



DEPARTMENT OF PLANNING, INDUSTRY & ENVIRONMENT

Expected diversity as an indicator of biodiversity status and trend

**A case example using the listed threatened species and
ecological communities of New South Wales, Australia**

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Acronyms and abbreviations

ALA	Atlas of Living Australia
BC Act	<i>Biodiversity Conservation Act 2016</i>
CSIRO	Commonwealth Scientific and Industrial Research Organisation
IBRA	Interim Biogeographic Regionalisation for Australia
IMCRA	Integrated Marine and Coastal Regionalisation of Australia
IUCN	International Union for Conservation of Nature
MDCC	Most derived consensus clade
NSW	New South Wales
SoS	<i>Saving our Species</i>

Context

The New South Wales (NSW) Government has introduced new legislation for biodiversity conservation, the *Biodiversity Conservation Act 2016* (the BC Act), which commenced on 25 August 2017, replacing the *Threatened Species Conservation Act 1995*. The goals of the BC Act include the conservation of biodiversity at bioregional and state levels, a reduction in the rate of species loss, and effective management to maintain or enhance the integrity of natural habitats. To contribute to assessing the performance of the new legislation, the former Office of Environment and Heritage NSW established the Biodiversity Indicator Program to report on the status of biodiversity and ecological integrity at regular intervals. The responsibility of implementing this program now rests with the Department of Planning, Industry and Environment / Environment, Energy and Science.

Monitoring of biodiversity across New South Wales is a large, complex task requiring novel approaches to data collection and use, including the application of models to help track change. The three indicators, reported here, are components of biodiversity in New South Wales for which the status and change over time are being assessed. The overarching monitoring framework, which outlines how indicators are related and derived, is presented in *Measuring Biodiversity and Ecological Integrity in New South Wales: Method for the Biodiversity Indicator Program* (OEH & CSIRO 2019).

The method for the Biodiversity Indicator Program establishes a nested design within which all **indicators**, as they are developed, have a place. Each indicator is nested with others of its type in an **indicator family**, and each family is nested within one of five **themes** which are associated with either the biodiversity or ecological integrity **class** of indicators (as shown in Figure 1).

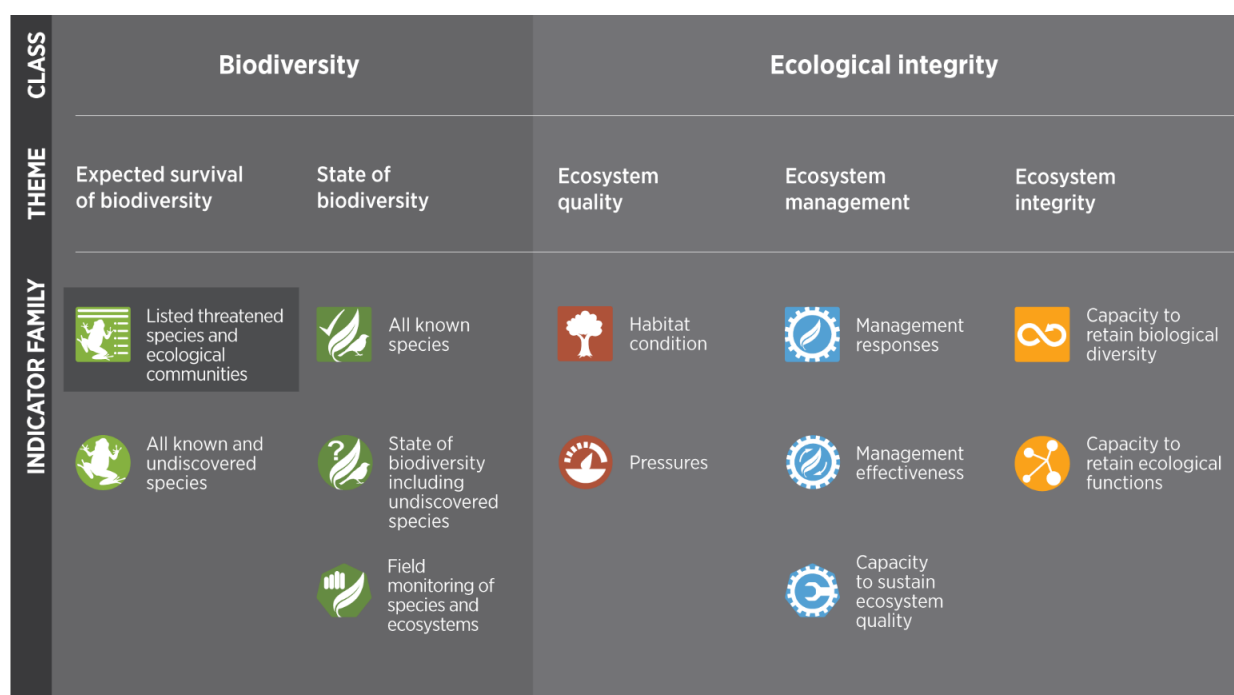


Figure 1 Nested structure used to arrange indicators for measuring biodiversity and ecological integrity in New South Wales. This implementation report addresses **the indicator family**: Expected survival of listed threatened species and ecological communities (shown by the darker grey box).

The indicators in the **expected survival of biodiversity** theme assess both listed threatened species and ecological communities as well as all known and undescribed species in New South Wales.

This indicator implementation report details how three indicators for the expected survival of biodiversity theme were measured/assessed. The key results and highlights are presented in one of several report cards in the first *NSW Biodiversity Outlook Report* (DPIE 2020). The indicators detailed in this report sit within the nested framework as follows:

Class:	Biodiversity
Theme:	1. Expected survival of biodiversity
Indicator family:	1.1 Expected survival of listed threatened species and ecological communities
Indicator:	1.1a Expected survival of listed threatened species <i>Number of listed threatened species expected to survive in 100 years</i>
Indicator:	1.1b Expected existence of listed threatened ecological communities <i>Number of listed threatened ecological communities expected to exist in 100 years</i>
Indicator:	1.1c Expected survival of phylogenetic diversity for listed threatened species <i>The length of evolutionary history that is maintained in the species of a biological group that is expected to survive in 100 years</i>

The **expected survival of biodiversity** indicator family allows the assessment of the survival (continued existence) in 100 years of species and ecological communities that have already been determined by the NSW Threatened Species Scientific Committee to be at risk of extinction. The indicator family also includes a measure of the risk of losing unique evolutionary heritage (via phylogenetic diversity). In the future, this indicator can be updated based on monitoring of successful management actions that result in secure wild populations of threatened species or ecological communities as determined by the *Saving our Species* (SoS) program.

Summary

The BC Act requires a program for monitoring biodiversity for the state of New South Wales. Consequently, the former Office of Environment and Heritage collaborated with the Commonwealth Scientific and Industrial Research Organisation (CSIRO), Macquarie University and the Australian Museum to develop indicators for biodiversity at regional and statewide scales. The method specifically detailed in this report describes the first assessment (at the commencement of the BC Act) and temporal trends for indicators that measure the rate of loss of biodiversity in New South Wales from scheduled lists of threatened species and ecological communities, in accordance with the regulations under the BC Act.

Expected diversity measures the rate of loss by determining the amount of biodiversity expected to still exist at some point in the future (e.g. 100 years from now). Expected diversity provides a measure for assessing change in the threatened status of biodiversity, and was the basis for the three indicators reported here:

- expected survival of listed threatened species
- expected existence of listed threatened ecological communities
- expected survival of phylogenetic diversity for listed threatened species.

Expected survival was estimated from the listed status (i.e. vulnerable, endangered, critically endangered or extinct) of species and ecological communities. Phylogenetic diversity measures evolutionary heritage by quantifying the amount of evolutionary history (sum of 'branch lengths' on a phylogenetic tree) for any given set of species. The expected survival of phylogenetic diversity quantifies the amount or proportion of the tree expected to survive.

Determining temporal trends in the indicators required the interpolation of the listed status of threatened species and ecological communities over time. In the 'best case' scenario, species and ecological communities were assumed to maintain the same status over time unless specifically changed by a determination of the NSW Threatened Species Scientific Committee (or its predecessor). In the 'worst case' scenario, species and ecological communities were assumed to be secure (i.e. not threatened) prior to being first listed as threatened.

Results for each indicator are reported for the first assessment (i.e. at the time of the commencement of the BC Act in 2017) and temporal trends (i.e. from the inception of threatened species legislation in New South Wales in 1995 to the first assessment in 2017). Results are summarised in the key findings section below. Declines, robust to assumptions, have occurred since 1995 in the expected survival of listed threatened species and phylogenetic diversity, but not of listed ecological communities. Phylogenetic diversity was only conducted on selected vertebrate groups (i.e. birds, mammals and frogs).

Extrapolating trends in threatened species and ecological communities to rates of biodiversity loss requires that lists of threatened entities are representative of the overall biodiversity of New South Wales. The representativeness of the lists is unknown but is clearly biased towards well-known groups such as terrestrial vertebrates and flowering plants, and within these groups, the well-known species.

The accuracy with which the expected diversity indicators described here are able to track changes in the loss of biodiversity hinges on the rate of reassessment of listed species and ecological communities. This could be achieved by either a formal process (through the NSW Threatened Species Scientific Committee) or by translating results of monitoring populations through programs such as SoS. Establishing an up-to-date extinction risk assessment for all species and ecological communities and reassessing already listed entities on a regular basis would improve the sensitivity of the indicators to true changes in the rate of loss of NSW biodiversity.

To facilitate future iterations of the indicators, new data products need to be maintained, namely:

1. official lists of NSW species and subspecific taxa (with standardised taxonomy) for selected groups
2. phylogenies matching the official species lists
3. a database documenting the rationale behind each determination of the NSW Threatened Species Scientific Committee.

These indicators can be updated as new data become available, either as determinations of the NSW Threatened Species Scientific Committee, or from monitoring outcomes through programs such as SoS.

Key findings

Indicator: 1.1a Expected survival of listed threatened species

1.1b Expected existence of listed threatened ecological communities

- Of the 1003 NSW species and subspecific taxa that were either listed as threatened or extinct under the BC Act in 2017 (991 taxa) or had been assessed and not listed (12 taxa), 507 (50.5%) are expected to be still surviving in 100 years. Considering only listed species, 496 (50%) are estimated to be still surviving in 100 years.
- There is a clear decline in the expected survival of listed threatened species between 1995 (when threatened species legislation was first enacted in New South Wales) and 2017. For the 'best case' scenario (assuming the smallest possible change in the indicator), this decline reflects genuine changes in the threat status of species. This trend is not simply due to growth in the number of species on the list, nor to the critically endangered category not being available before 2006. Decline is more rapid in some groups, notably amphibians and birds.
- Of the 109 NSW ecological communities either listed as threatened under the BC Act in 2017 (108 communities), or assessed and not listed (1 community), 65 (60%) are expected to be still existing in 100 years. Considering only listed ecological communities, 64 (59%) are estimated to be still existing in 100 years.
- There is perhaps no decline in the expected existence of listed threatened ecological communities. For the 'best case' scenario (assuming the smallest possible change in the indicator), the number of communities expected to still exist did not change between 1995 and 2017. In the 'worst case', decline is apparent but may be simply due to growth in the number of listed communities.
- The assessment of listed threatened species and ecological communities highlighted the need for more explicit information to accurately capture the rationale behind each decision made by the NSW Threatened Species Scientific Committee, and for this information to be managed in a publicly accessible database.

Indicator: 1.1c Expected survival of phylogenetic diversity

- An average of 92% of the phylogenetic diversity of NSW birds, representing 10,563 million years of evolutionary heritage, is expected to be surviving in 100 years.
- An average of 84% of the phylogenetic diversity of NSW mammals, representing 3143 million years of evolutionary heritage, is expected to be surviving in 100 years.
- An average of 83% of the phylogenetic diversity of NSW frogs, representing 2246 million years of evolutionary heritage, is expected to be surviving in 100 years.
- Expected survival of phylogenetic diversity for all three groups (birds, mammals, frogs) is not significantly higher or lower than a random selection of species with the same probabilities of survival, indicating that the distribution of threatened species is not biased towards particular parts of the tree or to particularly distinct (or indistinct) species.
- There is a clear decline in the expected survival of phylogenetic diversity of birds, mammals and frogs since 1995. Because of a lack of phylogenetic bias in listed species, trends largely follow those for the expected survival of threatened species.
- Example evolutionary subtrees for boobook owls, bandicoots and the *Litoria aurea* species complex show that gains in phylogenetic diversity due to securing a target threatened species in New South Wales are most dramatic when nearest relatives are also threatened. Conversely, the continued survival in New South Wales of groups such as bandicoots depends heavily on the status of their remaining secure (non-threatened) members.

- New data have been generated for New South Wales that represent current scientific knowledge of the phylogeny of birds, mammals and frogs. Equivalent assessments of phylogenetic diversity for other biological groups, such as reptiles, plants, fungi and some invertebrate groups, requires similar processing of available phylogenies and name matching with official lists of NSW species and subspecific taxa.

Future assessments of the indicators

- These indicators can be updated as assessments are made by the NSW Threatened Species Scientific Committee, or over any period following assessments.

These indicators may also be updated based on population monitoring through programs such as SoS. Successful management actions of threatened species could result in secure populations, slowing, halting or reversing temporal trends in the expected survival of threatened species.

1. Introduction

The former Office of Environment and Heritage NSW collaborated with the Commonwealth Scientific and Industrial Research Organisation (CSIRO), Macquarie University and the Australian Museum to develop a method for the collection, monitoring and assessment of biodiversity information in New South Wales at regional and statewide scales (OEH & CSIRO 2019). The technical implementation of the method specifically detailed in this report establishes a 'first assessment' (i.e. at the commencement of the *Biodiversity Conservation Act 2016* (the BC Act)), and temporal trends, for one family of indicators that measure biodiversity known to be threatened in New South Wales.

Consistent with the BC Act, 'biodiversity' is here defined as 'the variety of living animal and plant life from all sources, and includes diversity within and between species and diversity of ecosystems'. This definition deals exclusively with composition (variety of life) and does not include structural and functional attributes that are often conflated with composition in a broader definition of biodiversity (c.f. Noss 1990). It is important to note that the biodiversity of New South Wales includes all those species and ecosystems yet to be discovered, catalogued and assessed for their conservation status. The definition of plant life for the purposes of the BC Act in New South Wales includes fungi. The definition of animal for the purposes of the BC Act does not include humans or fish within the meaning of the *Fisheries Management Act 1994*.

The variety of life includes not only the number of species or ecosystem types, and their abundances, but also the differences between them (MacLaurin & Sterelny 2008).

Phylogenetic diversity (Faith 1992) captures information on the differences between species by measuring the evolutionary heritage represented by a set of species (Figure 2). Evolutionary heritage provides a currency for biodiversity (Mooers & Atkins 2003) by measuring biodiversity as millions of years of independent evolutionary history.

A core purpose of the BC Act is to 'support conservation and threat abatement action to slow the rate of biodiversity loss and conserve threatened species and ecological communities in nature'. This implies an indicator is needed to measure the rate of biodiversity loss (Pereira & Cooper 2006). Successful conservation programs would slow or even reverse the rate of loss at the state level. The goal of slowing or halting the rate of biodiversity loss is a globally recognised requirement for conservation programs and is a central mission for the Convention on Biological Diversity (Secretariat of the Convention on Biological Diversity 2010).

Expected diversity (Weitzman 1992) provides a means of measuring the rate of loss by determining the amount of biodiversity expected to still exist at some point in the future (e.g. 100 years from now), derived from estimated survival probabilities of species or ecological communities. Rate of loss is simply the difference in diversity between now and that expected in the future. The key indicator of conservation success is then a reduction in the rate of loss. The expected diversity framework resembles the Red List Index (Butchart et al. 2004; Butchart et al. 2007), in that species (or, potentially, ecological communities) are weighted according to their relative risk of loss, but differs in being a more directly probabilistic approach that is extensible to a variety of measures of biological diversity.

Conservation of phylogenetic diversity is important because, by retaining evolutionary heritage, 'option values' are also retained. The accumulation of unique evolutionary adaptations represented by phylogenetic diversity is a source of as-yet undiscovered uses (e.g. novel antibiotics); options that will be lost to humanity if evolutionary heritage is lost (Díaz et al. 2015). **Expected phylogenetic diversity**, part of the expected diversity framework (Faith 2008), provides an indicator that is sensitive to the loss of evolutionary heritage. Further, phylogenetic diversity provides a means of dealing with subspecific taxa more appropriately than if they were counted as equivalent to species. Loss of a subspecific

taxon (but not the parent species) in New South Wales would result in a lesser reduction in phylogenetic diversity than if the full species (including all NSW subspecific taxa) were lost.

An expected diversity indicator is constrained by available information on biodiversity, requiring survival probabilities be specified. Ideally, specific population viability assessments for individual species and ecological communities would form the basis for determining survival probabilities. As these data are not generally available, one proxy is to use assessments of extinction risk from standardised scientific determinations and threat-based listings. Only those species or ecological communities described, catalogued and assessed to determine their threatened status can be included in the calculation. Further, when considering phylogenetic diversity, evolutionary relationships between all included species must also be known. However, threatened species listings are typically a subset of all known species within a group and may not represent the risk of extinction to all species in the group. For example, less than 2% of NSW listed threatened species are invertebrates despite being about 67% of known Australian species (Chapman 2009; Nipperess 2015), and a much larger proportion of all Australian species, known and unknown (Taxonomy Decadal Plan Working Group 2018).

Information on the threatened status of species, subspecific taxa, populations and ecological communities is provided by the NSW Threatened Species Scientific Committee (NSW TSSC). The NSW TSSC is an independent body of scientists appointed by the NSW Minister for the Environment. Originally established under the *Threatened Species Conservation Act 1995*, as the NSW Scientific Committee, it continues to operate under the BC Act and its Regulation (i.e. Biodiversity Conservation Regulation 2017). The acronym 'NSW TSSC' will be used in this report to refer to the committee under either title (i.e. 'NSW Scientific Committee' or 'NSW Threatened Species Scientific Committee') as it is a continuously operating entity (with changing membership) over the period covered by this report and into the foreseeable future. While the NSW TSSC is responsible for assessing and listing threatened entities in the schedules of the BC Act, only species not covered by the Fisheries Management Act can be considered. The Fisheries Scientific Committee, established under the Fisheries Management Act, is responsible for assessing threatened status for fish, aquatic invertebrates, marine plants and aquatic ecological communities. All other vertebrates, even those that are aquatic (e.g. whales, seabirds, turtles and frogs), remain the responsibility of the NSW TSSC.

