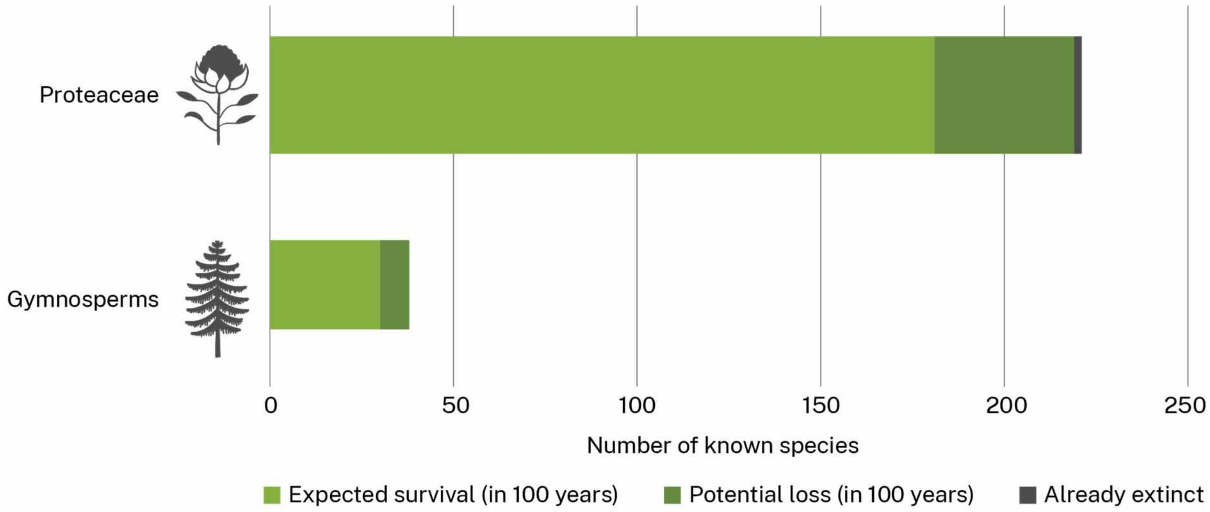

Figure 19 **Count of all known NSW species of Proteaceae and gymnosperms in 2020 expected to survive in 100 years**

Table 11 **Count (and percentage) of all known NSW species of tetrapods, gymnosperms and Proteaceae expected to survive in 100 years, by reporting year and biological group**

	2017			2020		
	Expected survival	Potential loss	Already lost	Expected survival	Potential loss	Already lost
All tetrapods	**922 (86%)**	**116 (11%)**	**38 (4%)**	**921 (86%)**	**117 (11%)**	**38 (4%)**
Birds	498 (89%)	49 (9%)	12 (2%)	497 (89%)	50 (9%)	12 (2%)
Reptiles	225 (89%)	26 (11%)	1 (0%)	225 (89%)	26 (10%)	1 (0%)
Mammals	133 (73%)	24 (13%)	25 (14%)	133 (74%)	23 (13%)	25 (14%)
Frogs	67 (79%)	17 (21%)	0 (0%)	66 (79%)	18 (21%)	0 (0%)
Proteaceae	–	–	–	181 (82%)	38 (17%)	2 (1%)
Gymnosperms	–	–	–	30 (80%)	8 (20%)	0 (0%)

All vascular plants

For all known NSW species of vascular plants, including gymnosperms and Proteaceae, the **percentage of species expected** to survive in 100 years was estimated. Two estimates of expected survival of all known species were calculated based on a statistical model. Firstly, the mean of 9 representative species sets (each comprising about 1,000 species with adequate predictive data) for 2007, 2013, 2017 and 2020 was calculated (see Table 12 'Representative species sets'). Secondly, for comparison, expected survival was calculated for a dataset of 4,683 NSW vascular plant species that had adequate predictive data (after data cleaning) (see Table 12 'Model species dataset'). Only results for representative species sets are included in the report card (see 'More information' section).

Expected survival of vascular plants was consistently lower when calculated from representative species sets than when calculated from the model species dataset. Generally, expected survival from the model species dataset was greater than 1 standard deviation (SD) higher than the mean across representative species sets (Table 12). This discrepancy was most pronounced for the 2020 reporting year (76.4% c.f. 80.7%), although variation across representative species sets was also relatively large for that year (SD 4.1%). This discrepancy appears to be driven by a bias towards species with smaller ranges in the representative species sets. Mean area of occupancy of all species in the model species dataset was 1,689 km^2. Across representative species sets, the overall mean was 1,220 km^2 with a SD of 100 km^2.

Table 12 **Percentage of all known NSW species of vascular plants expected to survive in 100 years, by reporting year**

Year	Representative species sets (mean ± SD)	Model species dataset (n = 4,683)
2007	78.5 ± 3.1%	81.9%
2013	79.1 ± 2.1%	82.5%
2017	78.9 ± 2.5%	82.6%
2020	76.4 ± 4.1%	80.7%

For all species not listed as threatened in New South Wales, an **extinction risk category** was predicted using the decision-tree model in Figure 9. The model outputs a probability of membership of each species in each risk category. The sum of the probabilities across species gives the prediction of how many species are in each category. Two estimates of the number of species in each risk category were made: one based on the representative species sets and one based on the model species dataset (see Table 13). Taking the mean proportions across 9 representative sets and applying those to the total count of 6,125 known species of vascular plants in New South Wales (from PlantNET) gives an estimation of how many species are in each category for 'all known species'. For comparison, the risk categories for the 4,683 vascular plants in the model species dataset were predicted using the decision-tree model. For NSW listed threatened species, the extinction risk was the NSW Biodiversity Conservation Act category for each species as of 2020.

Table 13 **Count of NSW vascular plant species in 2020 estimated, predicted or formally listed in each extinction risk category**

	LC	NT	VU	EN	CR	EX	Total
All known species (estimate based on representative species sets)	2,791	353	1,238	1,533	185	25	6,125
Model species dataset (predicted)	2,504	313	787	961	93	25	4,683
NSW listed threatened species (as of 2020)	–	–	212	303	72	28	615

Notes:
Total species count according to NSW PlantNET. Count does not include listed subspecies, varieties or populations.
LC = least concern; NT = near threatened; VU = vulnerable; EN = endangered; CR = critically endangered; EX = extinct.

4. Discussion

4.1 Interpretation

Despite some substantive changes in method, results for expected survival indicators were broadly similar to the first assessment. Following a core principle of the Biodiversity Indicator Program (OEH and CSIRO 2019), changes to method are both desirable and necessary as new data sources become available and technical developments are made. Where changes are made, results for earlier reporting periods are themselves updated to ensure that indicator trends are reflective of true changes in biodiversity status and pattern and do not merely mirror methodological alterations over time.

There is an ongoing trend of decline in the expected survival of biodiversity. Despite a highly conservative approach to interpreting the history of listing, the proportion of threatened species expected to survive continues to decline, including during the most recent interval from 2017 to 2020. When considering all known species of tetrapods and vascular plants, including those species not currently listed as threatened in New South Wales, overall survival remains relatively high, although both groups have continued to decline. For tetrapods, there is also a small decline in expected phylogenetic diversity from 2017 to 2020.

Decline in the expected survival of **all known species of vascular plants** from 2017 to 2020 was due to the modelled impact of the 2019–20 bushfires. Change in this indicator is driven by corresponding changes in habitat intactness. Further, changes in habitat intactness from 2017 to 2020 were entirely determined by the intersection of the 2017 mapping with fire extent and severity mapping (Gibson et al. 2020). Thus, the estimated decline in expected survival should be considered provisional until modelling of habitat intactness can be updated for the 2020 reporting year (DCCEEW 2025). Habitats are expected to recover over time, which should result in an increase in the expected survival indicator in subsequent years, assuming no impacts on habitat intactness of similar spatial magnitude. However, many vascular plant species are sensitive to fire history and thus some species may not recover even as habitat condition improves, especially if longer term fire regimes have been altered by this catastrophic event (Gallagher et al. 2021).

The decline in the expected survival of **listed threatened species** cannot be attributed to the 2019–20 bushfires as the impact of that event had not been assessed in time to influence species listings up to the end of 2020. Nevertheless, many vascular plant species have been provisionally assessed as negatively impacted by the fires (Auld et al. 2022) and these species are being prioritised for listing or reassessment. Other species (for example, *Androcalva rosea*) have germinated from seed banks post-fire, resulting in significant increases in number and extent (Gallagher et al. 2023). Some recent declines can be directly ascribed to the rapidly emergent threat of myrtle rust (*Austropuccinia psidii*) which has triggered critically endangered listings in 2019 for the native guava

(*Rhodomyrtus psidioides*) and the scrub turpentine (*Rhodamnia rubescens*). However, the basis for most listings continues to be declines in range area driven by habitat clearing.

Expected survival of **phylogenetic diversity** remained relatively high. Generally, declines in phylogenetic diversity are proportionally less than loss in species count because of the relatively small chance of loss of internal branches – a branch can only be lost if all descendent species are lost (Witting and Loeschcke 1995). However, if there is a phylogenetic bias in extinction risk, either towards distinctive species or towards clusters of related species, then loss of phylogenetic diversity can be significantly greater than expected given a certain level of species loss. This is marginally the case for gymnosperms (Figure 17) where 2 distinctive families (Araucariaceae and Podocarpaceae) are represented by very few NSW native species (Figure 4). Further, both of these families contain a highly distinctive and threatened species: in the case of Araucariaceae, the Wollemi pine (*Wollemia nobilis*), and for the family Podocarpaceae, the dwarf mountain pine (*Pherosphaera fitzgeraldii*).

Reporting expected survival for all known species of a biological group gives a much more complete perspective on the overall level of extinction threat. For **tetrapods**, expected survival in 100 years of the entire group is estimated at 86% in 2020 (Table 11), versus 56% when considering only those species listed as threatened in New South Wales (Table 6). Clearly, focussing only on those species listed as threatened gives a biased view of extinction risk. It is much more helpful, where the data allow, to survey the whole group. For some groups, like tetrapods and gymnosperms, comprehensive assessments have been completed for the IUCN Red List of Species and these assessments can be substituted for those species not listed in New South Wales. Non-threatened species are not formally listed by NSW or national legislation and species assessed but rejected for listing as threatened are not given any specific status. However, the *Nature Conservation (Animals) Regulation 2020* of the Queensland Government has provisions and criteria for formally listing species as ‘near threatened’ and ‘least concern’ as well as the threatened categories.

In the absence of comprehensive assessments for a biological group, extinction risk category can be modelled from known predictors such as effective range area. For vascular plants, in the 2020 reporting year it was estimated that 76.4% of all known NSW species of vascular plants were expected to survive in 100 years (Table 12). When looking at only threatened vascular plant species, 49% of species were expected to survive (Table 6). However, the higher estimate is derived from a sample of ~1,000 species (out of 6,125 known species) averaged over 9 representative species sets. When estimating from a larger sample of 4,683 species, expected survival is higher still at 81.7% (Table 12).

The representative species sets show some bias towards species with higher predicted extinction risk and this appears to be an outcome of a bias towards small-ranged species. This potential for bias was recognised in the first assessment as the algorithm selecting a species to represent a particular point in environmental space may bias that selection towards a species with a small geographic range around that point (Nipperess et al. 2020b). Diagnostics were used to select a sufficiently large number of species to adequately represent both the diversity of environmental niches and geographic ranges of plant species. However, a species set designed to evenly represent environmental space may inevitably be biased towards small-ranged species because distinctive environments that are geographically rare (such as alpine meadows) will support specialised small-ranged species but few if any large-ranged species. There was also an environmental bias in the geographic distribution of the 2019–20 bushfires towards the relatively rugged and heavily forested parts of the Great Dividing Range, thus having a disproportionate impact on species with relatively small ranges occurring in distinctive and geographically rare environments (Auld et al. 2022). This is likely reflected in the relatively more pronounced discrepancy in expected survival for the 2020 reporting year (Table 12).

Expected survival of listed **threatened ecological communities** remained steady throughout the entire reporting period. However, this result should be treated very cautiously because no threatened ecological community has been assessed more than once by the NSW Threatened Species Scientific Committee. Other sources of information on risk category (national and global lists) are difficult to access because of the lack of equivalency in how these ecological units are defined at national and global scales (section 4.2).

4.2 Future directions

Standardisation of reporting to all known species

Due to the inherent bias in lists of threatened species, expected survival indicators should be standardised to report as a count and percentage of all known species, that is, threatened and not threatened species. In addition to the obvious problem that extinction risk is, on average, higher for species formally listed as threatened, the length of lists of threatened species tend to get longer over time (Rodríguez 2008) as new species are added. Increase in the length of a list is often interpreted as an increasing risk of biodiversity loss but this interpretation is overly simplistic because species may have been threatened for some time before being formally added to a list. The overall length of the list is essentially arbitrary, being those species that have been assessed and listed, and will grow over time largely as a function of the effort put into assessments and listing, and thus makes a poor standard against which to report a proportion or percentage. In contrast, the taxonomic list of all known species, at least for well-known biological groups, will be relatively stable over time and a reported percentage has a more straightforward interpretation.

The challenge with reporting expected survival of all known species is the very incomplete information available on extinction risk for many biological groups. For groups that have been comprehensively assessed by the IUCN Red List of Species, such as birds and mammals, a list unification process can be used to integrate this information with the list of NSW threatened species. For other biological groups, such as vascular plants, it is possible to predict extinction risk category from other suitable variables if the data are available. Standardising expected survival to all known species might therefore result in the exclusion of some biological groups (for example, most invertebrates) from the indicator because the available data are far too sparse, even though they may have member species formally listed as threatened in New South Wales. Predicting overall expected survival in a group from a sample can be effective if that sample is representative. Species sets designed to be environmentally representative may not be representative of the distribution of extinction risk (see section 4.1) and, perhaps, should not be used when ad hoc or random samples are large enough to make statistically valid inferences.

Standardisation of classification of ecological communities

Reporting expected survival of all known ecological communities is complicated by the way threatened communities are defined. Operationally, listed threatened ecological communities are defined as lists of characteristic species (NSW Scientific Committee 2014). Listed communities are not directly comparable or functionally equivalent when they are defined by characteristic species from different biological groups. In New South Wales, threatened ecological communities have been defined for assemblages of vascular plants, fungi, gastropods (slugs and snails) and seabirds. Further, listed communities need not be comparable in their relative distinctness or spatial specificity (NSW Scientific Committee 2014). Counts of such disparate and idiosyncratically defined entities are, therefore, difficult to interpret and, in the absence of a standardised definition, it is impossible to estimate a count of all known such entities.

Hierarchical standardised classifications, such as the NSW vegetation classification framework and the *IUCN Global Ecosystem Typology* (Keith et al. 2020), comprehensively list all known, functionally equivalent, ecological communities, providing a relatively stable basis for reporting expected survival. It would be possible to provisionally assess these ecological units for risk of collapse by a predictive modelling approach. The NSW State Vegetation Type Map (SVTM) provides rich data on the spatial distribution, both original and current, of plant community types and can be intersected with mapping of habitat intactness (DCCEEW 2025). Parameterising the model for risk of collapse in New South Wales will be difficult however, because of the lack of equivalency of listed threatened ecological communities with the ecological units in standard classifications. For example, it would not be possible to create a training set of plant community types (used by the SVTM) with listed categories because these ecological units are not formally assessed by NSW Threatened Species Scientific Committee.

Although lacking the richness of data for New South Wales that is available from the SVTM, the *IUCN Global Ecosystem Typology* may be a preferable classification for indicator development. This is because ecosystem types are assessed by the IUCN for risk of collapse (allowing model parameterisation) and because ecosystem types are defined based on their functional characteristics, rather than lists of characteristic species, providing more stable definitions that allow for natural change in species composition over time (Keith et al. 2022).

Improved estimation of extinction risk

While the categories and criteria of the IUCN Red List of Species are a robust global standard, there remains considerable uncertainty in inferring extinction risk from state, national and global listings. In the case of New South Wales, many species were first listed in 1995 under the Threatened Species Conservation Act, and have not been formally assessed since. Thus, the risk category of a historical listing may not be a good guide for current extinction risk, especially in the light of more recent data on population recovery or decline, or the discovery of previously unknown populations. The NSW Threatened Species Scientific Committee is required by the Biodiversity Conservation Act to review listings 'at least every 5 years' (s 4.18) but there is no requirement to undertake detailed regular assessments of all listed species.