The NSW TSSC makes determinations on whether nominated species, subspecific taxa, populations or ecological communities should be listed as threatened or extinct in New South Wales. Listed species and subspecific taxa are categorised as either vulnerable, endangered, critically endangered, extinct (formerly the presumed extinct category) or extinct in the wild. Similarly, listed ecological communities are classified as either vulnerable, endangered, critically endangered or collapsed. Populations may be listed if the species to which the population belongs is not separately listed as threatened, and the population is, in the opinion of the NSW TSSC, of significant conservation value based on its role in the conservation of the species or a number of other species. The categories for populations follow those as for species. The listing of an entity requires a rigorous assessment of available evidence, with assignment to a category requiring qualification for specific criteria. The quantitative criteria of the NSW TSSC follow those of the International Union for Conservation of Nature (IUCN), specifically, the *IUCN Red List of Threatened Species* (IUCN 2018) and the *IUCN Red List of Ecosystems* (IUCN 2016) and are designed to measure the widely recognised symptoms of extinction risk and ecosystem collapse (Mace et al. 2008; Keith et al. 2013).

This report provides technical detail on the methods and results for a family of indicators on the status of biodiversity in New South Wales, based on the expected diversity framework. The primary data for this assessment are provided by the lists of threatened species and ecological communities as scheduled under the BC Act. The indicators report on expected diversity of species and ecological communities in New South Wales that have been formally

assessed for threatened status and, therefore, estimate rate of loss on only a specific and small subset of NSW biodiversity. In the case of threatened species, expected phylogenetic diversity is also reported for selected groups (i.e. birds, mammals and frogs). The first assessment is at the commencement of the BC Act on 25 August 2017. In addition, temporal trends are reported from 1995 to 2017 by interpolating the status of currently threatened species and ecological communities over time. This assessment does not consider threatened populations.

Indicators included in this report are as follows:

- **Expected survival of listed threatened species**

Number of listed threatened species expected to survive in 100 years

Species listed as threatened or extinct in Schedules 1 and 3 (respectively) of the BC Act are assigned a probability of survival in 100 years. The indicator at the first assessment (i.e. 2017) is calculated by summing the probabilities of survival for all listed species. Future change in the value of the indicator can reflect either a change in the threat category of species due to a decision of the NSW TSSC or a change in the probability of survival due to effective management of the species.

- **Expected existence of listed threatened ecological communities**

Number of listed threatened ecological communities expected to exist in 100 years

Ecological communities listed in Schedule 2 of the BC Act are assigned a probability of survival in 100 years. The indicator at the first assessment is calculated by summing the probabilities of survival for all ecological communities for all threatened ecological communities. Future change in the value of the indicator can reflect either a change in the threat category of an ecological community due to a decision of the NSW TSSC or a change in the probability of survival due to effective management of the ecological community.

- **Expected survival of phylogenetic diversity for listed threatened species**

The length of evolutionary history that is maintained in the species of a biological group that is expected to survive in 100 years

A complete list is obtained of all species within New South Wales for a biological (i.e. taxonomic) group. How each species is related by shared ancestry over evolutionary timescales (in millions of years) is given by a phylogeny or evolutionary tree. For each biological group, this indicator requires a complete phylogeny for all species known from New South Wales. Species listed as threatened or extinct in Schedules 1 and 3 (respectively) of the BC Act are assigned a probability of survival in 100 years. Other species in the biological group are considered not threatened (i.e. 'secure').

Phylogenetic diversity is the sum of all the lengths of the branches in the evolutionary tree that span all species and their common ancestor, scaled in millions of years. The length of each branch is weighted by its probability of survival, giving the amount (and proportion) of the tree expected to be still surviving in 100 years. Future change in the value of the indicator can reflect either a change in the threat category of species due to a decision of the NSW TSSC or a change in the probability of survival due to effective management of the species.

2. Method design

2.1 Expected diversity framework

Expected diversity is formally defined as the number of biodiversity features expected to still exist at some specified point in the future (e.g. 100 years from now). ‘Features’ are defined broadly as units of biodiversity such as genes, species and ecological communities. Thus, species richness is a specific example of feature diversity which simply counts the number of species. Feature diversity is strictly concave (adding features always increases diversity, see Lande 1996), and thus features must be discrete entities that individually contribute to overall diversity. Then, for any class of features that fulfils this requirement, the expectation of the value of feature diversity ($\mathbb{E}[D]$) at some point in the future is given by equation 1, and is simply the sum of the probability (q_i) of survival of each feature (i) across a set of features (F) where $i \in F$ (Weitzman 1992).

$$\mathbb{E}[D] = \sum_{i \in F} q_i \quad \text{equation 1}$$

The expected diversity framework provides a measure for the rate of biodiversity loss. Slowing the rate of loss is a central goal of the BC Act, as well as global conservation efforts. Rate of loss is simply measured as the change in expected diversity between two time steps (Weitzman 1992; Faith 2008), where each feature (i) may have a new probability (\hat{q}) of survival (equation 2).

$$\Delta(\mathbb{E}[D]) = \sum_{i \in F} \hat{q}_i - \sum_{i \in F} q_i \quad \text{equation 2}$$

2.2 Expected phylogenetic diversity

Phylogenetic diversity is a special case of feature diversity where the length of a branch segment on a phylogenetic tree is interpreted as being proportional to the number of discrete features possessed by species descendent from that branch (Faith 1992). A ‘branch segment’ is here defined as the edge on a phylogenetic tree that connects nodes (branching points) or connects a node to a tip. Given that feature diversity is simply a count of features, phylogenetic diversity is then the sum of branch lengths connecting some set of species to the root of the tree (Figure 2).

Expected phylogenetic diversity ($\mathbb{E}[PD]$) is then the sum of the length (L_j) of each branch segment (j) in a phylogenetic tree ($T, j \in T$) multiplied by its probability (q_j) of survival (equation 3). 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.

$$\mathbb{E}[PD] = \sum_{j \in T} \left[L_j * \left(1 - \prod_{i \in S_j} (1 - q_i) \right) \right] \quad \text{equation 3}$$

Branch lengths on phylogenetic trees are often scaled in units of character changes (genetic or morphological) which will vary depending on the set of characters used. A common currency is, however, provided by evolutionary time where branching nodes (and thus branch lengths) are scaled by estimated divergence dates, and phylogenetic diversity is thus measured in units of millions of years of evolutionary heritage (Mooers & Atkins 2003).

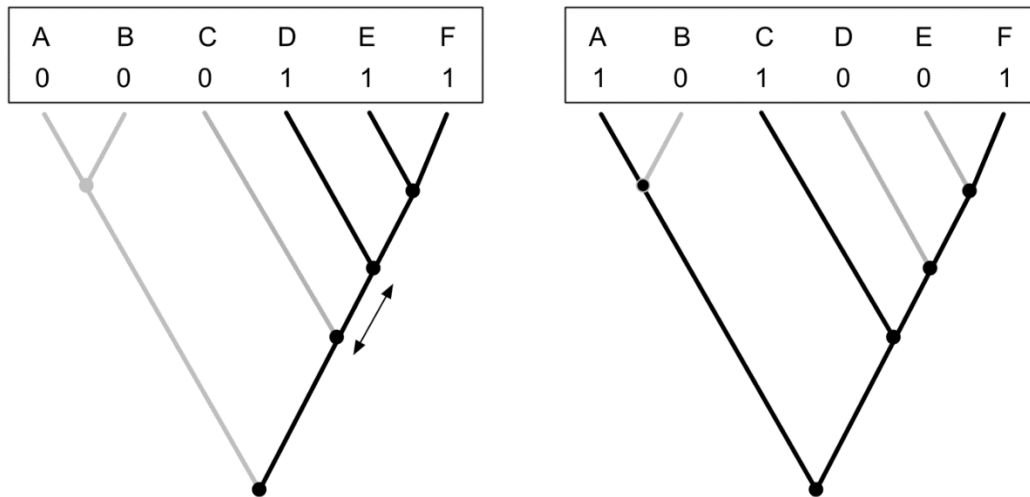


Figure 2 Hypothetical example showing two scenarios where species A–F are either retained (1) or lost (0) in the future

The length of a single branch segment is indicated by the double-headed arrow. Branch segments that are retained (due to survival of descendent species) are shown in black while branch segments that are lost are shown in grey. Phylogenetic diversity expected in the future is then the sum of the lengths of the black branch segments. The left-hand example retains less phylogenetic diversity than the right-hand example, even though the number of surviving species are the same.

2.3 Probabilities of survival of threatened species and ecological communities

The probability of survival (and thus of extinction) for species adopted here must be consistent with the definition of extinct used by the BC Act and the *IUCN Red List of Threatened Species* (IUCN 2018). Thus, if any individuals of the species persist in New South Wales in 100 years, then it has ‘survived’ even if the population is not viable in the longer term. It is probably reasonable to assume that critically endangered species do not have viable populations in the long term (i.e. are functionally extinct) but are not and would not be classified as extinct until the last individual is lost (IUCN 2012).

While the true survival probabilities of individual species are not known, the IUCN does give estimates for probability of extinction for criterion E for specific threat categories (vulnerable, endangered and critically endangered) for both the the *IUCN Red List of Threatened Species* (IUCN 2018) and the *IUCN Red List of Ecosystems* (IUCN 2016). Criterion E gives critical thresholds for extinction probabilities (over specified time periods) determined from population viability analysis (Brook et al. 2000) or the equivalent for ecosystems. Based on these thresholds, Kindvall and Gärdenfors (2003) determined the per-year extinction probabilities for species and then extrapolated for other time periods (Figure 3). Following from Kindvall and Gärdenfors (2003), the *Saving our Species* (SoS) program (OEH 2013) derived survival probabilities (for a 100-year time period) in the development of a priority score for selecting projects. The SoS program also included a ‘secure’ category for non-threatened species, which was assigned a survival probability (over 100 years) of 0.95. The SoS values were adopted for the expected diversity indicators (Table 1).

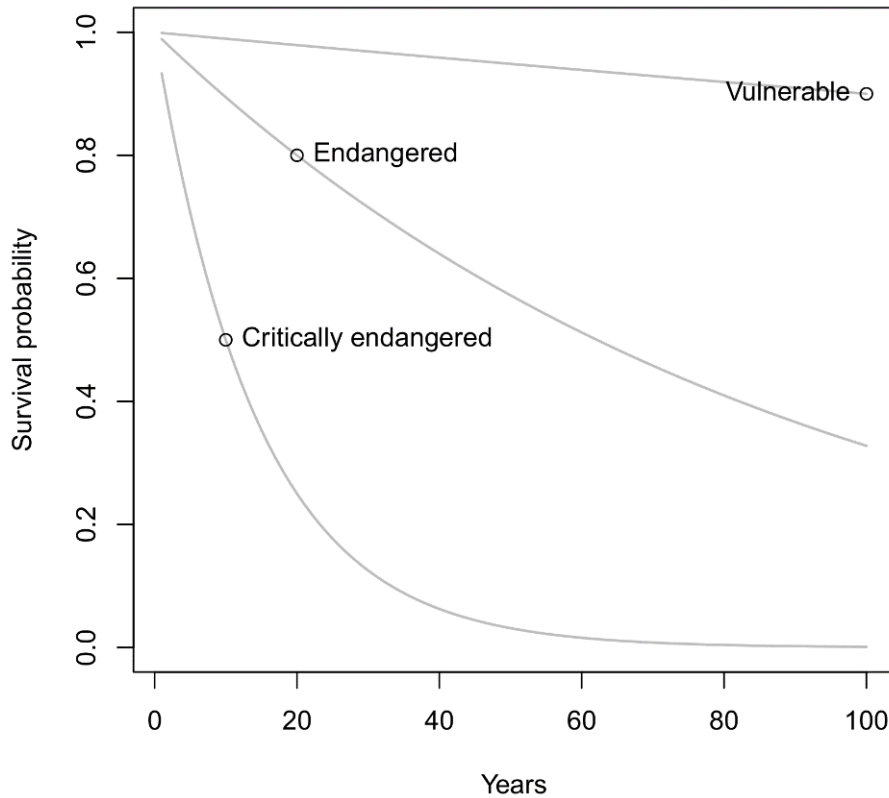


Figure 3 Extrapolation of survival probabilities of categories of threatened species over time derived from Criterion E of the *IUCN Red List of Threatened Species*. Original IUCN estimates are indicated as points for critically endangered, endangered and vulnerable. Calculations follow Kindvall and Gärdenfors (2003).

Table 1 Survival probabilities of species and ecological communities for risk of extinction categories adopted by this study

Risk category	Probability (<i>q</i>) of survival in 100 years	
	Species	Ecological communities
Secure	0.95	0.95
Vulnerable	0.90	0.90
Endangered	0.30	0.65
Critically endangered	0.05	0.25
Extinct	0.01	

Note: Values follow those used by the *Saving our Species* program where possible and are derived by extrapolation from IUCN criterion E (Kindvall & Gärdenfors 2003). The exception is the extinct category, which is derived from a sighting model (Solow & Roberts 2003) of a hypothetical species last seen 50 years ago.

While SoS provides survival probabilities for threatened species and non-threatened species, there is no corresponding probability for species listed as extinct or extinct in the wild on Schedule 3 of the BC Act. It was considered desirable to include a small probability of survival for this category because species presumed to be extinct are occasionally

rediscovered, for example, the dusky hopping mouse (*Notomys fuscus*) was rediscovered in 2003 (NSW TSSC 2017). A scientifically supportable estimate was provided by sighting models. Solow and Roberts (2003) derived an equation for estimating probability of survival (q) based on the current year (T), the year of the most recent sighting (T_n), and the year of the second most recent sighting (T_{n-1}) (equation 4).

$$q = \frac{T_n - T_{n-1}}{T - T_{n-1}} \quad \text{equation 4}$$

If we define a hypothetical species last seen 50 years ago (and again in the previous year), the probability that it will still be extant in 100 years is given in equation 5. The choice of 50 years is based on a rule of thumb (previously used by the IUCN) that a species not seen for more than 50 years is extinct in the wild.

$$q = \frac{T_n - T_{n-1}}{T - T_{n-1}} = \frac{1967 - 1966}{2117 - 1966} \sim 0.01 \quad \text{equation 5}$$

Extinction probabilities for ecological communities are given as criterion E of the *IUCN Red List of Ecosystems* (Bland et al. 2017). The approach of Kindvall and Gärdenfors (2003) can again be adopted by temporally extrapolating from criterion E to derive survival probabilities for a period of 100 years (Figure 4 and Table 1). For ecological communities deemed to be non-threatened (secure), we adopted the same value (0.95) used for species in the SoS program. As there are no ecological communities listed as collapsed in New South Wales, a survival probability equivalent to extinct for ecological communities was not derived.

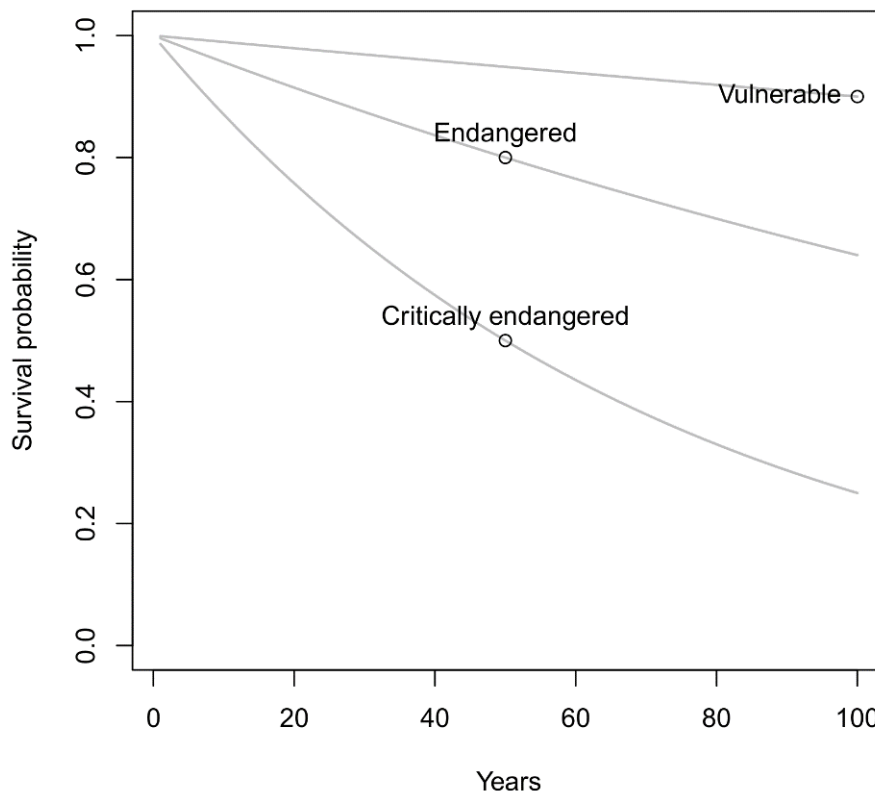


Figure 4 Extrapolation of survival probabilities of categories of threatened ecological communities over time derived from criterion E of the *IUCN Red List of Ecosystems*. Original IUCN estimates are indicated as points for critically endangered, endangered and vulnerable. Calculations follow that of Kindvall and Gärdenfors (2003) for species.

2.4 Partition of diversity into expected survival and expected loss components

If total diversity (D) is defined as the number of features, then expected diversity ($\mathbb{E}[D]$) is the number of features expected to survive over some timeframe; that is, the **expected survival** component of total diversity. An **expected loss** component is then simply the difference between total and expected diversity ($D - \mathbb{E}[D]$) or, alternatively, the sum of extinction probabilities ($\sum_{i \in F} (1 - q_i)$). The expected loss component will include a contribution by features presumed to be extinct and thus it might be useful to further partition expected loss into that contributed by presumed extinct features and the remainder (that is, loss that has not yet occurred).