Rather than being inferred from a qualitative risk category, probabilities of survival should ideally be estimated directly from monitoring data. Trajectories of abundance or occupancy over an extended sampling period provide useful information on the likely long-term viability of populations from which probabilities of survival can be estimated (Boyce 1992). However, relatively few species have data of sufficient quality to allow this. Data from monitoring of conservation projects could be used to estimate survival probabilities. However, data on the abundance or occupancy of managed populations are available for only a few species and frequently only cover a relatively short period (Bayraktarov et al. 2021). Further, population-level outcomes at management sites do not necessarily translate to recovery at the species level, depending on the proportional coverage of conservation actions within the known geographic range of the species (Brazill-Boast et al. 2018).

In the absence of monitoring data, geographic range, both original and lost, provides a very useful surrogate for predicting probability of survival (Mace et al. 2008). However, the area of the former and current range of a species are often poorly known. The fundamental data on geographic range are occurrence records – observations of a species at points in time and space. These data can be sparse, leading to an underestimation of occupied area (Gaston and Fuller 2009). Trends in range area over time are even more obscure because there is rarely a sufficient time series of occurrence records available (Ribeiro et al. 2022).

The approach taken here is to estimate range area from all known records and infer the proportion of occupied or viable habitat by intersection with a model of habitat quality. This allows for a trend in range size over time as habitat quality changes. However, the relationship between the quality of habitat in a 2 km × 2 km grid cell and its viability to support a population will vary considerably among species. Ideally, the relationship between occupancy and habitat quality should be estimated separately for each species, according to its sensitivity to loss of condition and connectivity.

Statistical modelling provides a means to estimate expected survival for a large sample of species (Caetano et al. 2022) and can also factor in the differential responses of species to habitat loss. Rather than predicting qualitative categories, probability of survival could be modelled directly, given suitable data. Population viability analysis (Boyce 1992) could be implemented for a set of species for which population trajectory data are available, giving estimates of survival probabilities over 100 years. Assuming this set of species is sufficiently large and representative, traits, phylogeny, range area, and even listed extinction risk category can be used as predictors for other species in the same biological group. The differential responses of species to habitat loss could be modelled through an interaction between predictors, that is, species with different traits and/or in different clades can have different modelled responses to habitat loss. This approach seems to work particularly well in a hierarchical regression tree model, as implemented in this report.

If predictors of probability of survival are universal, a training set of species used to parameterise the model does not necessarily need to be species known from New South Wales. Further, not all species (in a biological group) known from New South Wales need to be assessed by the model, so long as there is a sufficiently large and representative sample from which to estimate a proportional indicator. The database maintained for the *Threatened Species Index* (Bayraktarov et al. 2021) on population trajectories could provide the basis for a useful training set.

Improved ecological data for modelling, inference and reporting

The greatest challenge to reporting on the security of biodiversity in New South Wales is the lack of regularly collected, standardised and comprehensive data. Lists of threatened species are inherently incomplete and biased. Occurrence records, from which we can infer range area, are commonly sparse over space and time, accumulate haphazardly, and reflect collecting efforts that are transient and, collectively, unorganised. Modelling can attempt to address many of these deficiencies but is itself ultimately subject to the quality of the underlying data.

An ecological observation network of sites that are surveyed regularly, covering the full range of environments present in New South Wales, and targeting a representative sample of species and ecological communities, would provide a much firmer basis for inference and reporting. Such an ambitious monitoring program is not without precedent – the Alberta Biodiversity Monitoring Institute is a large, intensive region-wide program designed to monitor status and trend of biodiversity and ecological integrity with 1,656 sites across the entire province of Alberta, Canada (Sólymos et al. 2015). In New South Wales, comprehensive assessments of flora and fauna were completed as part of the North East Forest Biodiversity Study (Hines et. al 2000) and later to support regional forestry agreements (Ferrier et al. 2002) and this work could form the basis of a renewed program (Lindenmayer et al. 2015). Combining standardised monitoring data with modelling approaches would provide a powerful framework for prediction, scenario analysis, program evaluation and decision-making (Haughland et al. 2010).

Next steps

Where to from here?

Now that you have read this report, you have 3 main options for more information. This information can be accessed via the links in the ‘More information’ section at the end of the report.

Firstly, 2 report cards present results for the expected survival of biodiversity indicator theme in plain English:

- Expected survival of listed threatened species and ecological communities
- Expected survival of all known species.

This implementation report is designed to support the report cards by providing technical detail on the calculation of the results presented in the report card.

Secondly, the NSW biodiversity outlook reports provide a high-level summary of our indicators. The latest outlook report at the time of the release of this implementation report is the *NSW biodiversity outlook report 2024*, which includes summary results for 13 indicators as well as case studies and research highlights.

Thirdly, the NSW SEED (Sharing and Enabling Environmental Data) portal provides access to the data underlying our indicators. The Expected survival of listed threatened species and ecological communities and Expected survival of all known species data packages provide detailed derived data for technical users.

Appendices

Appendix A Indicator workflow diagrams

The following figures present workflow diagrams showing both data and processes used in the development of the updated expected survival of biodiversity indicators. High-resolution versions of the diagrams are available in the data packages.

Workflow for indicator: Expected survival of listed threatened species

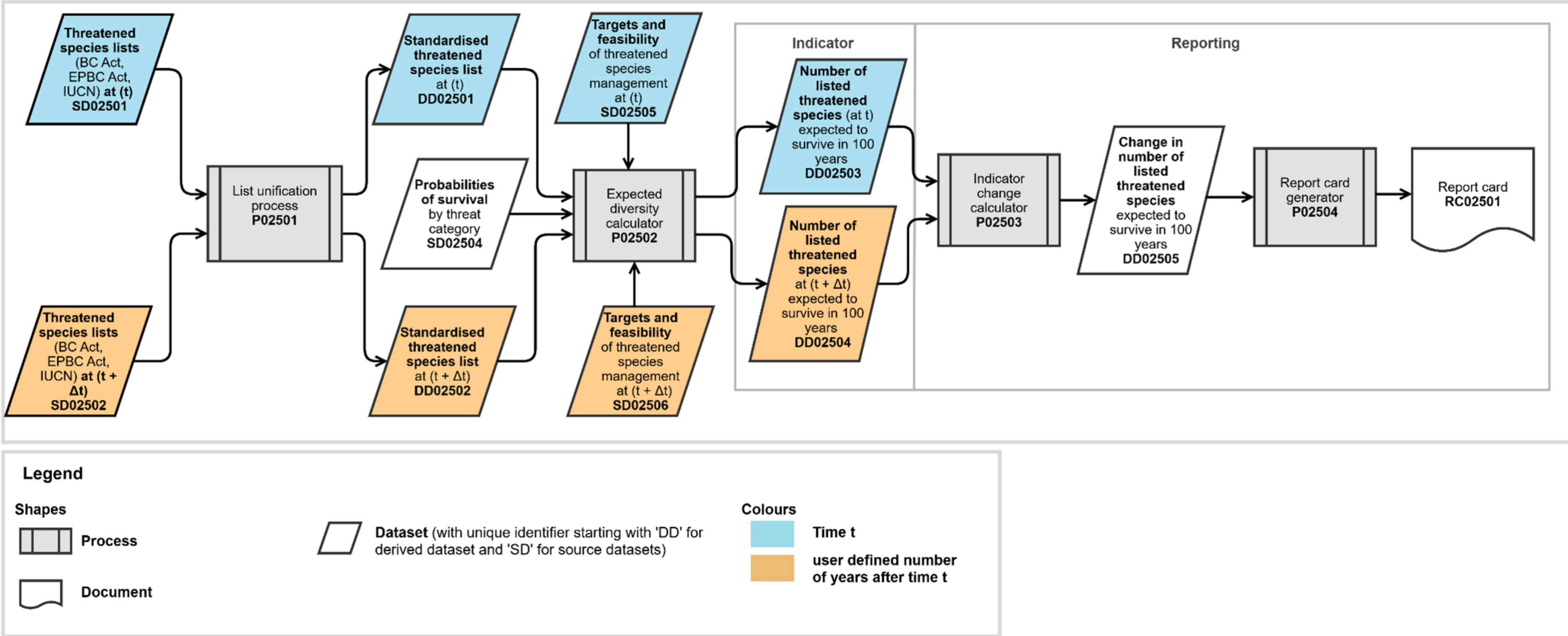

Figure 20 Workflow for expected survival of listed threatened species

Table 14 **Workflow for indicator: expected survival of listed threatened species (Figure 20) in table format. The ID prefix 'P' denotes a process, 'D' denotes a document, 'DD' denotes a derived dataset and 'SD' denotes a source dataset**