The contribution to expected loss made by features presumed to be already extinct ($\mathbb{E}[D_X]$) is the sum of extinction probabilities of that subset (F_X) of features (equation 6).

$$\mathbb{E}[D_X] = \sum_{i \in F_X} (1 - q_i) \quad \text{equation 6}$$

The contribution to expected loss made by features not already extinct can then be determined by subtraction ($D - \mathbb{E}[D] - \mathbb{E}[D_X]$).

Expected loss of phylogenetic diversity, as a component of total phylogenetic diversity (PD), can be determined by simple subtraction ($PD - \mathbb{E}[PD]$). The contribution of presumed extinct species can be determined from the difference in probabilities if one assumes they are truly extant ($q = 1$) versus having a small survival probability (e.g. $q = 0.01$) (equation 7). In equation 7, S_{Y_j} is the subset of species, descendent from branch segment j , that are *not* extinct and S_{X_j} is the subset of descendent species that are presumed extinct.

$$\mathbb{E}[PD_X] = \sum_{j \in T} \left[L_j * \left(\left(1 - \left(\prod_{i \in S_{Y_j}} (1 - q_i) * \prod_{i \in S_{X_j}} 0 \right) \right) - \left(1 - \prod_{i \in S_j} (1 - q_i) \right) \right) \right] \quad \text{equation 7}$$

The contribution to expected loss of phylogenetic diversity made by species not already extinct can then be determined by subtraction ($PD - \mathbb{E}[PD] - \mathbb{E}[PD_X]$).

3. Method implementation

3.1 Data sourcing, cleaning and manipulation

3.1.1 Lists of threatened species and ecological communities

The primary data for the analyses in this report are the species, subspecific taxa and ecological communities listed in the schedules of the BC Act. Species and aquatic communities listed under the Fisheries Management Act are not included. When referring to lists of threatened entities (i.e. species, subspecific taxa and ecological communities) in this report, it is intended to mean those entities listed in the schedules of the BC Act. This includes species presumed to be extinct in New South Wales, which are not considered 'threatened' in the legislation.

Subspecific taxa (i.e. subspecies and varieties) are included in analyses, and 'species' will generally be used as a shorthand for referring to species-level and subspecific taxa. Where a subspecific taxon is listed, the NSW TSSC does not also list the parent species-level taxon. Note that the BC Act also lists threatened populations (see section 5.3.4), and more determinations at this level are anticipated, but these are not presently included in this family of indicators. For the expected survival of listed threatened species indicator, taxa ranked below species level were treated as equivalent to species. For the expected survival of phylogenetic diversity for listed threatened species indicator, taxa below species level were inserted as short branches in a phylogenetic tree (see section 3.1.3) and thus were generally given a smaller weighting than full species.

Data on threatened entities were downloaded from NSW BioNet (<http://www.bionet.nsw.gov.au/>) by calling the BioNet Open Application Programming Interface with the 'jsonlite' (Ooms 2014) package in *R: A language and environment for statistical computing* (R Core Team 2017, referred to in this report as '*R*'). These data included the name of the listed entity (as currently accepted by the NSW TSSC), the current threatened status in New South Wales, and the year that the entity was listed with its current threatened status.

To enable hindcasting of the indicators, it was necessary to reconstruct the history of determinations of listed entities from 1995 (Threatened Species Conservation Act) to commencement of the BC Act in 2017. This information was not available through NSW BioNet, which only records the current status of listed entities. Using the *Index of Final Determinations* (NSW TSSC 2017) as a starting point, each final determination of the NSW TSSC (available from: www.environment.nsw.gov.au/committee/finaldeterminations.htm) was assessed as to whether that determination resulted in a change in status for an entity. Changes due to taxonomic revision were not included *unless* that revision also resulted in a genuine change in status of the newly accepted taxon. Taxonomy was standardised to that of the current 2017 list (as provided by BioNet). From these data, a new listing database was generated with one row for every determination resulting in an assignment of a threatened status for a particular entity.

As a result of determinations of the NSW TSSC, some entities were either removed from the list (delisted) or rejected (after nomination) from inclusion on the list on the basis that the entity was found to not (or no longer) qualify for listing. As these determinations involved a rigorous assessment of extinction risk by the NSW TSSC, these events were recorded in the new listing database as entities within the secure category. Species previously listed as threatened before being delisted had their earlier status recorded in the listing database, provided the change in status was due to a genuine change in extinction risk and not simply due to a taxonomic revision (e.g. a formerly recognised species being lumped within a secure species).

3.1.2 Lists of New South Wales species (birds, mammals and frogs)

Expected phylogenetic diversity requires a comprehensive list of all species and subspecific taxa for a taxonomic group, along with survival probabilities for all those species. This is because the calculation for internal branches in the phylogenetic tree requires the survival probabilities of all descendent species (equation 3). Thus, it was necessary to acquire lists of species of birds, mammals and frogs known to occur in New South Wales, including islands under jurisdiction (such as Lord Howe Island). These fauna groups were chosen because they have comprehensive phylogenies available (see section 3.1.3). As the threatened species list for New South Wales includes sea mammals and seabirds, a land mask applied to species occurrence records (from NSW BioNet or the Atlas of Living Australia) would not be appropriate in this case. It was a further requirement that these lists be standardised to an accepted taxonomy to facilitate matching across datasets.

Therefore, a biogeographic approach was taken whereby a species recorded as occurring in a terrestrial or marine biogeographic region intersecting with (terrestrial), or adjacent to (marine), the jurisdictional boundary of New South Wales was included in the list (Figure 5). The Australian Faunal Directory provides a standardised, accepted taxonomy for animal species occurring in Australia and includes information about the biogeographic regions in which those taxa are known to occur. The bioregionalisation schemes used by the Directory are the Interim Biogeographic Regionalisation for Australia (IBRA) (Thackway & Cresswell 1995) version 6.1 for terrestrial bioregions, and the Integrated Marine and Coastal Regionalisation of Australia (IMCRA) version 4.0 (IMCRA Technical Group 2006) for marine bioregions. All species and subspecies for each group corresponding to this spatial filter were downloaded from the Australian Faunal Directory Advanced Search tool (<https://biodiversity.org.au/afd/search/advanced?>).

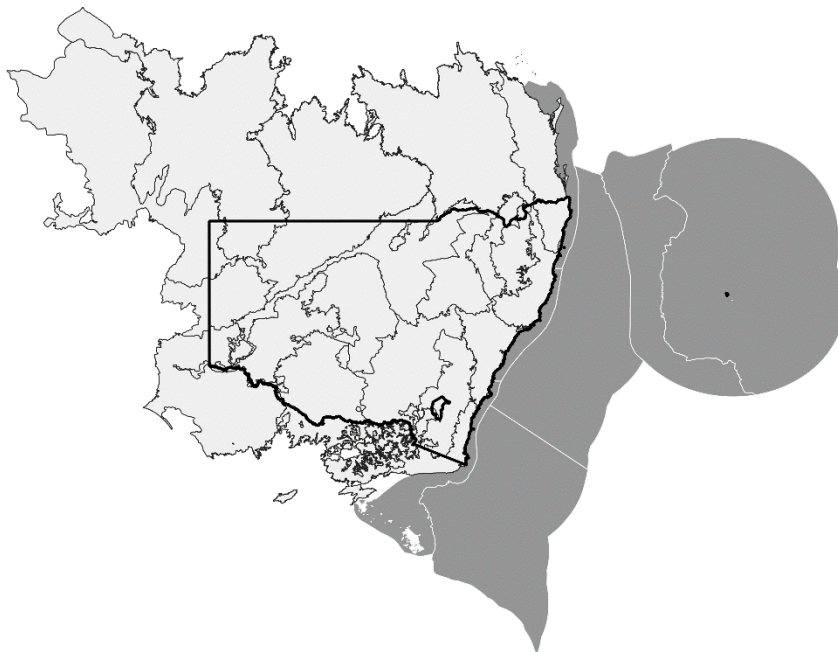


Figure 5 Bioregions used to generate a species list for New South Wales for birds, mammals and frogs

Terrestrial bioregions correspond to Interim Biogeographic Regionalisation for Australia (IBRA) and are shown in light grey. Marine bioregions correspond to Integrated Marine and Coastal Regionalisation of Australia (IMCRA) and are shown in dark grey. Boundary of New South Wales indicated by thick black line.

These lists were then searched for species or subspecies that are unlikely to have a NSW distribution. Species that qualified for one or more of the following criteria were removed from the list:

1. lacking current or historical occurrence records in New South Wales (or offshore) in the Atlas of Living Australia
2. having an expert range map (sourced from the Atlas of Living Australia or the IUCN Red List) that did not intersect with New South Wales or offshore waters
3. were delisted by the NSW TSSC due to no evidence of distribution in New South Wales.

3.1.3 Phylogenetic trees (birds, mammals and frogs)

Birds, mammals and frogs were chosen as good first candidates for the calculation of expected phylogenetic diversity because these groups have comprehensive phylogenetic trees that include almost all known extant species and are fully dated (i.e. branch lengths are scaled in millions of years of evolutionary history).

For mammals, the phylogenetic tree was originally compiled by Bininda-Emonds et al. (2007) and included 4510 species. Fritz et al. (2009) produced an updated version (with 5020 out of 5417 known extant species) with an improved species-level taxonomy matched to *Mammal Species of the World* (Wilson & Reeder 2005). The mammal phylogenetic tree contains many polytomies (i.e. nodes with more than two descendent branches), which are the result of uncertainty about the exact branching order in parts of the tree. Polytomies are a strict consensus among competing hypotheses of the pattern of evolutionary history but are problematic in ecological analyses because they result in over-estimation of branch lengths (Rangel et al. 2015). The problem of polytomies can be resolved, while still preserving the extent of uncertainty about evolutionary relationships, by producing multiple phylogenetic trees, each with only two descendants per node, with each tree representing a competing hypothesis on the true branching order and branch lengths (Rangel et al. 2015). To this end, Kuhn et al. (2011) applied a birth–death model to produce 100 fully resolved (i.e. no polytomies) versions of the tree updated by Fritz et al. (2009). It is recommended that ecological analyses, such as the calculation of expected phylogenetic diversity, be conducted on each fully resolved tree separately and the mean and variance calculated from the resulting range of values (Rangel et al. 2015). The fully resolved set of 100 trees produced by Kuhn et al. (2011) (available as Supporting Information) formed the source phylogenetic data for this study.

For birds, a comprehensive phylogenetic tree was compiled by Jetz et al. (2012), containing all 9993 known extant species and is fully dated. The tree was built upon an earlier ‘backbone’ tree (Hackett et al. 2008), which resolved the major branching points in bird evolutionary history but did not include all known species. Jetz et al. (2012) used a novel Bayesian method that produced 10,000 fully resolved trees that are equally plausible, thus solving the problem of polytomies. This set of trees (based on the Hackett et al. (2008) backbone tree) formed the source phylogenetic data for this study and was downloaded from BirdTree.org (<http://birdtree.org/>). To reduce substantial computational overheads, and allow direct comparison with the mammal trees, 100 trees were selected at random from the 10,000 available trees.

For frogs, this project used a comprehensive phylogenetic tree of amphibians (including frogs) compiled by Isaac et al. (2012), that included 5713 amphibian species (out of 5866 known extant species) and is fully dated. Similar to the original mammal tree of Bininda-Emonds et al. (2007), the amphibian tree comprises a single topology with a large proportion of polytomies. For this project, polytomies were resolved by a simple random process described by Rangel et al. (2015). In this algorithm, two branch segments are selected at random from a polytomy, joined with a new node (with an age determined from a random uniform distribution), and reconnected to their original parent node by a new branch

segment. The process is repeated until no nodes have more than two descendants. This algorithm was implemented using the 'bifurcatr' function in the 'PDcalc' package (Nipperess & Wilson 2017). To allow direct comparison with the mammal and bird trees, and to cover a range of possible phylogenetic hypotheses, 100 fully resolved trees were generated from the original tree using the algorithm.

To produce phylogenetic trees compatible with the NSW species lists and threatened species list, it was necessary to match species names across all three sources and resolve all mismatches. Where taxonomic conflicts about accepted names occurred, the Australian Faunal Directory name was used, *except* where a different name was used in the threatened species list. In that rare case, the name as it appears in the threatened species list was used. To resolve mismatches (i.e. where a name in the NSW species list or threatened species list was not found in the tree), a semi-automated decision tree process was adopted (Figure 6). Synonyms for non-matching names were retrieved from the Atlas of Living Australia (<https://www.ala.org.au/>) by calling the Application Programming Interface using the 'ALA4R' package (Raymond et al. 2017) in *R*. When a species could not be matched (usually a species in the extinct category), it was inserted as a new tip in the tree.

Insertion of new species required, in each case, the identification of the 'most derived consensus clade' (MDCC). The MDCC is the smallest group of species to which the missing species could be confidently assigned (Rangel et al. 2015). In the majority of cases, the MDCC was identified as the genus. In these cases, the missing species was inserted at a random position within the subtree containing all members of a genus using the 'add.species.to.genus' function in the 'phytools' package (Revell 2012) in *R*. This procedure was repeated for all 100 versions of the tree, being placed at a random position each time, to allow for phylogenetic uncertainty.

One extinct mammal species, the pig-footed bandicoot (*Chaeropus ecaudatus*), could not be inserted into a genus because it is the only member and thus the entire genus is missing from the tree. This bandicoot is considered to be a very distinctive species belonging to its own family (Chaeropidae) and is probably the sister to all living bandicoots (Westerman et al. 2012). Therefore, the pig-footed bandicoot was inserted at a random position on the branch segment immediately below the most recent common ancestor of living bandicoots. The insertion was implemented using the 'bind.tip' function in the 'phytools' package (Revell 2012) in *R* and were repeated for all 100 versions of the tree to allow for phylogenetic uncertainty.

Because subspecies are listed in the threatened species list, all NSW subspecies of a animal species for which there are threatened subspecies were also included in the tree. Where only one subspecies occurred in New South Wales, the species name in the tree was simply replaced with the subspecies name. Where there were two NSW subspecies, the species name was replaced with one of the subspecies names and the other subspecies was inserted by attaching it at a random position on the terminal branch of the parent species. Where there were more than two NSW subspecies, the first subspecies replaced the species name, the second was attached to the terminal branch, and the third (and subsequent) were attached at a random position within the subtree containing all members (thus far inserted) of the species. Insertions were implemented using the 'bind.tip' function in the 'phytools' package in *R* and were repeated for all 100 versions of the tree to allow for phylogenetic uncertainty.

The final step in phylogenetic tree processing was to trim away all species not included in the NSW species list. If internal branches had no remaining descendants after removal of tips, these were also removed. The final NSW mammal tree had 189 tips (species and subspecies), the bird tree had 582 tips (species and subspecies) and the frog tree had 85 tips (species and subspecies). These trees represent new data for New South Wales that represent current scientific knowledge of the phylogeny of these groups.

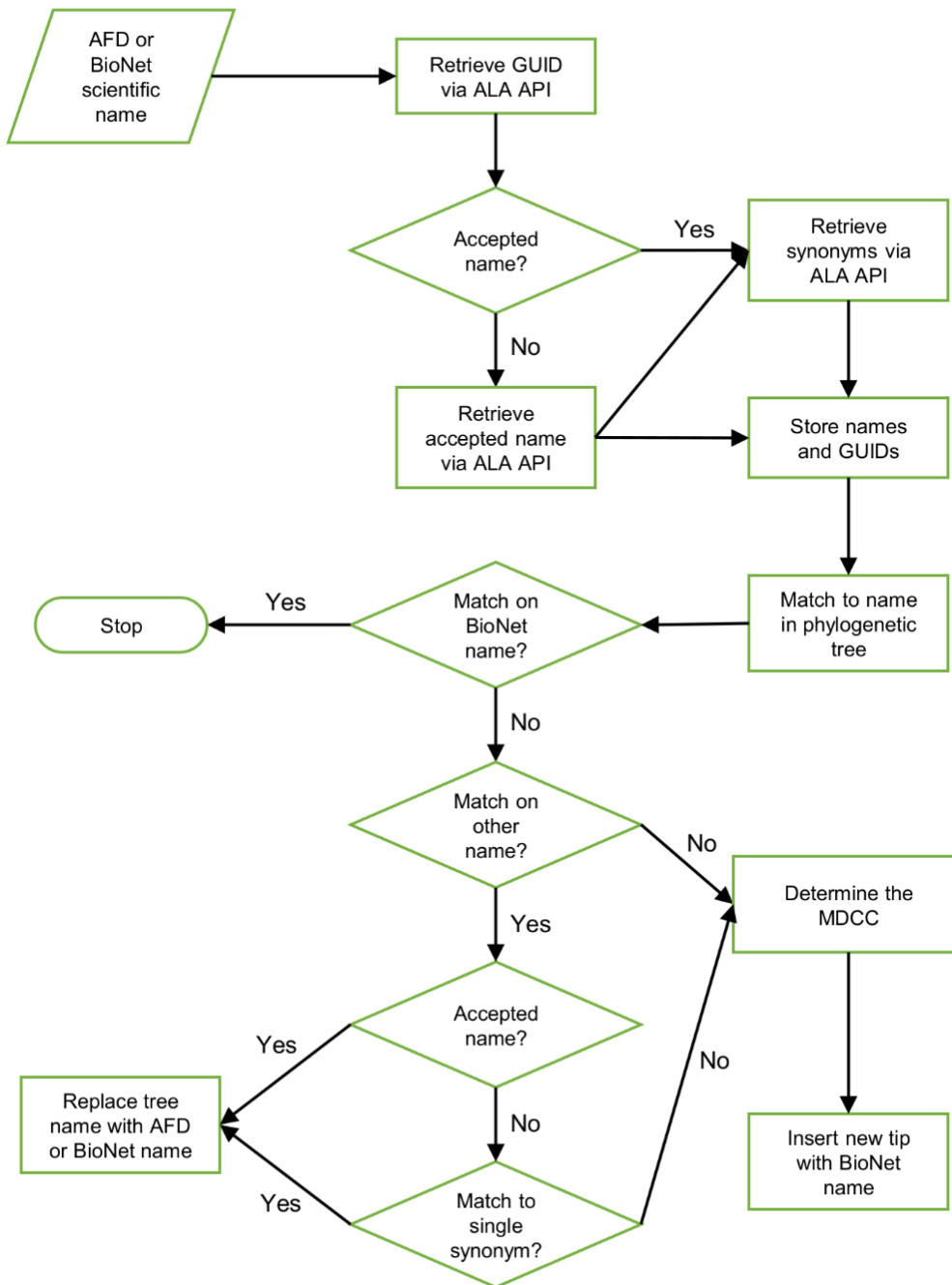


Figure 6 Decision tree used to resolve taxonomic mismatches between the NSW species list (for birds, mammals and frogs), the NSW threatened species list, and the names on the corresponding phylogenetic tree.

Globally unique identifiers (GUIDs, assigned by the Australian Faunal Directory, AFD) were used to retrieve synonyms stored in the Atlas of Living Australia Application Programming Interface (ALA API) and, where possible, matched to a name on the tree. Where no match could be found, or where there was a complex relationship with synonyms (due to splitting or lumping), species were inserted as new tips in the tree within the most derived consensus clade (MDCC).

3.2 Analyses

3.2.1 First assessment values and temporal trajectories

A first assessment value for each indicator calculated using expected diversity was generated from the survival probabilities inferred from the current (2017) threatened status of species and ecological communities, according to Table 1 and equations 1 and 3. In the case of expected phylogenetic diversity, there was no single value for the first assessment, but rather a mean across equally plausible phylogenetic trees.

Expected diversity values were calculated for annual time steps from 1995 to 2017. This covers the period from the first NSW threatened species list provided under the Threatened Species Conservation Act to that in force at the time of commencement of the BC Act. To build a temporal trajectory of expected diversity, it is necessary to make an important assumption about the threatened status of entities prior to their first listing. In these analyses, three possible states were assumed:

1. entities were secure prior to being first listed as a threatened species or ecological community
2. entities were the same status as at the time of first listing as a threatened species or ecological community
3. entities had an equal chance of being either secure or the same status prior to first listing.

Assumptions 1 and 2 effectively bracket the range of uncertainty in the indicator prior to the first assessment, while assumption 3 is a compromise solution. Assumption 2 (best case) is the most conservative option and effectively assumes the threatened status of entities awaits discovery by the NSW TSSC. Meanwhile, assumption 1 (worst case) models the other extreme where entities are nominated for threatened status solely due to a sudden shift in conservation status from secure to threatened.

An additional adjustment for assumption 2 was made for entities listed as endangered prior to 2006 and subsequently changed to critically endangered status. Because the critically endangered category was not available for NSW threatened entities prior to 2006, it is likely that this shift in status is simply due to a reassignment to the newly available category rather than a genuine shift in extinction probability. For consistency with the principle of assumption 2 that, in the absence of new information, entities retain the same status over time, entities that were listed as endangered prior to 2006, and subsequently reclassified as critically endangered, were assumed to be critically endangered for the whole period. Note that this adjustment only applied to assumption 2. Under assumption 1, and consistent with the 'worst case' principle, a shift from endangered to critically endangered was treated as a genuine shift in extinction probability.

3.2.2 Sensitivity to phylogenetic uncertainty

Sensitivity analysis for expected phylogenetic diversity was provided by the distribution of possible values calculated from each of 100 equally plausible phylogenetic trees, which assessed sensitivity to phylogenetic uncertainty. The first assessment and temporal values are reported as means across the 100 trees.

3.2.3 Permutation test of expected phylogenetic diversity

If species with a relatively high risk of extinction tended to be phylogenetically distinctive (no near relatives), then expected phylogenetic diversity would be lower than the case where there was no relationship between extinction risk and phylogenetic distinctiveness.

Alternatively, if phylogenetically distinctive species tended to have a lower risk of extinction than other species, expected phylogenetic diversity would be higher than the case where there is no relationship. Lower expected phylogenetic diversity could also occur if threat was concentrated among species representing a subsection of the tree, which would place that entire subsection (representing a whole group of related species) at risk of extinction. More generally, given a fixed number of species in each threat category, the specific location of those species on a phylogenetic tree can lead to either higher or lower expected phylogenetic diversity than if those species were placed randomly. If the deviation from random is statistically significant, this would indicate a 'phylogenetic bias', that is, the distribution of threat on the tree is biased towards phylogenetic distinctive species (or the opposite) or is concentrated in particular parts of the tree.

To test whether expected phylogenetic diversity was unusually high or low (compared to a null model), the assignment of species to threat categories was permuted 1000 times and expected phylogenetic diversity was calculated for each permutation for each of the 100 trees for each group (birds, mammals and frogs). For each permutation, the mean across trees was then calculated. The observed expected phylogenetic diversity for a group (mean across 100 trees) was then compared to the corresponding null model comprising the distribution of means across trees. If the observed value was outside the 95% confidence limits of the model (lower than the lowest 2.5% of the null model or higher than the highest 2.5% of the null model), then the pattern of threat was considered significantly phylogenetically biased (two-tailed test).

3.2.4 Gains in expected phylogenetic diversity from conservation action

Three species listed as threatened in New South Wales were selected to demonstrate how a hypothetical change in survival probability from conservation action flows on to gains in expected phylogenetic diversity. The chosen species were the barking owl (*Ninox connivens*), representing birds, the southern brown bandicoot (*Isoodon obesulus obesulus*), representing mammals, and the yellow-spotted tree frog (*Litoria castanea*), representing frogs. For each of these species, survival probability was altered to secure ($q = 0.95$) and the consequent changes in survival of internal nodes calculated. The gain in expected phylogenetic diversity from hypothetical conservation action was then simply expected phylogenetic diversity with conservation action minus the original expected phylogenetic diversity.

4. Results

4.1 Indicator: Expected survival of listed threatened species

4.1.1 First assessment value at commencement of the BC Act, 25 August 2017

At the commencement of the BC Act in 2017, there were 1003 species and subspecific taxa that were either listed as threatened or extinct (991 taxa), or had been assessed by the NSW TSSC and not listed (12 taxa) due to not qualifying as threatened.

Of these 1003 species and subspecific taxa, 507 (51%) are expected to be still surviving in 100 years. Ignoring assessed but not listed species, 495.5 (50%) are estimated to be still surviving in 100 years. See Table 2. The count of species in each threat category and taxonomic group is given in Table 3.

Table 2 Number of species (including subspecific taxa) expected to survive in 100 years; expected to be lost in 100 years (not counting diversity already extinct); and presumed to be already extinct in New South Wales

Number (and percent) of species in 2017				
	Surviving (in 100 years)	Loss (in 100 years)	Presumed extinct (in NSW)	Total
Listed	495.5 (50%)	422 (43%)	73 (7%)	991
Assessed	507 (51%)	423 (42%)	73 (7%)	1003

Notes: 'Listed' species are those listed as threatened or extinct in the schedules of the Biodiversity Conservation Act (BC Act) at the date of commencement of the Act (2017).
 'Assessed' species are those assessed as being taxonomically valid and either listed as threatened or extinct in the schedules of the BC Act, or rejected from listing (due to not qualifying as threatened or extinct).
 See section 2.4 for a mathematical definition of components.
 The number of species expected to survive or be lost in 100 years can be a fraction because the index is calculated from the sum of probabilities of survival.

Table 3 Number of species (including subspecific taxa) in each threat category in each major taxonomic group and the corresponding number of species expected to survive in 100 years

Taxonomic group	Number of species in 2017						Number of species surviving in 100 years	
	VU	EN	CR	EX	Listed	Assessed	Listed	Assessed
Algae	0	1	0	0	1	1	<1 (30%)	<1 (30%)
Amphibians	11	13	5	0	29	29	14 (48%)	14 (48%)
Birds	93	21	13	13	140	141	91 (65%)	92 (65%)
Fungi	4	5	0	0	9	9	5 (57%)	5 (57%)
Invertebrates	0	15	6	1	22	22	5 (22%)	5 (22%)
Mammals	43	18	3	26	90	94	44.5 (49%)	48 (51%)
Plants	229	335	58	33	655	662	310 (47%)	316 (48%)
Reptiles	22	21	1	1	45	45	26 (58%)	26 (58%)
Total	402	429	86	74	991	1003	495.5 (50%)	507 (51%)

Notes: 'Listed' species are those listed as threatened or extinct in the schedules of the Biodiversity Conservation Act (BC Act) at the date of commencement of the Act (2017).
 'Assessed' species are those assessed as being taxonomically valid and either listed as threatened or extinct in the schedules of the BC Act, or rejected from listing (due to not qualifying as threatened or extinct).
 VU = vulnerable; EN = endangered; CR = critically endangered; and EX = extinct in New South Wales.

4.1.2 Temporal trajectory

Temporal change in the expected survival of listed threatened species indicator was assessed for all three types of assumption (see section 3.2.1). The range of possible values, given these assumptions, is shown in Figure 7. A breakdown of the trend in expected survival into major taxonomic groups is given in Figure 8.

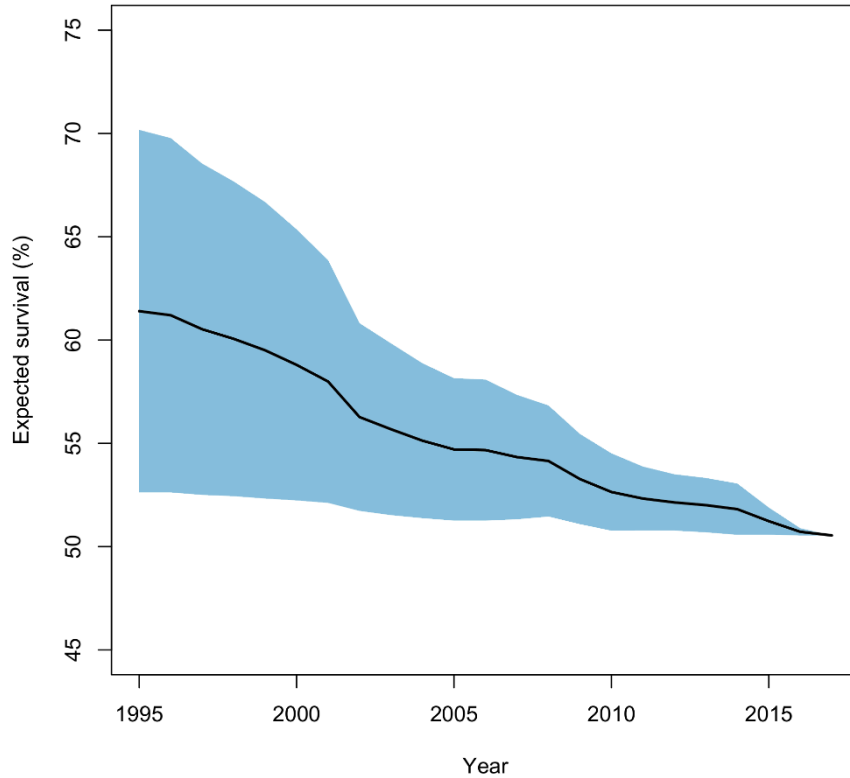


Figure 7 Range of possible values from 1995 to 2017 for the indicator: Expected survival of listed threatened species

Upper limit (worst case) assumes species are secure prior to being listed as threatened (assumption 1). Lower limit (best case) assumes species are the same status prior to listing as when first listed (assumption 2). Solid line assumes species have an equal chance of being either secure or the same status prior to first listing (assumption 3). Expected survival is a percentage of all assessed species (including those assessed but not listed). See section 3.2.1 for a description of assumptions.

Expected diversity as an indicator of biodiversity status and trend

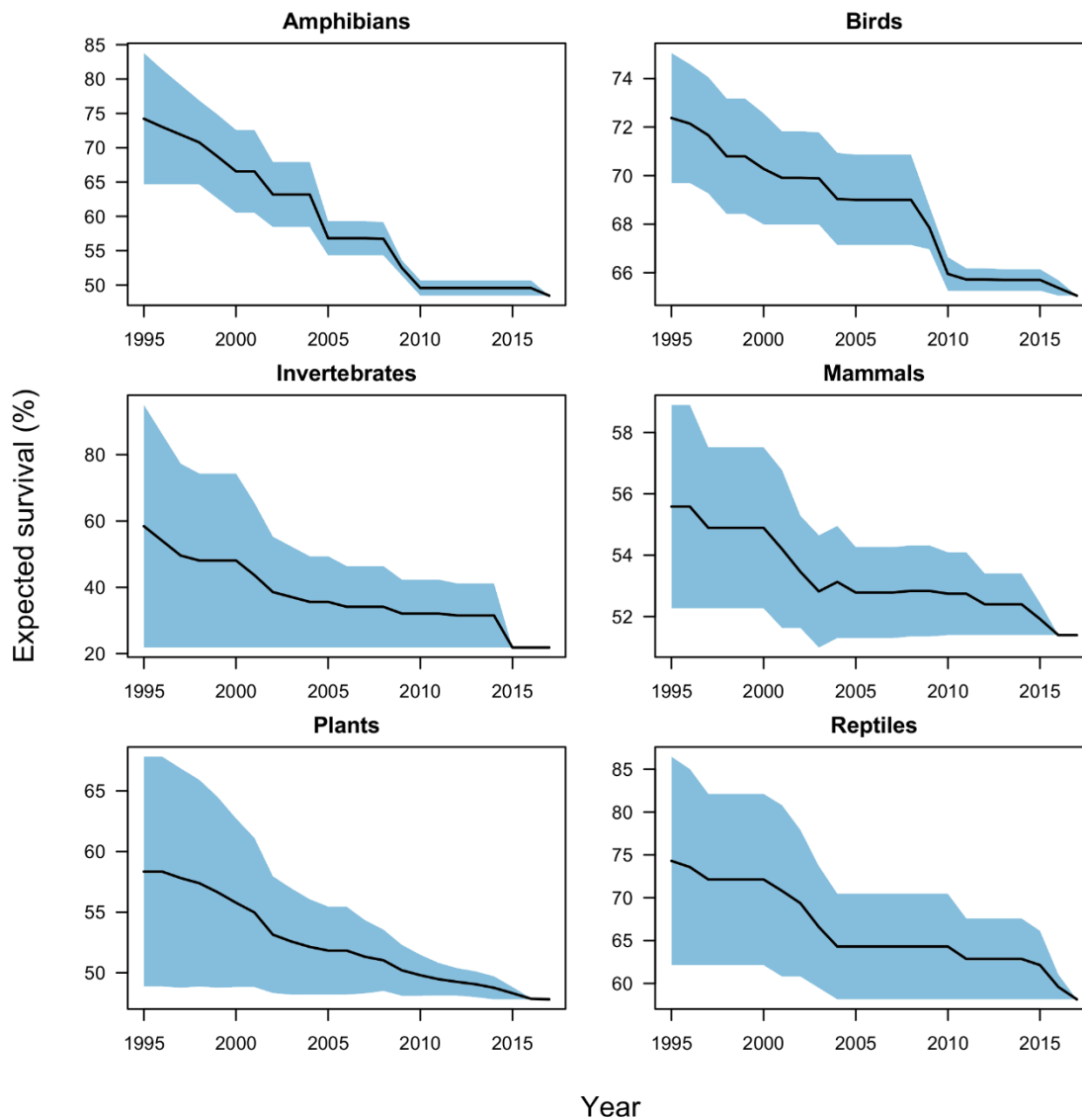


Figure 8 Range of possible values from 1995 to 2017 for major taxonomic groups for the indicator: Expected survival of listed threatened species

Upper limit (worst case) assumes species are secure prior to being listed as threatened (assumption 1). Lower limit (best case) assumes species are the same status prior to listing as when first listed (assumption 2). Solid line assumes species have an equal chance of being either secure or the same status prior to first listing (assumption 3). Expected survival is a percentage of all assessed species (including those assessed but not listed). See section 3.2.1 for a description of assumptions.

4.2 Indicator: Expected existence of listed threatened ecological communities

4.2.1 First assessment value at commencement of the BC Act, 25 August 2017

Of the 109 ecological communities either listed as threatened in 2017 or assessed by the NSW TSSC and not listed (i.e. assumed to be secure), 65 (60%) are expected to be still existing in 100 years (Table 4). Ignoring the presumed secure category, 64 (59%) listed threatened ecological communities are estimated to be still in existence in 100 years.

Table 4 Number of ecological communities expected to survive in 100 years; and expected to be lost in 100 years

Category	Number of ecological communities in 2017		
	Surviving (in 100 years)	Loss (in 100 years)	Total
Vulnerable ecological community	3.6	0.4	4
Endangered ecological community	55.9	30.1	86
Critically endangered ecological community	4.5	13.5	18
Total listed	64 (59%)	44 (41%)	108
Total assessed	65 (60%)	44 (40%)	109

Notes: 'Listed' ecological communities are those listed as threatened in Schedule 2 of the BC Act at the date of commencement of the Act (2017).
 'Assessed' ecological communities are those assessed as being operationally valid and either listed in Schedule 2 of the BC Act, or rejected from listing (due to not qualifying as threatened).
 See section 2.4 for a mathematical definition of components.
 The number of communities expected to survive or be lost in 100 years can be a fraction because the index is calculated from the sum of probabilities of survival.

4.2.2 Temporal trajectory

Temporal change in the expected existence of threatened ecological communities indicator was assessed for all three types of assumption (see section 3.2.1). The range of possible values, given these assumptions, is shown in Figure 9.