ID	Name	Flows to:
SD02501	Threatened species lists (BC Act, EPBC Act, IUCN) at (t)	P02501
SD02502	Threatened species lists (BC Act, EPBC Act, IUCN) at (t + Δt)	P02501
P02501	List unification process	DD02501, DD02502
DD02501	Standardised threatened species list at (t)	P02502
DD02502	Standardised threatened species list at (t + Δt)	P02502
SD02504	Probabilities of survival by threat category	P02502
SD02505	Targets and feasibility of threatened species management at (t)	P02502
SD02506	Targets and feasibility of threatened species management at (t + Δt)	P02502
P02502	Expected survival calculator	DD02503, DD02504
DD02503	Number of listed threatened species (at t) expected to survive in 100 years	P02503
DD02504	Number of listed threatened species (at t + Δt) expected to survive in 100 years	P02503
P02503	Indicator change calculator	DD02505
DD02505	Change in number of listed threatened species expected to survive in 100 years	P02504
P02504	Report card generator	RC02501
RC02501	Report card	

Workflow for indicator: Expected existence of listed threatened ecological communities

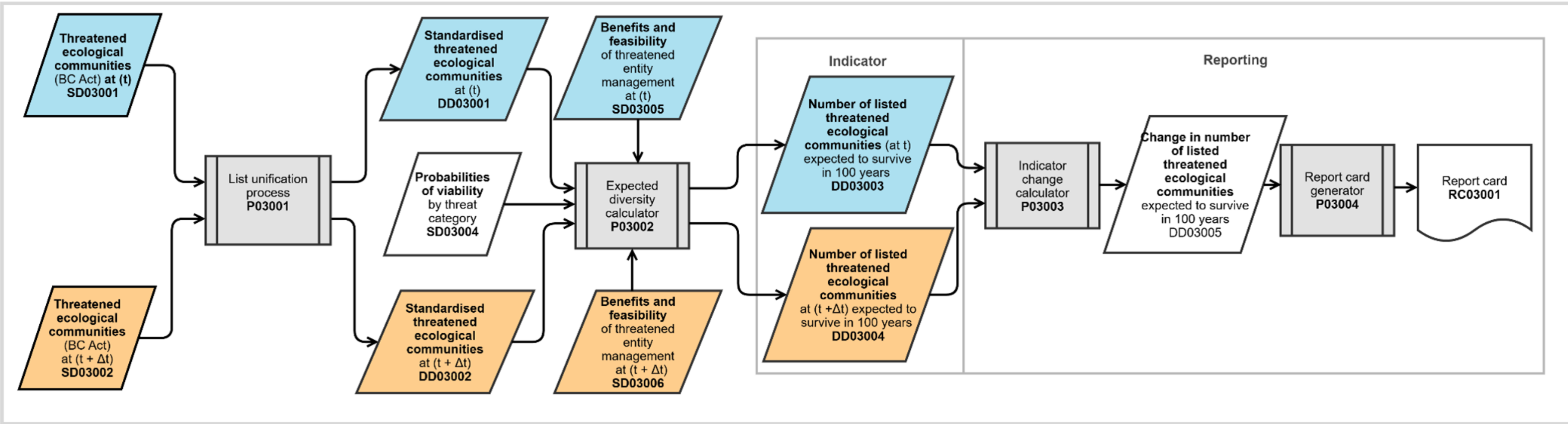

Figure 21 **Workflow for expected existence of listed threatened ecological communities**

Table 15 **Workflow for indicator: expected survival of listed threatened ecological communities (Figure 21) in table format. The ID prefix 'P' denotes a process, 'D' denotes a document, 'DD' denotes a derived dataset and 'SD' denotes a source dataset**

ID	Name	Flows to:
SD03001	Threatened ecological communities (BC Act) at (t)	P03001
SD03002	Threatened ecological communities (BC Act) at (t + Δt)	P03001
P03001	List unification process	DD02501, DD02502
DD03001	Standardised threatened ecological communities at (t)	P03002
DD03002	Standardised threatened ecological communities at (t + Δt)	P03002
SD03004	Probabilities of viability by threat category	P03002
SD03005	Benefits and feasibility of threatened entity management at (t)	P03002
SD03006	Benefits and feasibility of threatened entity management at (t + Δt)	P03002
P03002	Expected diversity calculator	DD03003, DD03004
DD03003	Number of listed threatened ecological communities (at t) expected to survive in 100 years	P03003
DD03004	Number of listed threatened ecological communities (at t + Δt) expected to survive in 100 years	P03003
P03003	Indicator change calculator	DD03005
DD03005	Change in number of listed threatened ecological communities expected to survive in 100 years	P03004
P03004	Report card generator	RC03001
RC03001	Report card	

Workflow for indicator: Expected survival of phylogenetic diversity for listed threatened species

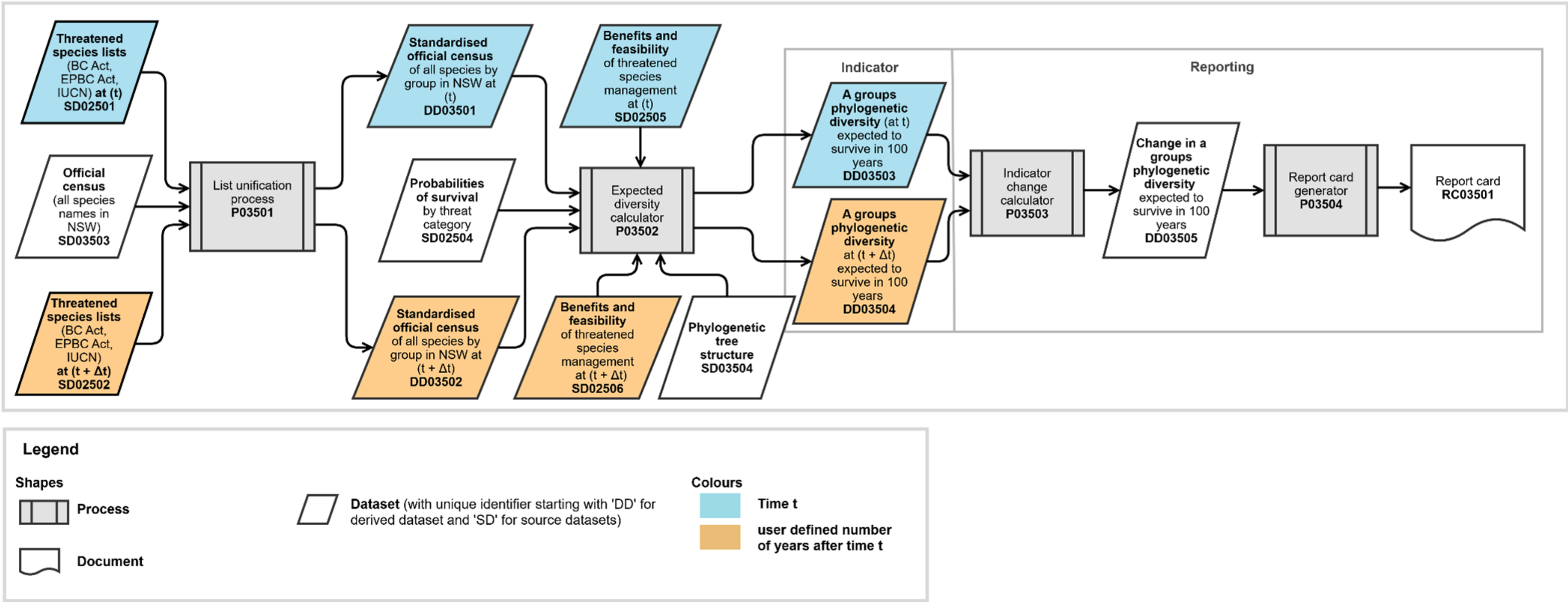

Figure 22 Workflow for expected survival of phylogenetic diversity for listed threatened species

Table 16 **Workflow for indicator: expected survival of phylogenetic diversity for listed threatened species (Figure 22) in table format. The ID prefix 'P' denotes a process, 'D' denotes a document, 'DD' denotes a derived dataset and 'SD' denotes a source dataset**