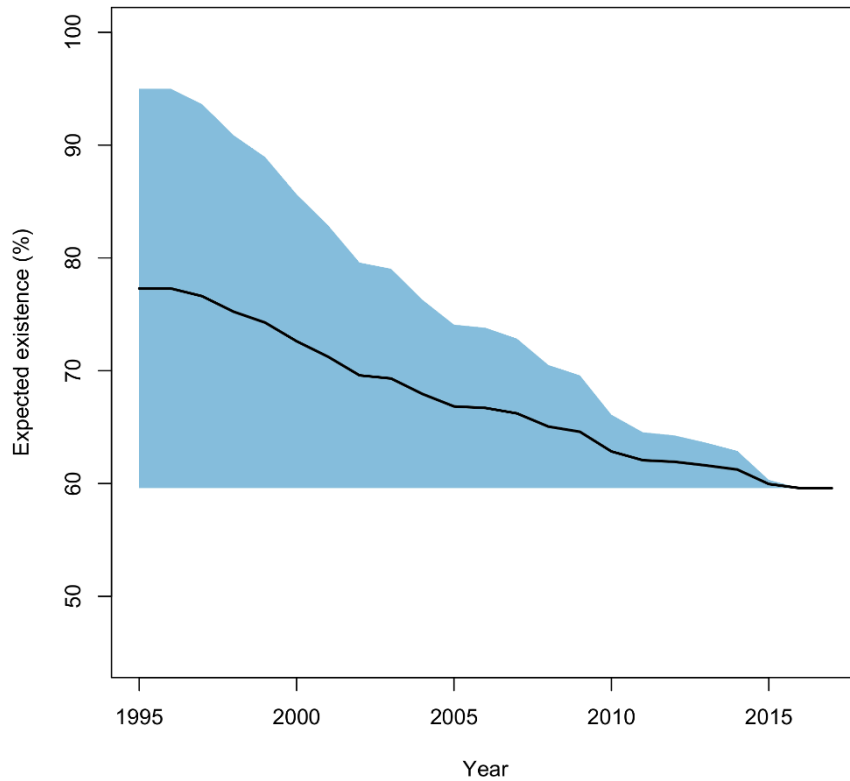


Figure 9 Range of possible values from 1995 to 2017 for the indicator: Expected existence of ecological communities

Upper limit (worst case) assumes communities are secure prior to being listed as threatened (assumption 1). Lower limit (best case) assumes communities are the same status prior to listing as when first listed (assumption 2). Solid line assumes communities have an equal chance of being either secure or the same status prior to first listing (assumption 3). Expected existence is a percentage of all assessed ecological communities (including those assessed but not listed). See section 3.2.1 for a description of assumptions.

4.3 Indicator: Expected survival of phylogenetic diversity for listed threatened species

4.3.1 First assessment value at commencement of the BC Act, 25 August 2017

Expected phylogenetic diversity values and the number of NSW species for each of birds, mammals and frogs are given in Table 5. For the purposes of this indicator, all other bird, mammal and frog species in New South Wales not previously assigned a threat category were treated as secure. This is likely to be an over-estimate because many species in these groups that are less well known or data deficient, and have not yet been assessed by the NSW TSSC as secure, may in fact be at risk of extinction within 100 years, assuming current processes that threaten species survival remain unchanged over that period.

Table 5 Number of species (and subspecies) and phylogenetic diversity of birds, mammals and frogs in New South Wales

Taxonomic group	Number of species		Phylogenetic diversity			
	Listed species	Total species	Surviving (in 100 years)	Loss (in 100 years)	Presumed extinct (in NSW)	Total
Birds	140	582	92% (10,563 Ma)	7% (857 Ma)	1% (115 Ma)	11,536 Ma
Mammals	90	189	84% (3,143 Ma)	9% (335 Ma)	8% (285 Ma)	3,762 Ma
Frogs	29	85	83 % (2,246 Ma)	17 % (466 Ma)	0 % (0 Ma)	2,712 Ma

Notes: Phylogenetic diversity is partitioned into the components: expected to survive in 100 years; expected to be lost in 100 years (not counting diversity already extinct); presumed to be already extinct in New South Wales.

'Listed species' are those listed as either threatened or extinct in the schedules of the Biodiversity Conservation Act (BC Act) at the date of commencement of the Act in 2017. For the purposes of this indicator, all other bird, mammal and frog species in New South Wales not previously assigned a threat category were treated as secure.

'Total species' refers to the number of species originally existing in New South Wales in the pre-industrial era (c. 1750).

See section 2.4 for a mathematical definition of components.

Phylogenetic diversity is given as both the percentage of original and as millions of years (Ma) of evolutionary heritage.

The original (c. 1750) evolutionary heritage for the 582 species and subspecies of NSW birds (including species presumed to be extinct in New South Wales) is estimated to be 11,563 million years (Table 5), averaged across 100 equally plausible phylogenetic trees. As of 2017, an average of 92% of this original phylogenetic diversity is expected to survive in 100 years, representing approximately 10,563 million years of evolutionary heritage (Table 5). The distribution of possible values of expected phylogenetic diversity from 100 equally plausible trees is given in Figure 10. Expected phylogenetic diversity was not unusually high or low, given the number of species in each threat category. In a permutation test that randomly reassigned species to threat categories, the observed value was within the 95% confidence interval of the 1000 trials of the permutation test (Figure 11). See Table 3 for a count of bird species among threat categories.

The original evolutionary heritage for the 189 species and subspecies of NSW mammals (including species presumed to be extinct in New South Wales) is estimated to be 3762 million years (Table 5), averaged across 100 equally plausible phylogenetic trees. As of 2017, an average of 84% of this original phylogenetic diversity is expected to survive in 100 years, representing approximately 3143 million years of evolutionary heritage (Table 5). The distribution of possible values of expected phylogenetic diversity from 100 equally plausible trees is given in Figure 10. Expected phylogenetic diversity was not unusually high or low, given the number of species in each threat category. In a permutation test that randomly reassigned species to threat categories, the observed value was within the 95% confidence interval of the 1000 trials of the permutation test (Figure 11). See Table 3 for a count of mammal species among threat categories.

The original evolutionary heritage for the 85 species and subspecies of NSW frogs is estimated to be 2712 million years (Table 5), averaged across 100 equally plausible phylogenetic trees. As of 2017, an average of 83% of this original phylogenetic diversity is expected to survive in 100 years, representing approximately 2246 million years of evolutionary heritage (Table 5). The distribution of possible values from 100 equally plausible trees is given in Figure 10. Expected phylogenetic diversity was not unusually high or low, given the number of species in each threat category. In a permutation test that randomly reassigned species to threat categories, the observed value was within the 95% confidence interval of the 1000 trials of the permutation test (Figure 11). See Table 3 for a count of frog species among threat categories.

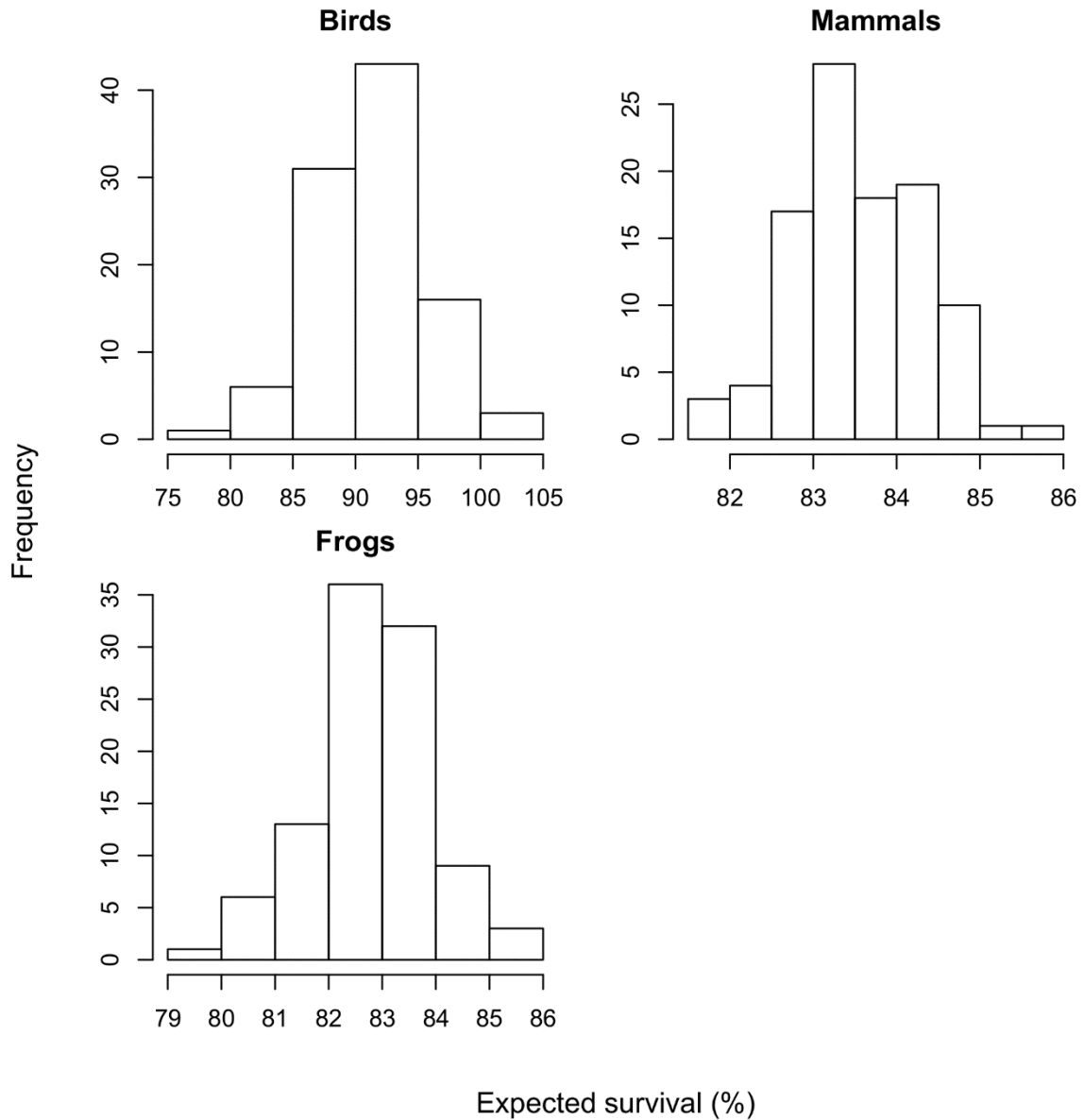


Figure 10 Distribution of the indicator: Expected survival of phylogenetic diversity for listed threatened species as of the commencement of the Biodiversity Conservation Act, for each of birds, mammals and frogs, across 100 equally plausible phylogenetic trees. Expected survival is given as the percentage of original phylogenetic diversity expected to be still surviving in 100 years.

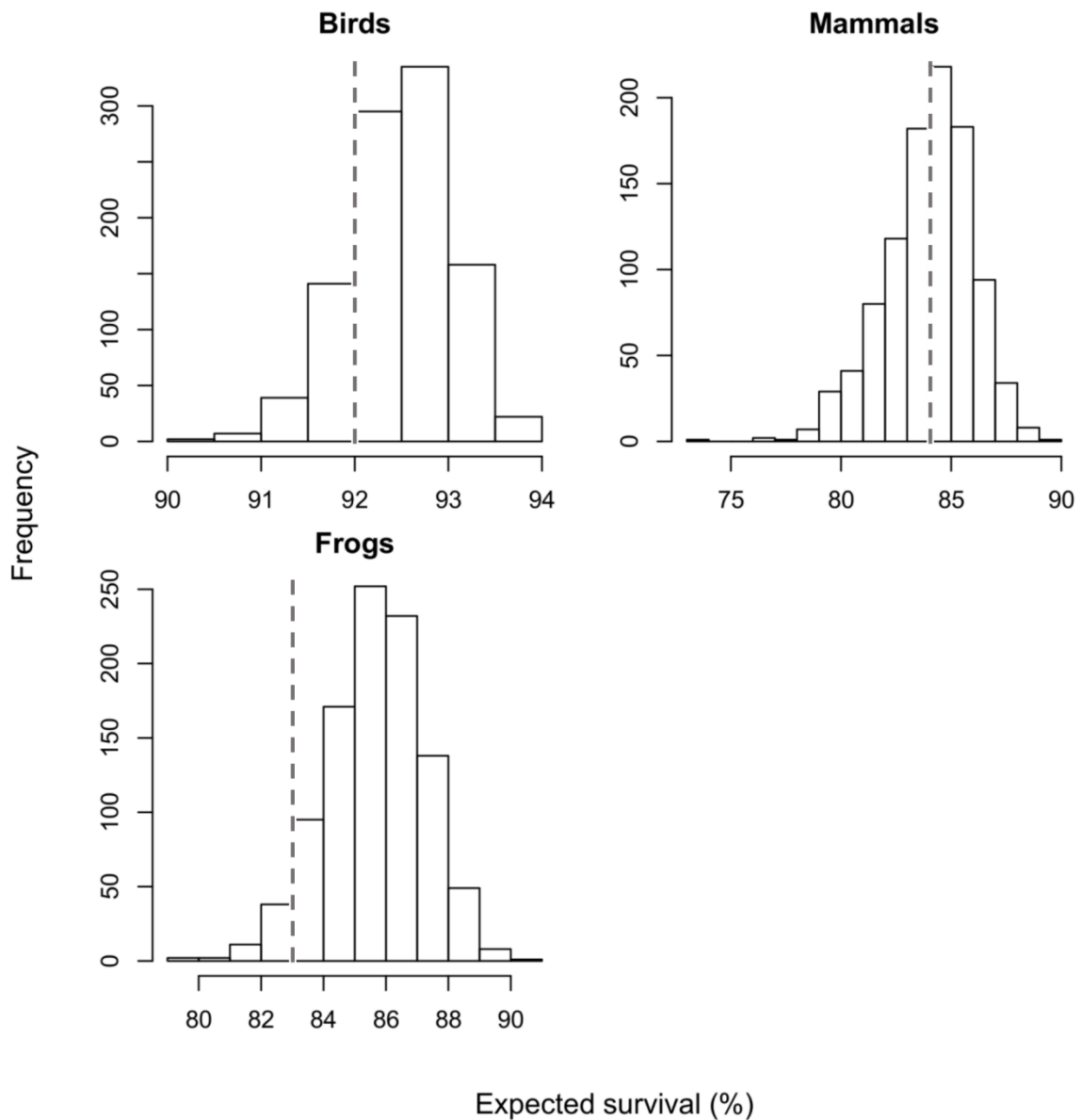


Figure 11 Distribution of the indicator: Expected survival of phylogenetic diversity for listed threatened species as of the commencement of the Biodiversity Conservation Act, for each of birds, mammals and frogs, for 1000 random permutations of species to threat category

Dashed vertical line indicates the observed expected survival for each group. The list of threatened species would be phylogenetically biased if the observed value differed from the majority of permuted values. Expected survival is given as the percentage of original phylogenetic diversity expected to be still surviving in 100 years.

4.3.2 Temporal trajectory

Temporal change in the expected survival of phylogenetic diversity for listed threatened species indicator (for three taxonomic groups) was assessed for all three types of assumption (see section 3.2.1). The range of possible values, given these assumptions, is shown in Figure 12. Mean values and 95% confidence intervals across 100 equally plausible trees for each assumption for each year (1995 to 2017) is given in Table 6 (birds), Table 7 (mammals) and Table 8 (frogs).

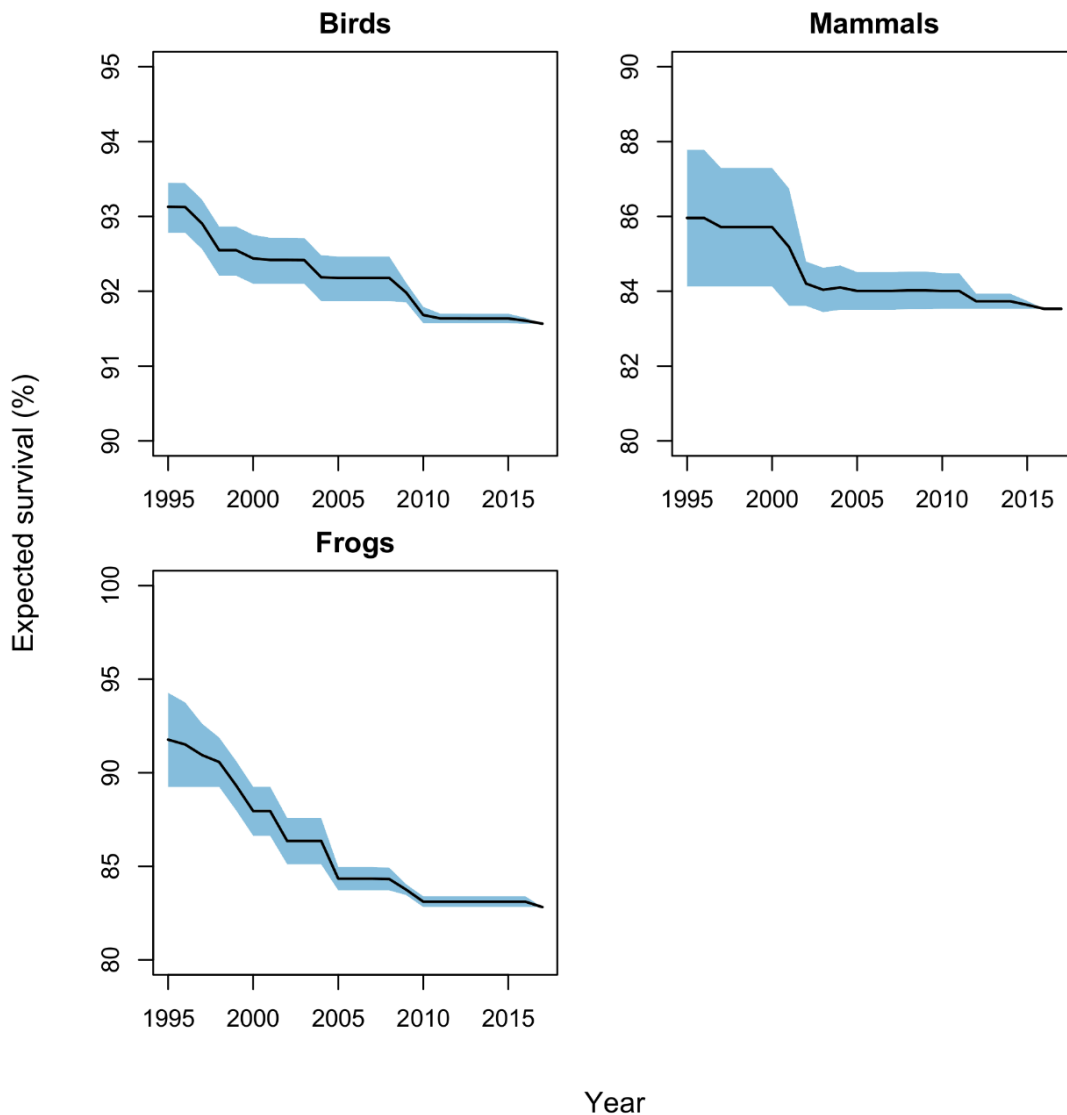


Figure 12 Range of possible mean values from 1995 to 2017 of the indicator: Expected survival of phylogenetic diversity of threatened species, for each of birds, mammals and frogs

Upper limit (worst case) assumes species are secure prior to being listed as threatened (assumption 1). Lower limit (best case) assumes species are the same status prior to listing as when first listed (assumption 2). Solid line assumes species have an equal chance of being either secure or the same status prior to first listing (assumption 3). Expected survival is given as the percentage of original phylogenetic diversity expected to be still surviving in 100 years. See section 3.2.1 for a description of assumptions.

Table 6 Mean and 95% confidence limits across 100 phylogenetic trees for the indicator: Expected survival of phylogenetic diversity of listed species (birds), for each type of assumption, for each year from 1995 to 2017

Year	Type 1 assumption			Type 2 assumption			Type 3 assumption		
	Mean	Upper tail	Lower tail	Mean	Upper tail	Lower tail	Mean	Upper tail	Lower tail
1995	10,781	11,810	9,808	10,704	11,732	9,743	10,744	11,772	9,776
1996	10,780	11,809	9,807	10,704	11,732	9,743	10,743	11,772	9,775
1997	10,754	11,786	9,783	10,678	11,710	9,720	10,718	11,749	9,752
1998	10,713	11,743	9,744	10,637	11,666	9,681	10,677	11,706	9,713
1999	10,713	11,743	9,744	10,637	11,666	9,681	10,677	11,706	9,713
2000	10,700	11,727	9,729	10,625	11,651	9,667	10,664	11,690	9,699
2001	10,696	11,723	9,726	10,625	11,651	9,667	10,662	11,688	9,697
2002	10,696	11,723	9,726	10,625	11,651	9,667	10,662	11,688	9,697
2003	10,695	11,723	9,726	10,625	11,651	9,667	10,661	11,688	9,697
2004	10,669	11,692	9,706	10,598	11,621	9,647	10,635	11,658	9,677
2005	10,667	11,690	9,704	10,598	11,621	9,647	10,634	11,657	9,676
2006	10,667	11,690	9,704	10,598	11,621	9,647	10,634	11,657	9,676
2007	10,667	11,690	9,704	10,598	11,621	9,647	10,634	11,657	9,676
2008	10,667	11,690	9,704	10,598	11,621	9,647	10,634	11,657	9,676
2009	10,626	11,650	9,670	10,596	11,622	9,649	10,611	11,636	9,659
2010	10,589	11,607	9,633	10,564	11,584	9,617	10,577	11,595	9,625
2011	10,579	11,595	9,626	10,564	11,584	9,617	10,572	11,590	9,621
2012	10,579	11,595	9,626	10,564	11,584	9,617	10,572	11,590	9,621
2013	10,579	11,595	9,626	10,564	11,584	9,617	10,571	11,589	9,621
2014	10,579	11,595	9,626	10,564	11,584	9,617	10,571	11,589	9,621
2015	10,579	11,595	9,626	10,564	11,584	9,617	10,571	11,589	9,621
2016	10,573	11,588	9,620	10,563	11,583	9,617	10,568	11,585	9,618
2017	10,563	11,583	9,617	10,563	11,583	9,617	10,563	11,583	9,617

Note: Type 1 assumes species are secure prior to being listed as threatened. Type 2 assumes species are the same status prior to listing as when first listed. Type 3 assumes species have an equal chance of being either secure or the same status prior to first listing. See section 3.2.1 for a description of assumptions. Diversity values are in units of millions of years of evolutionary history.

Table 7 Mean and 95% confidence limits across 100 phylogenetic trees for indicator: Expected survival of phylogenetic diversity of listed species (mammals), for each type of assumption, for each year from 1995 to 2017

Year	Type 1 assumption			Type 2 assumption			Type 3 assumption		
	Mean	Upper tail	Lower tail	Mean	Upper tail	Lower tail	Mean	Upper tail	Lower tail
1995	3,303	3,361	3,249	3,165	3,214	3,106	3,234	3,286	3,177
1996	3,303	3,361	3,249	3,165	3,214	3,106	3,234	3,286	3,177
1997	3,284	3,341	3,230	3,165	3,214	3,106	3,225	3,276	3,168
1998	3,284	3,341	3,230	3,165	3,214	3,106	3,225	3,276	3,168
1999	3,284	3,341	3,230	3,165	3,214	3,106	3,225	3,276	3,168
2000	3,284	3,341	3,230	3,165	3,214	3,106	3,225	3,276	3,168
2001	3,264	3,321	3,209	3,146	3,195	3,087	3,205	3,256	3,148
2002	3,190	3,242	3,138	3,146	3,195	3,087	3,168	3,218	3,112
2003	3,184	3,235	3,132	3,139	3,189	3,081	3,162	3,212	3,105
2004	3,186	3,238	3,134	3,142	3,192	3,083	3,164	3,215	3,108
2005	3,180	3,229	3,123	3,142	3,192	3,083	3,161	3,209	3,103
2006	3,180	3,229	3,123	3,142	3,192	3,083	3,161	3,209	3,103
2007	3,180	3,229	3,123	3,142	3,192	3,083	3,161	3,209	3,103
2008	3,180	3,229	3,124	3,142	3,193	3,084	3,161	3,210	3,104
2009	3,180	3,229	3,124	3,142	3,193	3,084	3,161	3,210	3,104
2010	3,179	3,228	3,123	3,143	3,193	3,084	3,161	3,210	3,104
2011	3,179	3,228	3,123	3,143	3,193	3,084	3,161	3,210	3,104
2012	3,158	3,207	3,102	3,143	3,193	3,084	3,150	3,199	3,093
2013	3,158	3,207	3,102	3,143	3,193	3,084	3,150	3,199	3,093
2014	3,158	3,207	3,102	3,143	3,193	3,084	3,150	3,199	3,093
2015	3,151	3,199	3,093	3,143	3,193	3,084	3,147	3,196	3,089
2016	3,143	3,193	3,084	3,143	3,193	3,084	3,143	3,193	3,084
2017	3,143	3,193	3,084	3,143	3,193	3,084	3,143	3,193	3,084

Note: Type 1 assumes species are secure prior to being listed as threatened. Type 2 assumes species are the same status prior to listing as when first listed. Type 3 assumes species have an equal chance of being either secure or the same status prior to first listing. See section 3.2.1 for a description of assumptions. Diversity values are in units of millions of years of evolutionary history.

Table 8 Mean and 95% confidence limits across 100 phylogenetic trees for indicator: Expected survival of phylogenetic diversity of listed species (frogs), for each type of assumption, for each year from 1995 to 2017

Year	Type 1 assumption			Type 2 assumption			Type 3 assumption		
	Mean	Upper tail	Lower tail	Mean	Upper tail	Lower tail	Mean	Upper tail	Lower tail
1995	2,556	2,637	2,471	2,420	2,503	2,345	2,489	2,565	2,408
1996	2,543	2,622	2,456	2,420	2,503	2,345	2,482	2,560	2,401
1997	2,512	2,591	2,425	2,420	2,503	2,345	2,466	2,545	2,389
1998	2,492	2,571	2,408	2,420	2,503	2,345	2,456	2,535	2,380
1999	2,458	2,530	2,377	2,386	2,459	2,312	2,422	2,492	2,348
2000	2,420	2,485	2,350	2,349	2,412	2,281	2,385	2,446	2,316
2001	2,420	2,485	2,350	2,349	2,412	2,281	2,385	2,446	2,316
2002	2,375	2,438	2,301	2,308	2,371	2,237	2,342	2,404	2,268
2003	2,375	2,438	2,301	2,308	2,371	2,237	2,342	2,404	2,268
2004	2,375	2,438	2,301	2,308	2,371	2,237	2,342	2,404	2,268
2005	2,304	2,367	2,245	2,270	2,332	2,207	2,287	2,350	2,226
2006	2,304	2,367	2,245	2,270	2,332	2,207	2,287	2,350	2,226
2007	2,304	2,367	2,245	2,270	2,332	2,207	2,287	2,350	2,226
2008	2,303	2,365	2,244	2,270	2,332	2,207	2,287	2,349	2,225
2009	2,279	2,338	2,222	2,263	2,323	2,204	2,271	2,330	2,213
2010	2,262	2,321	2,203	2,246	2,306	2,185	2,254	2,313	2,194
2011	2,262	2,321	2,203	2,246	2,306	2,185	2,254	2,313	2,194
2012	2,262	2,321	2,203	2,246	2,306	2,185	2,254	2,313	2,194
2013	2,262	2,321	2,203	2,246	2,306	2,185	2,254	2,313	2,194
2014	2,262	2,321	2,203	2,246	2,306	2,185	2,254	2,313	2,194
2015	2,262	2,321	2,203	2,246	2,306	2,185	2,254	2,313	2,194
2016	2,262	2,321	2,203	2,246	2,306	2,185	2,254	2,313	2,194
2017	2,246	2,306	2,185	2,246	2,306	2,185	2,246	2,306	2,185

Note: Type 1 assumes species are secure prior to being listed as threatened. Type 2 assumes species are the same status prior to listing as when first listed. Type 3 assumes species have an equal chance of being either secure or the same status prior to first listing. See section 3.2.1 for a description of assumptions. Diversity values are in units of millions of years of evolutionary history.

4.3.3 Gains in expected phylogenetic diversity from hypothetical conservation action

Example subtrees from within the bird (Figure 13), mammal (Figure 14) and frog (Figure 15) phylogenetic trees are provided to demonstrate how the survival probabilities of tips affect the survival of internal nodes and the flow-on effects of potential improvements to conservation outcomes of targeted species/subspecies. Securing the barking owl, southern brown bandicoot and yellow-spotted tree frog would result in average gains in expected survival of 0.3, 5 and 18 million years, respectively.

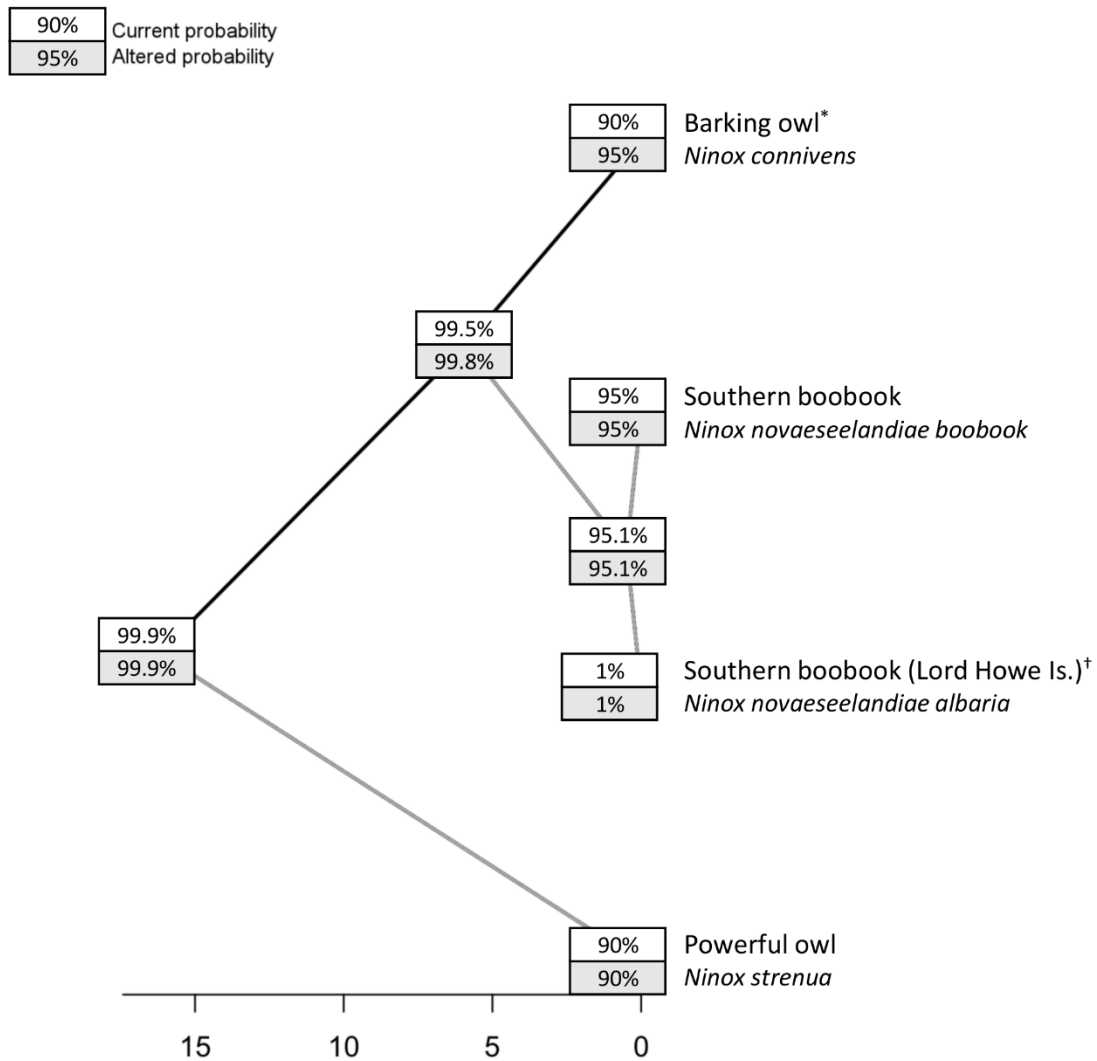


Figure 13 Phylogenetic relationships of boobook owls (*Ninox* spp.) for one of 100 equally plausible trees

Scale indicates the age of internal nodes and is in units of millions of years. Percentage values in upper (white) boxes show the current probability of survival of each tip and node in 100 years. Values in lower (grey) boxes show the altered probabilities if the vulnerable barking owl (marked with an asterisk) were to be secured by conservation action. Extinct taxa are marked with a dagger (†) symbol. Probability of survival of an internal node (and the branch immediately below it) is the probability that at least one descendant survives in 100 years (equation 3). Black branches have increased survival from the conservation action while grey branches are unaffected. Across 100 equally plausible trees, securing the barking owl will increase the expected survival of phylogenetic diversity of NSW birds by an average of 0.3 million years.

Expected diversity as an indicator of biodiversity status and trend

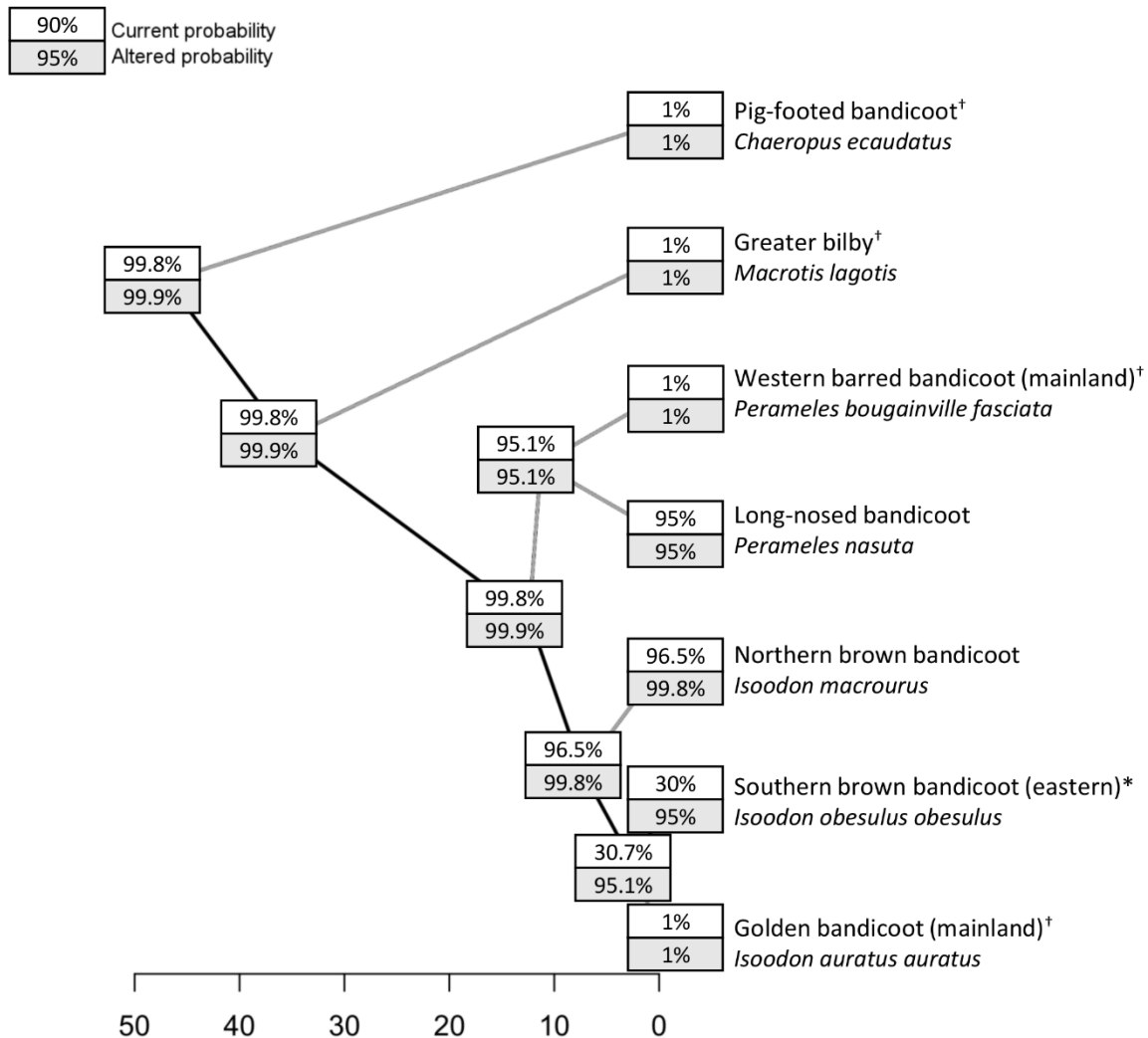


Figure 14 Phylogenetic relationships of bandicoots (order Peramelemorphia) for one of 100 equally plausible trees

Scale indicates the age of internal nodes and is in units of millions of years. Percentage values in upper (white) boxes show the current probability of survival of each tip and node in 100 years. Values in lower (grey) boxes show the altered probabilities if the endangered southern brown bandicoot (marked with an asterisk), were to be secured by conservation action. Extinct taxa are marked with a dagger (†) symbol. Probability of survival of an internal node (and the branch immediately below it) is the probability that at least one descendant survives in 100 years (equation 3). Black branches have increased survival from the conservation action while grey branches are unaffected. Across 100 equally plausible trees, securing the southern brown bandicoot will increase the expected survival of phylogenetic diversity of NSW mammals by an average of 5 million years.