ID	Name	Flows to:
SD02501	Threatened species lists (BC Act, EPBC Act, IUCN) at (t)	P03501
SD02502	Threatened species lists (BC Act, EPBC Act, IUCN) at (t + Δt)	P03501
SD03503	Official census (all species names in NSW)	P03501
P03501	List unification process	DD03501, DD03502
DD03501	Standardised official census of all species by group in NSW at (t)	P03502
DD03502	Standardised official census of all species by group in NSW at (t + Δt)	P03502
SD02504	Probabilities of survival by threat category	P03502
SD02505	Benefits and feasibility of threatened species management at (t)	P03502
SD02506	Benefits and feasibility of threatened species management at (t + Δt)	P03502
SD03504	Phylogenetic tree structure	P03502
P03502	Expected diversity calculator	DD03503, DD03504
DD03503	A groups phylogenetic diversity (at t) expected to survive in 100 years	P03503
DD03504	A groups phylogenetic diversity (at t + Δt) expected to survive in 100 years	P03503
P03503	Indicator change calculator	DD03505
DD03005	Change in a groups phylogenetic diversity expected to survive in 100 years	P03504
P03504	Report card generator	RC03501
RC03501	Report card	

Workflow for indicator: Expected survival of all known species (comprehensively assessed biological group)

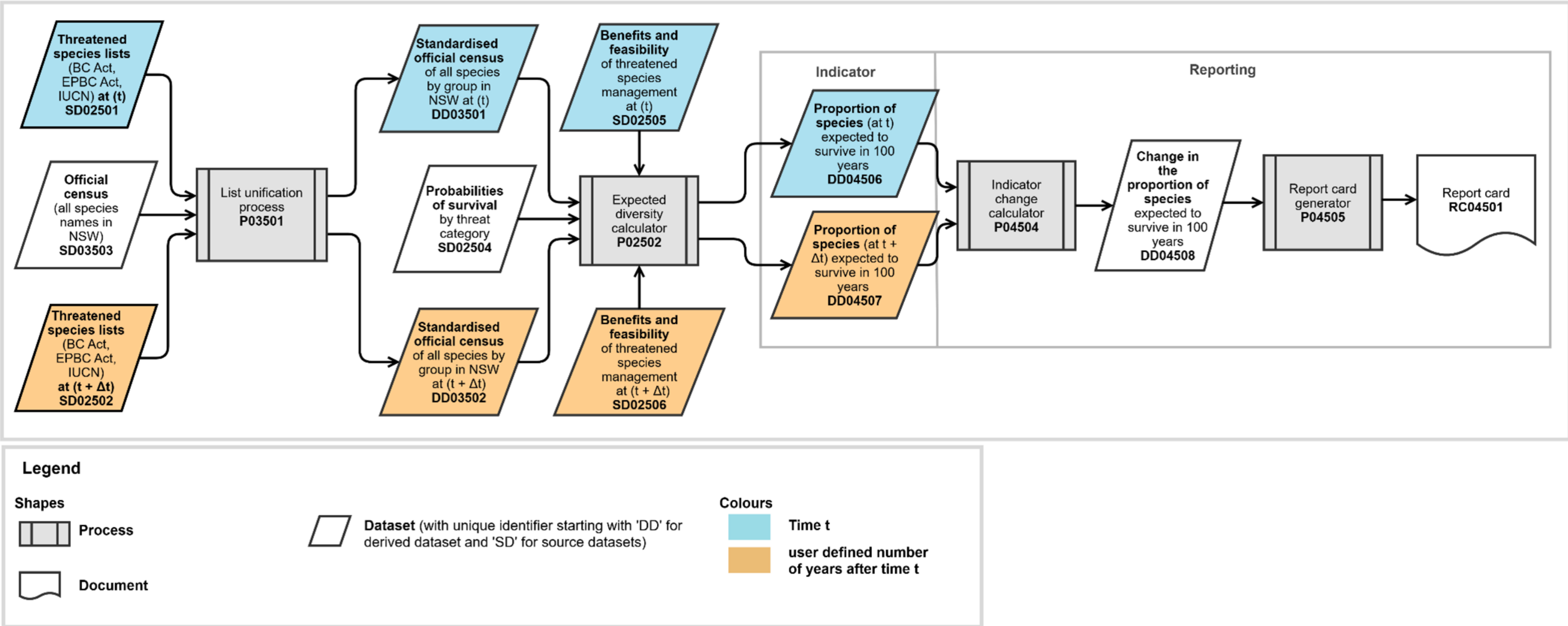

Figure 23 **Workflow for expected survival of all known species (comprehensively assessed biological group)**

Table 17 Workflow for indicator: expected survival of all known species (comprehensively assessed biological group) (Figure 23) in table format. The ID prefix 'P' denotes a process, 'D' denotes a document, 'DD' denotes a derived dataset and 'SD' denotes a source dataset

ID	Name	Flows to:
SD02501	Threatened species lists (BC Act, EPBC Act, IUCN) at (t)	P03501
SD02502	Threatened species lists (BC Act, EPBC Act, IUCN) at (t + Δt)	P03501
SD03503	Official census (all species names in NSW)	P03501
P03501	List unification process	DD03501, DD03502
DD03501	Standardised official census of all species by group in NSW at (t)	P03502
DD03502	Standardised official census of all species by group in NSW at (t + Δt)	P03502
SD02504	Probabilities of survival by threat category	P03502
SD02505	Benefits and feasibility of threatened species management at (t)	P03502
SD02506	Benefits and feasibility of threatened species management at (t + Δt)	P03502
P02502	Expected diversity calculator	DD04506, DD04507
DD04506	Proportion of species (at t) expected to survive in 100 years	P04504
DD04507	Proportion of species (at t + Δt) expected to survive in 100 years	P04504
P04504	Indicator change calculator	DD04508
DD04508	Change in the proportion of species expected to survive in 100 years	P04505
P04505	Report card generator	RC04501
RC04501	Report card	

Workflow for indicator: Expected survival of all known species (representative species set)

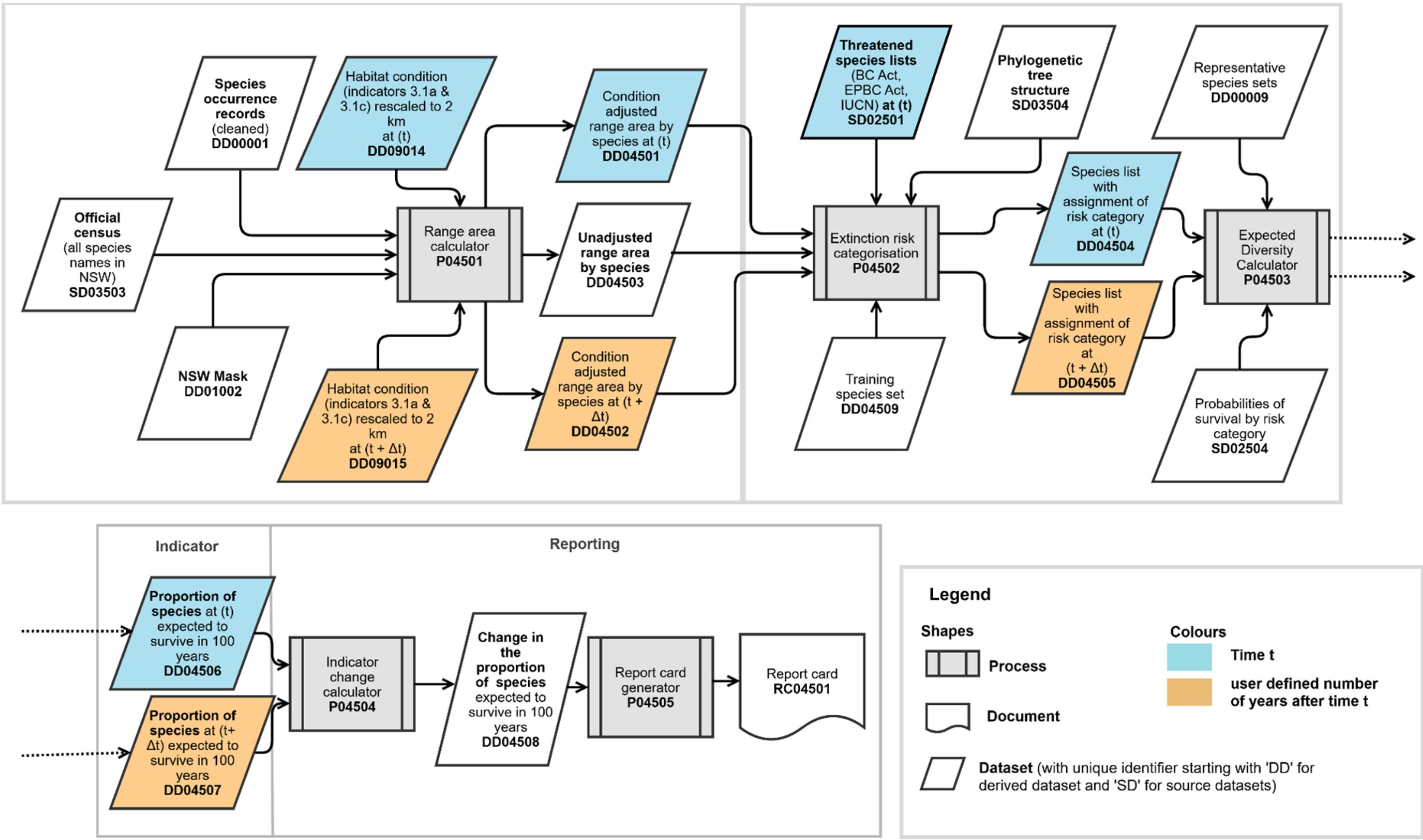

Figure 24 **Workflow for expected survival of all known species (representative species set)**

Table 18 **Workflow for indicator: expected survival of all known species (representative species set) (Figure 24) in table format. The ID prefix 'P' denotes a process, 'D' denotes a document, 'DD' denotes a derived dataset and 'SD' denotes a source dataset**

ID	Name	Flows to:
DD00001	Species occurrence records (cleaned)	P04501
SD03503	Official census (all species names in NSW)	P04501
DD01002	NSW Mask	P04501
DD09014	Habitat condition (indicators 3.1a & 3.1c) rescaled to 2 km at (t)	P04501
DD09015	Habitat condition (indicators 3.1a & 3.1c) rescaled to 2 km at (t + Δt)	P04501
P04501	Range area calculator	DD04501, DD04502, DD04503
DD04501	Condition adjusted range area by species at (t)	P04502
DD04502	Condition adjusted range area by species at (t + Δt)	P04502
DD04503	Unadjusted range area by species	P04502
SD02501	Threatened species lists (BC Act, EPBC Act, IUCN) at (t)	P04502
DD04509	Training species set	P04502
SD03504	Phylogenetic tree structure	P04502
P04502	Extinction risk categorisation	DD04504, DD04505
DD04504	Species list with assignment of risk category at (t)	P04503
DD04505	Species list with assignment of risk category at (t + Δt)	P04503
SD02504	Probabilities of survival by threat category	P04503
DD00009	Representative species sets	P04503
P04503	Expected diversity calculator	DD04506, DD04507
DD04506	Proportion of species (at t) expected to survive in 100 years	P04504
DD04507	Proportion of species (at t + Δt) expected to survive in 100 years	P04504
P04504	Indicator change calculator	DD04508
DD04508	Change in the proportion of species expected to survive in 100 years	P04505
P04505	Report card generator	RC04501
RC04501	Report card	

Abbreviations

Abbreviation	Meaning
AOO	Area of occupancy
EOO	Extent of occurrence
EPSG	European Petroleum Survey Group
IUCN	International Union for Conservation of Nature
NSW	New South Wales
SEED	Sharing and Enabling Environmental Data
SD	Standard deviation
SPRAT	Species Profile and Threats Database
SVTM	State Vegetation Type Map

Glossary

Area of occupancy: the area within the total range area of a species (that is, its extent of occurrence) which is currently occupied, excluding unsuitable and unoccupied areas.

Biodiversity (biological diversity): variability among living organisms from all sources (including terrestrial, freshwater, coastal, marine and other ecosystems and ecological complexes of which they are part). It includes genetic diversity, species diversity and ecosystem diversity.

Biological group: a group of biological entities (such as species) sharing common characteristics and treated as a unit for analyses and reporting. Grouping could be based on common ancestry, shared habitat requirements, shared functional characteristics or other criteria.

Clade: a group of species and/or subspecific taxa that share a common ancestor and where all descendants of that ancestor are included in the group. Also known as a monophyletic group.

Connectivity: the degree to which the landscape facilitates animal or plant movement or spread and ecological flows.

Decision tree: a flow chart structure where each node represents a test or criterion leading to a branch for each outcome and ending in terminal branches that represent classes. The paths from root node to terminals are the rules for classification. In machine learning, decision trees can be constructed from training data such that error in classification from predictor variables is minimised.

Ecological carrying capacity: the ability of an area to maintain self-sustaining and interacting populations of all species naturally expected to occur there, given the habitat resources, such as food and water, and connections to other habitat needed for persistence.

Ecological community: an assemblage of species occupying a particular area at a particular time.

Ecological condition: the intactness and naturalness of habitat to support biodiversity, without considering the indirect effects of fragmentation or connections with surrounding suitable habitat.

Ecosystem: a dynamic complex of plant, animal and microorganism communities and their nonliving environment that interact as a functional unit. Ecosystems may be small and simple, like an isolated pond, or large and complex, like a specific tropical rainforest or a coral reef.

Effective habitat: the proportion of residual habitat quality at a site which remains effective in supporting native plants and animals following the impacts of clearing, degradation and fragmentation at that site and in its neighbourhood.

Eigenvector: a dimension in a multidimensional space that explains the relationship among objects arrayed in that space. See ordination.

Environmental space: a multidimensional mathematical space defined by environmental variables.

Evolutionary heritage: a common currency for measuring phylogenetic diversity where branch lengths in a phylogenetic tree are measured in millions of years of evolutionary history (between dated nodes). The sum of the lengths of branch segments by a set of species (or subspecific taxa) is then the cumulative amount of independent evolutionary history represented.

Expected diversity (survival): the number of features (species, genes, ecosystems) that are expected to be extant over some timeframe, for example 100 years.

Extent of occurrence: the area of the total geographic range that includes all extant populations of the species.

Extinct: no individuals are remaining, either within a region or globally. A species or subspecific taxon is regionally extinct if no individuals remain within a region but are present elsewhere. A species (or subspecific taxon) with individuals in captivity but no individuals living independently in the wild would be 'extinct in the wild'. A species or subspecific taxon without viable populations, that is functionally extinct, in the long term is not extinct until the last known individual has died. Due to the difficulty detecting rare species, species or subspecific taxa that are presumed to be extinct are assumed to have a small but non-zero probability of survival.

Extinction risk: a measure of the actual or potential decline and extinction over time of a species or other defined ecological unit, for example an ecological community.

Gymnosperm: a taxon (Gymnospermae) of seed-producing plants that includes conifers, cycads, ginkgo and gnetophytes.

Habitat: an area or areas occupied, or periodically or occasionally occupied, by a species, population or ecological community, including any biotic or abiotic component.

Habitat condition: the capacity of an area to provide the structures and functions necessary for the persistence of all species naturally expected to occur there in an intact state.

Habitat fragmentation: the emergence of discontinuities (fragmentation) in an organism's preferred environment (habitat), causing population fragmentation and ecosystem decay.

Hindcast (hindcasting): is a process that involves the re-running of mathematical models when new data become available, about a period of time in the past.

Model: an abstract, usually mathematical, representation of a system, which is studied to gain understanding of the real system.

Occurrence record: information about the presence of a species in a given location (usually a point with geographic coordinates, but may also refer to other geographic units such as a polygon area or a pixel in a regular grid). Occurrence records do not contain any information about the absence of a species from a given location. Absence of a species is instead inferred from the absence of information about its presence. Species occurrence records are also commonly referred to as presence-only records, detection records, locality records, distribution data or observations.

Ordination: an analytical technique that defines a multidimensional space which preserves the relationships (distances) between objects in that space. Dimensions (eigenvectors) are ordered according to the amount of variation among objects that they each explain.

Permutation: a statistical procedure where the original data are randomly reordered. This is done to generate random patterns within a dataset. By comparing an observed pattern to multiple random patterns, it can be determined whether the observed pattern can be reasonably expected to have arisen by a random process.

Phylogenetic diversity: a measure of biodiversity which incorporates the phylogenetic (evolutionary) differences between species. The phylogenetic diversity of a set of species (or subspecific taxa) is the sum of lengths of branch segments connecting those species together in a phylogenetic tree.