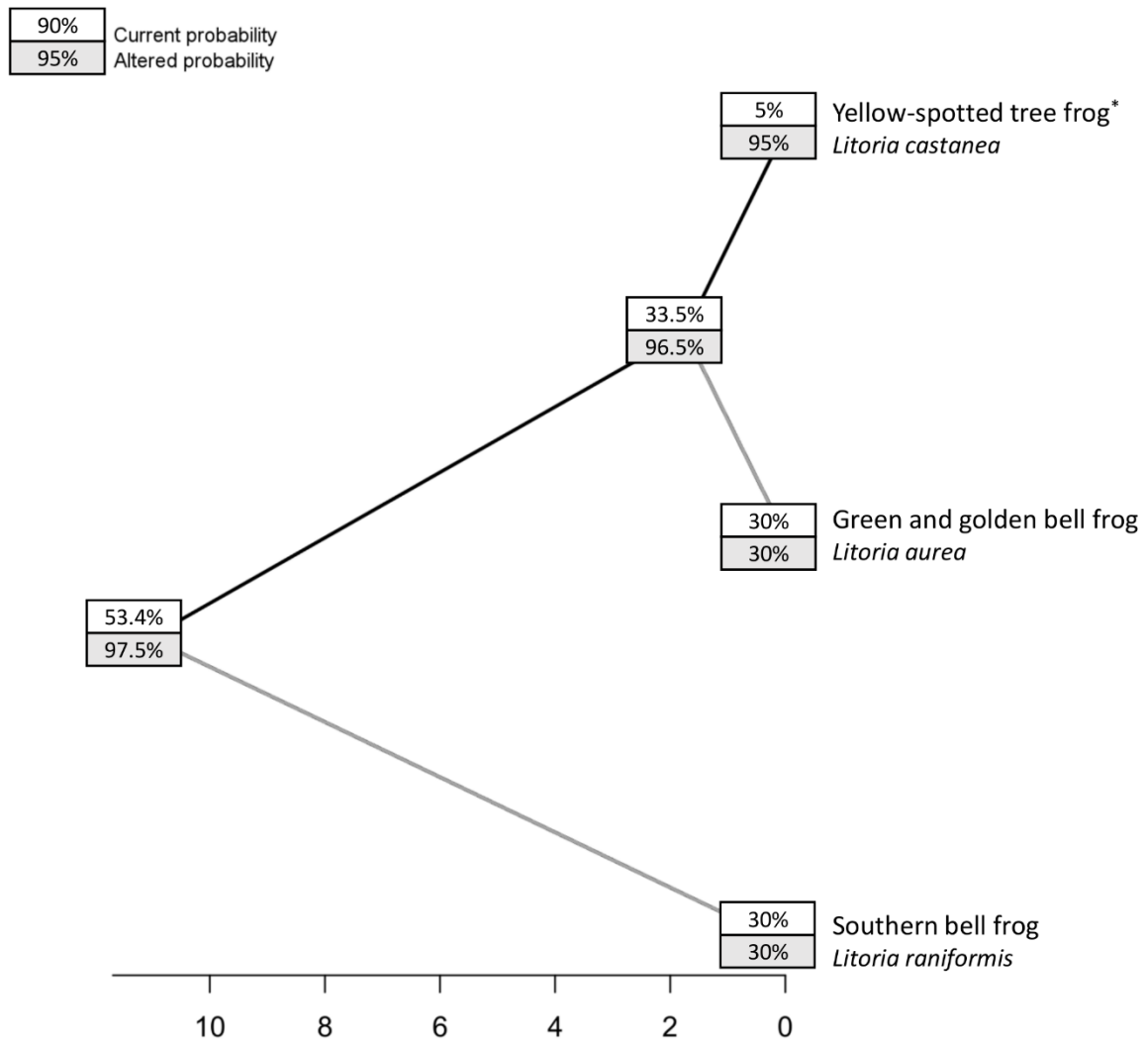


Figure 15 Phylogenetic relationships of the *Litoria aurea* species complex for one of 100 equally plausible trees

Scale indicates the age of internal nodes and is in units of millions of years. Percentage values in upper (white) boxes show the current probability of survival of each tip and node in 100 years. Values in lower (grey) boxes show the altered probabilities if the critically endangered yellow-spotted tree frog (marked with an asterisk) were to be secured by conservation action. Probability of survival of an internal node (and the branch immediately below it) is the probability that at least one descendant survives in 100 years (equation 3). Black branches have increased survival from the conservation action while grey branches are unaffected. Across 100 equally plausible trees, securing the yellow-spotted tree frog will increase the expected survival of phylogenetic diversity of NSW frogs by an average of 18 million years.

5. Discussion

5.1 Interpretation

Regardless of assumption (best case to worst case), there is a clear decline in the expected survival of threatened species since 1995 (Figure 7). For the 'best case' scenario (assuming the smallest possible change in the indicator), this decline reflects genuine changes in the threatened status of species, as determined by the NSW TSSC. Because of the way in which temporal values are determined in the best case, this trend is not due to simple growth in the number of species on the list nor to the critically endangered category not being available before 2006.

Decline is more rapid in some groups, notably amphibians and birds (Figure 8). For both groups, there is a particularly strong decline from 2008 to 2010, followed by a period of apparent stability, extending to the first assessment (2017). For birds, this rapid decline is mostly driven by changes in status of three species: the striated fieldwren (*Calamanthus fuliginosus*), the grey falcon (*Falco hypoleucos*) and the pied oystercatcher (*Haematopus longirostris*). For each of these species, there was a shift from vulnerable to endangered between 2008 and 2010, which is the largest possible decline in survival probability when shifting between adjacent threat categories (Table 1). Loss of key habitat is identified as a significant threat for all three species but there is no indication in the determinations that recent changes in habitat triggered these reassessments. For frogs, two species contributed to the rapid decline from 2008 to 2010: the peppered tree frog (*Litoria piperata*) and the northern corroboree frog (*Pseudophryne pengillyi*). Both species shifted from vulnerable to critically endangered. According to the determination, the peppered tree frog has not been seen since 1973 and the change in status reflects the view of the NSW TSSC that the species has a high probability of extinction in the wild, which is now more likely since its first listing in 1995. The northern corroboree frog has experienced significant declines in populations since first listed, likely due to infection by amphibian chytrid fungus (*Batrachochytrium dendrobatoides*).

Relatively few assessments of birds and frogs have been undertaken by the NSW TSSC since 2010, which explains the stability of expected survival over that period for those groups. While this pattern could be indicative of relatively little true change in threatened status for birds and frogs over this period, it may instead reflect the current priorities of the NSW TSSC and the taxa included in public nominations, particularly for reassessments of currently listed species.

Despite the strong trends in frogs and birds, the overall trend (Figure 7) follows that of plants (Figure 8). This is explained by plants constituting about 66% of the threatened species listed in the schedules of the BC Act (Table 3). Nevertheless, given that Australian plants are substantially more speciose than vertebrates (Chapman 2009; Nipperess 2015; Taxonomy Decadal Plan Working Group 2018), NSW plants are under-represented among listed threatened species when compared to vertebrates.

There is perhaps no trend in the expected existence of ecological communities (Figure 9). In the best case (assumption 2), there is no change for the entire period from 1995 to 2017. The only changes in threatened status were from endangered (declared before 2006) to critically endangered, which are assumed (under the best case) to not reflect a genuine change in extinction probability. Due to very little reassessment of threatened ecological communities, the worst-case trend may simply reflect growth of the list since 1995, rather than a genuine decline in community diversity.

Trends in phylogenetic diversity largely follow species diversity in the corresponding groups (Figure 8 and Figure 12). Further, there is no significant phylogenetic bias in the list of threatened and extinct species (Figure 11); distinctive species do not tend to be more

threatened nor is threat clustered in particular parts of the tree. Frogs come closest to being phylogenetically biased, with the majority of permutations having a higher expected survival than the observed value, although this difference is not significant.

Gains in the expected survival of phylogenetic diversity due to hypothetical conservation action range from relatively modest (for the barking owl) to substantial (for the yellow-spotted tree frog). Most obviously, the gain returned for conserving a species depends on the magnitude of the change in survival probability and the length of the terminal branch (leading to that species). However, because the change in survival probability of a tip has flow-on effects to the survival of internal nodes (Figure 13 to Figure 15), the relative security of nearest relatives is also important. When an entire clade is insecure, due to all or most members being threatened, a change in one species can have dramatic effects. This can be seen most clearly for the *Litoria aurea* species complex (Figure 15), where securing the yellow-spotted tree frog almost doubles the probability that at least one member will survive in 100 years. Not shown in Figure 15 is the relatively long branch leading to other members of the genus *Litoria*, which would also be secured in this case.

While not as dramatic, the bandicoot example (Figure 14) demonstrates how the conservation of an entire group may depend on a small number of secure members. Securing the southern brown bandicoot would represent an important gain in the conservation of evolutionary heritage. However, due to the large number of extinctions in this group (four out of seven NSW species), decline in either or both of the remaining secure species, long-nosed bandicoot (*Perameles nasuta*) and northern brown bandicoot (*Isoodon macrourus*), would lead to a dramatic reduction in the expected survival of the group as a whole.

When attempting to secure species with limited resources, predicting gains in phylogenetic diversity provides a means of prioritising conservation actions, such as under the SoS program. However, rather than simply ranking species by the predicted gain, benefits for the conservation of phylogenetic diversity need to be weighed against the feasibility of success and the cost of the action (Walker & Faith 1995; Possingham et al. 2002; Billionnet 2012). The SoS program has adopted a 'program prioritisation protocol' where costs, benefits and feasibility are all considered (Joseph et al. 2009). Evolutionary heritage provides a useful currency of conservation benefit that could be easily incorporated within this decision framework.

5.2 Caveats

5.2.1 Representativeness of listed entities

If the purpose of an indicator is to assess the rate of loss of biodiversity, then the pattern discerned should be *representative* of all biodiversity. However, lists of threatened entities (such as those included as schedules in the BC Act) tend to have strong taxonomic biases. For example, terrestrial vertebrates constitute about 31% of listed species despite being only about 2% of described species in Australia (Chapman 2009; Nipperess 2015; Taxonomy Decadal Plan Working Group 2018). Further, while it is certainly desirable to have a more comprehensive (and thus representative) list of threatened species in New South Wales, such a goal would be impractical when considering groups like terrestrial invertebrates (Mesibov 2001).

A better option is to choose a set of species that is designed to be representative (such as the expected survival of all known species indicator, Nipperess et al. 2020a) or to use a surrogate for the true proportions of biodiversity in particular threat categories (such as the expected survival of all known and undiscovered species indicator). These indicators fall into the expected survival of all known and undiscovered species indicator family within the indicator method framework (OEH & CSIRO 2019).

5.2.2 Uncertainty regarding the true probability of survival

As the survival (or otherwise) of a species is a future event, the true probability cannot be known. Population viability analysis provides a proven means for exploring the range of possible population trajectories (Brook et al. 2000) but can only be done on the relatively small number of species for which there is sufficient demographic data. However, IUCN Red List categories (and the categories used by the BC Act) can be assigned explicit probabilities via criterion E (Kindvall & Gärdenfors 2003) and are based on a rigorous evidence-based assessment process (Mace et al. 2008). Despite uncertainty about true survival probability, risk categories should be viewed as reliable indicators of the relative extinction risk of species or ecological communities. Thus, while the true value of expected survival may be unknown, changes in the indicator will reliably track changes in relative extinction risk, and therefore changes in the rate of biodiversity loss, at least with respect to listed threatened entities.

5.2.3 Uncertainty regarding the history of threatened status

The growth of a list of threatened entities over time may reflect two possible processes:

1. formerly secure entities becoming threatened
2. threatened entities becoming recognised as threatened and formally listed as such.

The former is a genuine change in the rate of loss of biodiversity, while the latter is a process of discovery of the true rate of loss. Some proportion of the entities will be listed due to the first process, and the remaining proportion will be listed due to the second. A simple way to reflect this uncertainty is to bracket the range of possible values by assuming all entities were secure (assumption 1) before listing versus all were threatened (assumption 2). Further, where proportions are unknown, a 50:50 split (assumption 3) is a reasonable compromise.

5.2.4 Uncertainty regarding the circumscription of listed entities

Whenever listing threatened entities, circumscription becomes an important consideration. While the objective reality of species remains a central problem in biology (Vane-Wright 2003), this concern is further amplified when attempting to circumscribe discrete ecological communities (Nicholson et al. 2015). A practical solution is to adopt operational concepts based on clear definitions (Keith et al. 2013). When making determinations, a review of the definition of the entity is conducted by the NSW TSSC. In the case of species, this includes a species description and the characteristics that discriminate it from other species. In the case of ecological communities, the entity is circumscribed by a listing of the characteristic species assemblage. Thus, the determinations of the NSW TSSC regarding circumscription are taken as the standard for this class of indicators because they provide clear operational definitions and because using a different standard would have meant resolving how threat status is translated across for split or lumped taxa. For species of frogs, birds and mammals, this meant, in some cases, using taxa that are not accepted names in the Australian Faunal Directory.

The problem of circumscription is less for expected phylogenetic diversity because species (and subspecific taxa) are treated as *relatively* distinct rather than *absolutely* distinct. That is, the extent to which a pair of tips are distinct from one another is the path length to their first common node (most recent common ancestor). Thus, the extent to which entities are discrete can be directly encoded in a phylogenetic tree, making phylogenetic diversity measures more robust to this form of uncertainty (Asmyhr et al. 2014).

5.2.5 Uncertainty regarding evolutionary relationships

It is important to realise that phylogenetic trees are hypotheses about the true evolutionary relationships of taxa. Those hypotheses that are better supported by the data are retained by phylogenetic analyses, while the remainder are discarded. When many potential trees are equally plausible, it is useful to calculate metrics like phylogenetic diversity for many versions of the tree (as done in this study) to capture information on phylogenetic uncertainty (Rangel et al. 2015). The mean of the metric across trees can then be interpreted as a consensus of the true value, while the variance provides an indicator of uncertainty.

5.2.6 Sensitivity to change in the rate of loss of biodiversity

The capacity of the three expected diversity indicators described here to track changes in the loss of biodiversity hinges on the responsiveness of the NSW TSSC and the rate of reassessment of listed species and communities. Similar to indicators based on the *IUCN Red List of Threatened Species*, temporal resolution can be coarse due to the delay between an entity undergoing a decline and a determination of change in conservation status being made (Butchart et al. 2004). It is important to note that reassessments are a relatively small proportion of the determinations of the NSW TSSC. The problem can be addressed if there were a requirement to reassess listed entities on a regular basis and the resources were made available to facilitate a higher rate of determinations.

Threat categories themselves are a relatively coarse way of tracking the rate of loss of biodiversity. A species or ecological community could be undergoing a decline (or a recovery) but, unless it crosses a critical threshold from one category to another, this will not result in a change in the indicator. This coarseness reflects uncertainty regarding the true survival probabilities.

Monitoring programs have the potential to provide better sensitivity to change in future iterations of the indicators. The SoS program aims to secure species in the wild through conservation actions, such as the amelioration of threatening processes and the securing of habitat, and uses population monitoring to determine the success (or otherwise) of these actions. Assessment of outcomes from monitoring at a population level could then be translated into changes in the probability of survival of the species at a state level. While this is a challenging proposition, changes in survival probability at a local level will change statewide survival as a function of the proportion of individuals in New South Wales that are affected. For example, in the extreme case that a species is represented in New South Wales by a single population, then any action to conserve that population will directly translate into a change in statewide survival. However, an important caveat to using monitoring outcomes to inform the rate of loss of biodiversity is that it may take some time (e.g. several years) before a change in a population due to conservation action becomes apparent (Nichols & Williams 2006).

5.3 Data gaps and considerations

This project identified some data gaps that could be usefully addressed for running the next assessment of the indicators.

5.3.1 History of threatened status of listed threatened entities

Schedules 1, 2 and 3 of the BC Act list the *current* status of threatened entities. These data are also replicated in machine-readable form in NSW BioNet. However, data were not readily available on the listing history of threatened entities. For example, if a species was listed as endangered in 1997 and then later reclassified as critically endangered in 2009, only the latter determination would be recorded in BioNet. The listing history of an entity can

be recovered by reviewing the final determinations made by the NSW TSSC, which are summarised in the *Index to Determinations* (NSW TSSC 2017). However, these data are only available as .pdf documents. Further, determinations are not only made to reassess threatened status but also to document taxonomic changes and changes to definitions. Taxonomic changes can also complicate the tracking of threatened status through time, due to the splitting and lumping of taxa.