Phylogenetic tree: a branching diagram that represents the pattern of evolutionary relationships between species or other taxa. A tree consists of branch segments (or edges) connected by nodes, representing evolutionary divergence events. Tips are terminal branch segments connected to the tree by a single node. When nodes are assigned ages, the lengths of the branches are proportional to the amount of the time between divergence events.

Population: a group of individuals of the same species or subspecific taxon occurring together in a particular area at a particular time.

Raster: spatial categorical or continuously valued data classifying or measuring some aspect of a region as a square grid of equally sized grid cells at a specified resolution.

Realm: in the *IUCN Global Ecosystem Typology*, the highest level grouping of ecosystem types. Five realms are recognised (terrestrial, freshwater, marine, subterranean, atmospheric), differing fundamentally in ecosystem organisation and function.

Representative species: a species (or set of species) that represents or is typical of that group of species.

Species: a taxon comprising one or more populations of individuals capable of interbreeding to produce fertile offspring.

Subspecific taxon: a taxon below the species level consisting of one or more populations that show some consistent differences in morphology, behaviour and/or genetic composition from other subspecific taxa of the same species. Subspecific taxa can be termed ‘subspecies’ (animals and plants) or ‘varieties’ (plants only).

Taxon (taxa): a grouping of populations that is recognised as biologically distinct from other taxa and is given a formal scientific name. Can also be referred to as a taxonomic group. A taxon is normally also a clade. A taxon can be comprised of several lower taxa and can itself be a member of a higher taxon.

Tetrapod: a taxon (superclass Tetrapoda) comprising all 4-limbed vertebrate animals, including amphibians, mammals, reptiles and birds. Also known as higher vertebrates.

Vascular plant: a taxon (phylum Tracheophyta) comprising all plants containing vascular tissue (tissue specialised for the conduction of fluids), including ferns, gymnosperms and flowering plants. Also known as higher plants.

References

Auld TD, Keith DA, Gallagher RV, Tozer M, Ooi MKJ, Breton TL, Allen S, Yates C, Leeuwen S van, Williams RJ and Mackenzie BDE (2022) ‘Frameworks for identifying priority plants and ecosystems most impacted by major fires’, *Australian Journal of Botany*, 70(7):455–493.

Bachman SP, Brown MJM, Leão TCC, Lughadha EN and Walker BE (2024) ‘Extinction risk predictions for the world’s flowering plants to support their conservation’, *New Phytologist*, 242(2):797–808.

Bayraktarov E, Ehmke G, Tulloch AIT, Chauvenet AL, Avery-Gomm S, McRae L, Wintle BA, O’Connor J, Driessen J, Watmuff J, Nguyen HA, Garnett ST, Woinarski J, Barnes M, Morgain R, Guru S and Possingham HP (2021) ‘A threatened species index for Australian birds’, *Conservation Science and Practice*, 3(2).

Bland LM, Keith DA, Miller RM, Murray NJ and Rodríguez JP (2017) *Guidelines for the application of IUCN Red List of Ecosystems categories and criteria*, International Union for Conservation of Nature and Natural Resources, Gland, Switzerland.

Boyce MS (1992) ‘Population viability analysis’, *Annual Review of Ecology and Systematics*, 23:481–506.

Brazill-Boast J, Williams M, Rickwood B, Partridge T, Bywater G, Cumbo B, Shannon I, Probert WJM, Ravallion J, Possingham H and Maloney RF (2018) ‘A large-scale application of project prioritization to threatened species investment by a government agency’, *PLoS ONE*, 13(8):e0201413.

Caetano GH de O, Chapple DG, Grenyer R, Raz T, Rosenblatt J, Tingley R, Böhm M, Meiri S and Roll U (2022) ‘Automated assessment reveals that the extinction risk of reptiles is widely underestimated across space and phylogeny’, *PLoS Biology*, 20(5):e3001544.

Colston TJ, Kulkarni P, Jetz W and Pyron RA (2020) ‘Phylogenetic and spatial distribution of evolutionary diversification, isolation, and threat in turtles and crocodilians (non-avian archosauromorphs)’, *BMC Evolutionary Biology*, 20(1):81.

Crawford NG, Parham JF, Sellas AB, Faircloth BC, Glenn TC, Papenfuss TJ, Henderson JB, Hansen MH and Simison WB (2015) ‘A phylogenomic analysis of turtles’, *Molecular Phylogenetics and Evolution*, 83:250–257.

De’ath G (2007) ‘Boosted trees for ecological modeling and prediction’, *Ecology*, 88(1):243–251.

Diniz-Filho J, Sant’ana C de and Bini L (1998) ‘An eigenvector method for estimating phylogenetic inertia’, *Evolution*, 52(5):1,247–1,262.

DCCEEW (2025) *Updating habitat condition indicators: implementation report supporting the NSW biodiversity outlook report 2024*, Department of Climate Change, Energy, the Environment and Water, Parramatta, Australia.

DPIE (Department of Planning, Industry and Environment, NSW) (2020a) *NSW biodiversity outlook report*, Department of Planning Industry and Environment, Sydney.

DPIE (2020b) *NSW Fire and the environment 2019–20 summary: biodiversity and landscape data and analyses to understand the effects of the fire events*, Department of Planning, Industry and Environment, Sydney, Australia.

Faith DP (1992) 'Conservation evaluation and phylogenetic diversity', *Biological Conservation*, 61(1):1–10.

Ferrier S, Watson G, Pearce J and Drielsma M (2002) 'Extended statistical approaches to modelling spatial pattern in biodiversity in northeast New South Wales. I. Species-level modelling', *Biodiversity & Conservation*, 11(12):2,275–2,307.

Gallagher RV, Allen S, Mackenzie BDE, Yates CJ, Gosper CR, Keith DA, Merow C, White MD, Wenk E, Maitner BS, He K, Adams VM and Auld TD (2021) 'High fire frequency and the impact of the 2019–2020 megafires on Australian plant diversity', *Diversity and Distributions*, 27(7):1,166–1,179.

Gallagher RV, Barrett S, Bell SAJ, Copeland LM, Dillon R, Gosper CR, Keith DA, Breton TDL, Mackenzie BDE, Messina A, Veldner VJ, Ngugi MR, Nolan RH, Ooi MKJ, Tasker EM, Tozer M, Walsh N, Yates CJ and Auld TD (2023) 'Blackened roots and green shoots: emerging trends in decline and recovery in Australian plant species after the 2019–20 wildfires', in L Rumpff, SM Legge, S van Leeuwen, BA Wintle, and JCZ Woinarski (eds) *Australia's megafires: biodiversity impacts and lessons from 2019-2020*, CSIRO Publishing.

Gaston KJ and Fuller RA (2009) 'The sizes of species' geographic ranges', *Journal of Applied Ecology*, 46(1):1–9.

Gibson R, Danaher T, Hehir W and Collins L (2020) 'A remote sensing approach to mapping fire severity in south-eastern Australia using sentinel 2 and random forest', *Remote Sensing of Environment*, 240:111702.

Haughland DL, Hero J-M, Schieck J, Castley JG, Boutin S, Solymos P, Lawson BE, Holloway G and Magnusson WE (2010) 'Planning forwards: biodiversity research and monitoring systems for better management', *Trends in Ecology & Evolution*, 25(4):199–200.

Hedges SB, Marin J, Suleski M, Paymer M and Kumar S (2015) 'Tree of Life Reveals Clock-Like Speciation and Diversification', *Molecular Biology and Evolution*, 32(4):835–845.

Heled J and Bouckaert RR (2013) 'Looking for trees in the forest: summary tree from posterior samples', *BMC Evolutionary Biology*, 13(1):221.

Hijmans RJ (2021) *raster: Geographic Data Analysis and Modeling*, https://CRAN.R-project.org/package=raster.

Hines H, Brown D and Scotts D (2000) 'Biological surveys', in D Brown, H Hines, S Ferrier and K McKay (eds) *Establishment of a biological information base for regional conservation planning in northeast New South Wales, Phase 1 (1991–1995)*, Occasional

Paper no. 26, New South Wales National Parks and Wildlife Service, Sydney, Australia, pp. 77–96.

IUCN (International Union for Conservation of Nature) (2012a) *IUCN Red List categories and criteria: version 3.1. 2nd edition*, IUCN, Gland, Switzerland.

IUCN (2012b) *Guidelines for application of IUCN Red List criteria at regional and national levels: Version 4.0*, IUCN, Gland, Switzerland.

Jarzyna MA and Jetz W (2016) 'Detecting the multiple facets of biodiversity', *Trends in Ecology & Evolution*, 31(7):527–538.

Jetz W and Pyron RA (2018) 'The interplay of past diversification and evolutionary isolation with present imperilment across the amphibian tree of life', *Nature Ecology & Evolution*, 2(5):850–858.

Jetz W, Thomas GH, Joy JB, Hartmann K and Mooers AO (2012) 'The global diversity of birds in space and time', *Nature*, 491:444–448.

Jin Y and Qian H (2019) 'V.PhyloMaker: an R package that can generate very large phylogenies for vascular plants', *Ecography*, 42(8):1,353–1,359.

Keith DA, Ferrer-Paris JR, Nicholson E, Bishop MJ, Polidoro BA, Ramirez-Llodra E, Tozer MG, Nel JL, Nally RM, Gregr EJ, Watermeyer KE, Essl F, Faber-Langendoen D, Franklin J, Lehmann CER, Etter A, Roux DJ, Stark JS, Rowland JA, Brummitt NA, Fernandez-Arcaya UC, Suthers IM, Wiser SK, Donohue I, Jackson LJ, Pennington RT, Iliffe TM, Gerovasileiou V, Giller P, Robson BJ, Pettorelli N, Andrade A, Lindgaard A, Tahvanainen T, Terauds A, Chadwick MA, Murray NJ, Moat J, Pliscoff P, Zager I and Kingsford RT (2022) 'A function-based typology for Earth's ecosystems', *Nature*, 610(7932).

Keith DA, Ferrer-Paris JR, Nicholson E and Kingsford RT (2020) *IUCN Global Ecosystem Typology 2.0*, International Union for Conservation of Nature, Gland, Switzerland.

Kindvall O and Gärdenfors U (2003) 'Temporal extrapolation of PVA results in relation to the IUCN Red List Criterion E', *Conservation Biology*, 17(1):316–321.

Lindenmayer DB, Blair D, McBurney L and Banks SC (2015) 'The need for a comprehensive reassessment of the Regional Forest Agreements in Australia', *Pacific Conservation Biology*, 21(4):266–270.

Love J, Drielsma M, Williams K and Thapa R (2020) *Integrated model–data fusion approach to measuring habitat condition for ecological integrity reporting*, Department of Planning, Industry and Environment, Sydney, Australia.

Lughadha EN, Bachman SP, Leão TCC, Forest F, Halley JM, Moat J, Acedo C, Bacon KL, Brewer RFA, Gâteblé G, Gonçalves SC, Govaerts R, Hollingsworth PM, Krisai-Greilhuber I, Lirio EJ, Moore PGP, Negrão R, Onana JM, Rajaovelona LR, Razanajatovo H, Reich PB, Richards SL, Rivers MC, Cooper A, Iganci J, Lewis GP, Smidt EC, Antonelli A, Mueller GM and Walker BE (2020) 'Extinction risk and threats to plants and fungi', *Plants, People, Planet*, 2(5):389–408.

Mace GM, Collar NJ, Gaston KJ, Hilton-Taylor C, Akcakaya HR, Leader-Williams N, Milner-Gulland EJ and Stuart SN (2008) 'Quantification of extinction risk: IUCN's system for classifying threatened species', *Conservation Biology*, 22(6):1,424–1,442.

Mooers AO and Atkins R (2003) 'Indonesia's threatened birds: over 500 million years of evolutionary heritage at risk', *Animal Conservation*, 6:183–188.

Mooers AO, Faith DP and Maddison WP (2008) 'Converting endangered species categories to probabilities of extinction for phylogenetic conservation prioritization', *PLoS One*, 3(11):e3700.

Nipperess DA, Faith DP, Auld TD, Brazill-Boast J and Williams KJ (2020a) *Expected diversity as an indicator of biodiversity status and trend*, Department of Planning Industry and Environment, Sydney, Australia.

Nipperess DA, Faith DP, Williams KJ, King D, Manion G, Ware C, Schmidt B, Love J, Drielsma M, Allen S and Gallagher RV (2020b) *Using representative sets of known species and habitat condition to inform change in biodiversity status*, Department of Planning Industry and Environment, Sydney, Australia.

Nipperess DA and Wilson PD (2023) *PDcalc: an implementation of the phylogenetic diversity (PD) calculus in R*, https://github.com/davidnipperess/PDcalc.

NSW Scientific Committee (2014) *Guidelines for interpreting listing criteria for species, populations and ecological communities under the NSW Threatened Species Conservation Act Version 1.4*, Office of Environment and Heritage, Sydney, Australia.

OEH and CSIRO (Office of Environment and Heritage and Commonwealth Scientific and Industrial Research Organisation) (2019) *Measuring biodiversity and ecological integrity in New South Wales*, OEH, Sydney.

Rangel TF, Colwell RK, Graves GR, Fučíková K, Rahbek C and Diniz-Filho JAF (2015) 'Phylogenetic uncertainty revisited: Implications for ecological analyses', *Evolution*, 69(5):1,301–1,312.

Ribeiro BR, Guidoni-Martins K, Tessarolo G, Velazco SJE, Jardim L, Bachman SP and Loyola R (2022) 'Issues with species occurrence data and their impact on extinction risk assessments', *Biological Conservation*, 273:109674.

Ripple WJ, Wolf C, Newsome TM, Hoffmann M, Wirsing AJ and McCauley DJ (2017) 'Extinction risk is most acute for the world's largest and smallest vertebrates', *Proceedings of the National Academy of Sciences*, 114(40):10678–10683.

Rodríguez N (2008) 'National Red Lists: the largest global market for IUCN Red List categories and criteria', *Endangered Species Research*, 6(2):193–198.

Rowe K, Aplin KP and Baverstock P (2011) 'Recent and rapid speciation with limited morphological disparity in the genus *Rattus*', *Systematic Biology* 60(2):188–203.

Schliep KP (2011) 'phangorn: phylogenetic analysis in R', *Bioinformatics*, 27(4):592–593.

Sólymos P, Morrison SF, Kariyeva J, Schieck J, Haughland DL, Azeria ET, Cobb T, Hinchliffe R, Kittson J, Mcintosh ACS, Narwani T, Pierossi P, Roy M, Sandybayev T, Boutin S and Bayne E (2015) ‘Data and information management for the monitoring of biodiversity in Alberta’, *Wildlife Society Bulletin*, 39(3):472–479.

Therneau T and Atkinson B (2019) *Rpart: recursive partitioning and regression trees*, CRAN (Comprehensive R Archive Network) website.

Tonini JFR, Beard KH, Ferreira RB, Jetz W and Pyron RA (2016) ‘Fully-sampled phylogenies of squamates reveal evolutionary patterns in threat status’, *Biological Conservation*, 204:23–31.

Upham NS, Esselstyn JA and Jetz W (2019) ‘Inferring the mammal tree: species-level sets of phylogenies for questions in ecology, evolution, and conservation’, *PLoS Biology*, 17(12):e3000494.

Weitzman M (1992) ‘On diversity’, *The Quarterly Journal of Economics*, 107(2):363–405.

Westgate M, Stevenson M, Kellie D and Newman P (2023) *galah: Atlas of Living Australia (ALA) Data and Resources in R*, CRAN (Comprehensive R Archive Network) website.

Witting L and Loeschcke V (1995) ‘The optimization of biodiversity conservation’, *Biological Conservation*, 71(2):205–207.

More information

Biodiversity Indicator Program links

- A Biodiversity Indicator Program for NSW – webpage
- Expected survival of listed threatened species and ecological communities: report card supplementing the NSW biodiversity outlook report 2024
- Expected survival of all known species: report card supplementing the NSW biodiversity outlook report 2024
- NSW biodiversity outlook report 2024 – outlook report
- Expected survival of listed threatened species and ecological communities 2024 data package
- Expected survival of all known species 2024 data package

Species and ecosystem online source data

- Atlas of Living Australia
- Australian Faunal Directory
- Australian National Species List
- Australian Plant Census
- IUCN Red List of Ecosystems
- IUCN Red List of Threatened Species
- IUCN Global Ecosystem Typology
- PlantNET (NSW Flora Online)
- NSW Threatened Species Scientific Committee – Final determinations
- Species Profile and Threats Database (SPRAT Database)

Other websites

- TimeTree of Life
- Feral predator-free areas project
- Fire extent and severity maps
- NSW State Vegetation Type Map
- NSW vegetation classification framework
- Threatened Species Index