A valuable data source for this project going forward would be a machine-readable database, preferably accessible through the BioNet Open Application Programming Interface, that records all determinations made by the NSW TSSC. This would need to track the type of determination being made (for which an ontology, describing the nature and rationale of decisions, would have to be developed) and changes to taxonomy, allowing the full history of an entity to be quickly recovered. The structure of the existing *Index to Determinations* could be used as a starting point for an ontology. The IUCN Red List Guidelines (IUCN 2017) also provide a basis for coding decisions related to species changing categories over time.

To implement this project, two spreadsheets have been created (one each for species and ecological communities), standardised on the current names for entities, with a row for each change in status of a particular entity, starting with initial listings for the Threatened Species Conservation Act. These spreadsheets could be periodically updated as an interim solution to running future assessments of the indicators. For example, a new set of determinations have been published subsequent to the mid-2017 commencement of the BC Act, and therefore an update to the indicators presented here could be developed by adding these determinations to the spreadsheets and re-running the respective expected diversity and expected phylogenetic diversity calculations.

5.3.2 Lists of NSW species for taxonomic groups

Three spreadsheets (one each for birds, mammals and frogs) were produced as a listing of species potentially existing in New South Wales (see section 3.1.2 for details). These lists should be considered provisional and reassessed prior to running future assessments of the indicators. Similar to the Australian Faunal Directory, it may be useful to maintain official lists of NSW species (and subspecific taxa) for particular groups. These should be standardised on the nationally accepted taxonomy (Australian Faunal Directory, Australian Plant Census) or at least matched to such. The spatial definition of New South Wales is somewhat problematic because it is difficult to choose a boundary that includes all terrestrial and marine species listed as threatened in New South Wales. Standardising to biogeographic regions is a useful operational solution, although more likely to include taxa with no known distribution in New South Wales. Because the index is standardised by the species included in the calculation, any additions or omissions in the future can be taken into account by using the same set of species and re-running the calculation for the history of determinations and deriving a revised version of the indicator and its trajectory.

5.3.3 Phylogenetic trees of NSW species for taxonomic groups

Following from the NSW species lists, corresponding phylogenetic trees have been produced for birds, mammals and frogs (see section 3.1.3 for details). Potentially, more taxonomic groups can be included in future assessments of the indicators if phylogenetic data are available and taxonomic mismatches between data sources can be resolved. Producing a phylogenetic tree of NSW reptiles would be quite useful as it would allow the linking of the frog, mammal and bird trees into a single, larger tree of tetrapods (i.e. terrestrial vertebrates). This would allow the reporting of an overall expected phylogenetic diversity for a significant proportion of the NSW threatened species list (304 out of 991 species), as well as results for particular groups within the list. A large, 4161-species,

time-calibrated phylogenetic tree does exist for squamate reptiles (i.e. lizards, snakes, worm lizards) (Pyron & Burbink 2014), which could form the basis of a NSW reptile tree. A phylogenetic tree for NSW flowering plants would also be very valuable, although a comprehensive (majority of known species represented) and time-calibrated tree currently does not exist for this taxonomic group. More feasible is to use a large and ecologically important plant family, such as the Myrtaceae, for which understanding of phylogenetic relationships is considerably more advanced. A comprehensive, 657-species tree exists for Australian Myrtaceae (González-Orozco 2016) but is currently not time-calibrated.

5.3.4 Threatened populations

The BC Act also allows for the listing of threatened populations where the species to which the population belongs is not separately listed as a threatened species, and the population is, in the opinion of the NSW TSSC, of significant conservation value based on its role in the conservation of the species or a number of other species. Prior to the commencement of the BC Act on 25 August 2017, 50 populations had been listed as endangered (Table 9), and the majority are plants. Integration of populations into an expected diversity measure would require consideration about how having threatened populations affects the statewide survival probability of a species, which might need information on distribution, abundance and within-species genetic diversity. Because listed populations are defined spatially, it will be possible to determine what proportion of a species' NSW range is represented by one or more threatened population(s), which could, in the absence of other information, be used to estimate an adjusted statewide survival.

Table 9 Count of populations in each threat category in each major taxonomic group

Taxonomic group	Threat category			
	Vulnerable	Endangered	Critically endangered	Total threatened
Amphibians	0	1	0	1
Birds	0	7	0	7
Invertebrates	0	1	0	1
Mammals	0	11	0	11
Plants	0	29	0	29
Reptiles	0	1	0	1
Totals	0	50	0	50

Note: Threatened populations are those listed in the schedules of the Biodiversity Conservation Act (BC Act) at the date of commencement of the BC Act (2017).

6. Guidelines for running the next assessment

The data and scripts provided in the data package for these indicators (Nipperess et al. 2020b) will allow the first assessment analyses to be re-run. The indicators and data are designed such that future assessments can be run on an annual basis if desired. Changes to taxonomy, future determinations of the NSW TSSC, and SoS reporting of effective threatened species management outcomes will require revision of the underlying data. Provided below are guidelines on how to re-run the analyses and to adapt the data package for future assessments of the indicators.

6.1 Software requirements

For each indicator, a custom script was written in *R*. Scripts are provided as part of the data package. Scripts for calculating expected diversity of threatened species and ecological communities require only the base installation of *R*. The custom script for expected phylogenetic diversity requires the additional installation of the ‘ape’ package (Paradis et al. 2004) and a custom function (‘*phylodiv.expected*’). The custom function is included in the data package.

6.2 Workflow

This section refers to the workflow diagrams for each indicator (included as appendices to the report). Object identifiers listed below relate directly to parts of the workflow.

6.2.1 List unification process (workflow objects P02501, P03001, P03501)

This process is essentially the same across all indicators and is not automated. The purpose of the process is to produce a spreadsheet (.csv file) that unifies threatened entity lists at different points in time into a single listing history (recording all changes in threat status) and standardises to a single taxonomy. This can be most simply done by manually updating the listing history databases (one each for species and communities, provided in the data package). Determinations by the NSW TSSC made since this first assessment should be reviewed and classified as follows:

1. *Change in name without change in threat category*

In the simplest case of a name being updated, then relevant entries in the listing database can be updated with the new name. If the name change is the result of a split AND the resulting taxa retain the same threat status, then the year of determination should be kept as the year the original taxon was listed.

2. *Change in name with change in threat category*

This will normally be because a taxon is split and the resulting taxa have a higher threat status OR because a taxon is lumped with another taxon, resulting in a lower threat status. In the former case, the new taxa should replace the old taxon in the database, with the newly recognised threat status, and the year of determination should be back-dated to the year the original taxon was listed. In the latter case, the name and status should be updated and the year of determination retained as for the original listing. Note that if a taxon is delisted due to being lumped with a secure taxon, then the entry in the database should be retained with the status of secure.

3. *Change in threat category*

If this change is not due to taxonomic changes, then it is interpreted as a genuine change in the threat status of the taxon. A new entry should be made in the database for the taxon, giving the new status and the year of determination. The older entry should be retained (thus recording the listing history).

4. *No distribution in New South Wales*

Occasionally, the NSW TSSC will determine that an entity should not have been listed because it is found to have no known distribution in New South Wales, including no historical records. In this case, the entity should be removed from the database.

5. *New listing*

This is the simple case of an entity being recognised as threatened without any prior history of determinations. A new entry is made in the database.

6. *Rejection of nomination for listing*

In the case where a nominated entity is determined by the NSW TSSC as not qualifying for any threat category AND there is sufficient data for a determination AND the rejection is not because the entity is not adequately circumscribed, then a new entry should be made in that database for an entity recognised as secure with the year of determination.

For expected phylogenetic diversity, the list unification process also must standardise taxonomy across an official census of NSW species (for a taxon), the threatened species list, and available phylogenetic trees. For this purpose, taxonomy was standardised to the Australian Faunal Directory except where this conflicted with the threatened species list. In that case, the name on the threatened species list had priority. Names on the source trees were changed to reflect this standard. Trees were then trimmed to remove all species not on the official census.

For the next assessment of the expected survival of phylogenetic diversity for listed threatened species indicator, the official census species lists should be reviewed and made compliant with the current taxonomic standard (where the threatened species list has precedence over the Australian Faunal Directory). Species and subspecific taxa should also be checked for distribution in New South Wales and, where there is confidence in a species' absence, that entry should be removed. Phylogenetic trees will need to be edited to reflect these changes. See section 3.1.3 for a description of the process.

6.2.2 Expected diversity calculator (workflow objects P02502, P03002, P03502) and Indicator change calculator (workflow objects P02503, P03003, P03503)

These processes are implemented in a custom *R* script: one each for each of the two expected diversity indicators, and one for each of the taxonomic groups used in the calculation of expected phylogenetic diversity (in this case, birds, mammals and frogs). The process includes assigning probabilities of survival to each entity, calculating current expected diversity, hindcasting the trajectory of change in expected diversity (based on assumptions described in section 3.2.1) and conducting sensitivity analyses.

6.2.3 Benefits and feasibility of threatened species management (workflow objects SD02505/6, SD03005/6, SD03505/6)

Note: This component was not implemented in this first assessment at commencement of the BC Act.

For future assessments of the indicators, survival probabilities may be adjusted to reflect demonstrated outcomes of threatened species management under the SoS and other programs. That is, we generate a new survival probability (\hat{q}) based on an assessment of the benefit (increase in survival probability) and the feasibility of the benefit. Following the decision process described in the *Saving our Species Technical Report* (OEH 2013), one could assume that the benefit is always an improvement to secure status (survival probability of 0.95 over 100 years). This value would then be down-weighted by a feasibility (f) score (a probability scaling 0–1) which reflects an assessment of the success of individual management actions and the translation of those actions to a statewide survival probability ($\hat{q} = 0.95 * f$). To implement this adjustment for expected diversity, a spreadsheet (saved as a .csv file) should be prepared with a column listing species names (one row per unique species name) for which management actions have been taken and a column for the feasibility score. Demonstration code is appended to the script for the two indicators reporting on listed threatened species and ecological communities that implements the adjustment to survival probabilities.

6.3 Report card

The expected diversity report card in the first *NSW Biodiversity Outlook Report* (DPIE 2020) provides a single value for the first assessment in 2017 for each indicator, and a range of values for the temporal trajectory showing the change in values. The range for the temporal values is that expected from assumptions 1–3 described in section 3.2.1. A trend is reported for the five-year period 2012–2017, but annual values (across assumptions) are also given. Values are given as percentages of total list (standardised to current year).

6.4 Triggers for running next assessment

New assessments of the indicator can be re-run any time new data become available. New data will become available from determinations of the NSW TSSC and management effectiveness reporting provided through the SoS program. While the TSSC meets multiple times a year, annual reporting would be sufficient to match the granularity of the hindcasting in this report. It is important to note that the present analysis reports the value of the indicator at the time of the **commencement of the BC Act on 25 August 2017**. The NSW TSSC has since released, during the remainder of 2017, final determinations for eight species (or subspecific taxa) and one ecological community (all dated 1 December 2017; available at: www.environment.nsw.gov.au/committee/finaldeterminations.htm). These determinations would need to be added to the 2017 data to reassess the temporal trajectory post-commencement and calculate annual values going forward.

7. Data products

The data used (where licences allow) and derived as a product of this analysis are publicly available through the CSIRO Data Access Portal (data.csiro.au). The following data package is available for download:

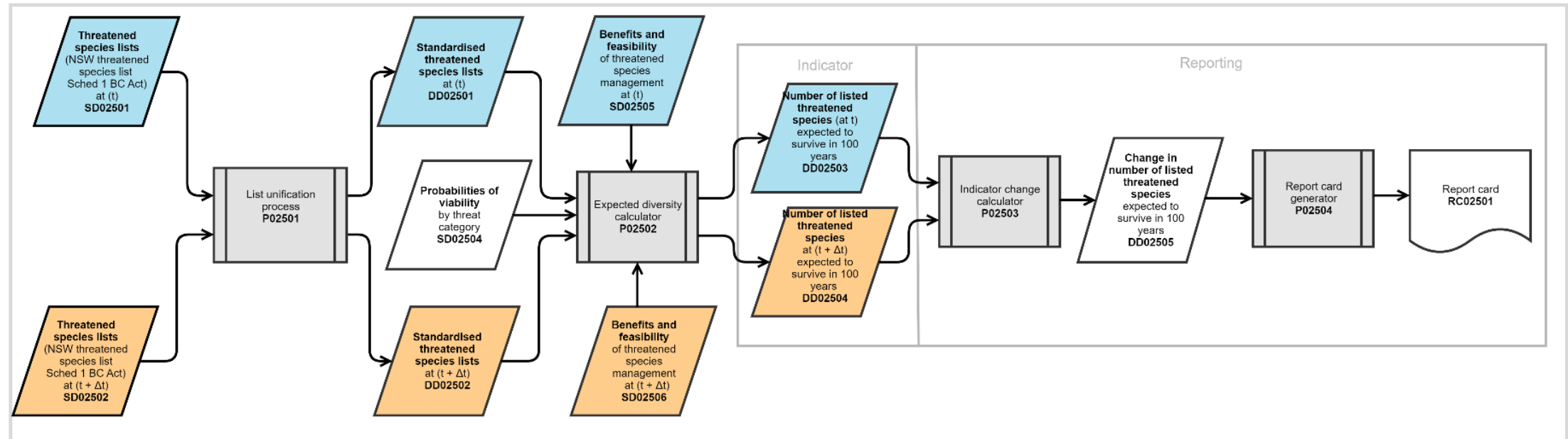
Nipperess DA, Faith DP, Auld TD, Brazill-Boast, Williams KJ & King D 2020, Expected survival of listed and threatened species and ecological communities: Data packages for the Biodiversity Indicator Program, first assessment, *SEED Portal*, datasets.seed.nsw.gov.au/dataset/biodiversity-indicator-program-data-packages.

The data package forms part of a collection hosted on the Sharing and Enabling Environmental Data (SEED) Portal (seed.nsw.gov.au). The collection includes links to all available data packages for the first assessment of the Biodiversity Indicator Program:

Department of Planning, Industry and Environment 2020, Data packages for the Biodiversity Indicator Program: First assessment, *SEED Portal*, Sydney, Australia, datasets.seed.nsw.gov.au/dataset/biodiversity-indicator-program-data-packages.

Appendices

Workflow for indicator: Expected survival of listed threatened species



Legend

Shapes



Process (with unique identifier starting with 'P')



Dataset (with unique identifier starting with 'DD' for derived dataset and 'SD' for source datasets)



Document (with unique identifier starting with 'RC' for report cards)



Decision variable (treated like a source data set but separately defined in the workflow)

Colours



Time t

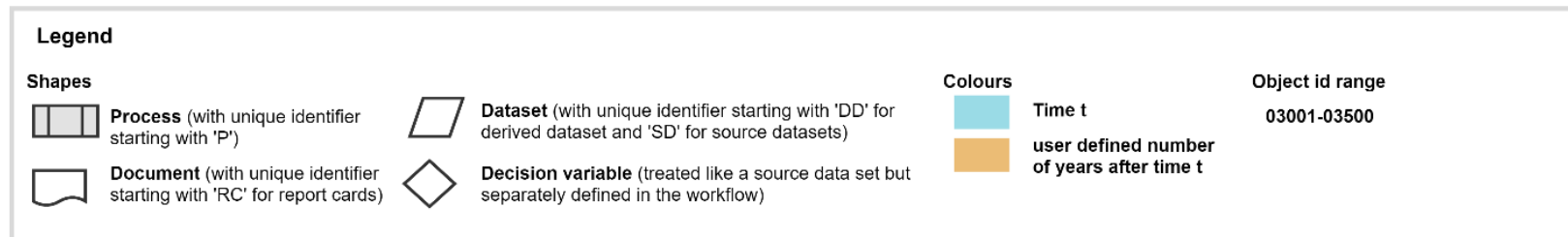
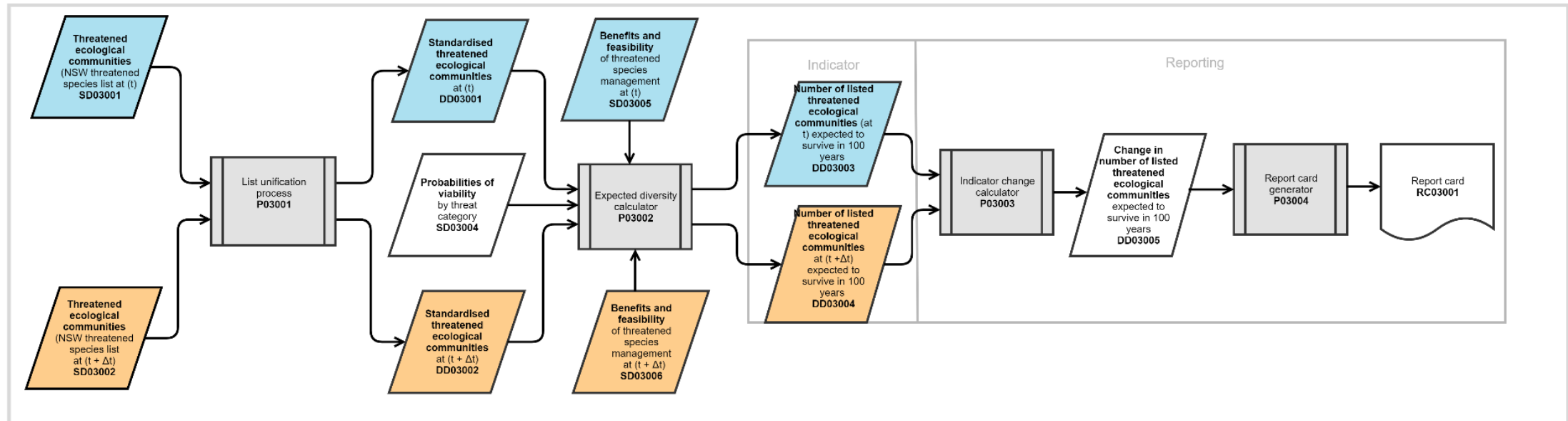


user defined number of years after time t

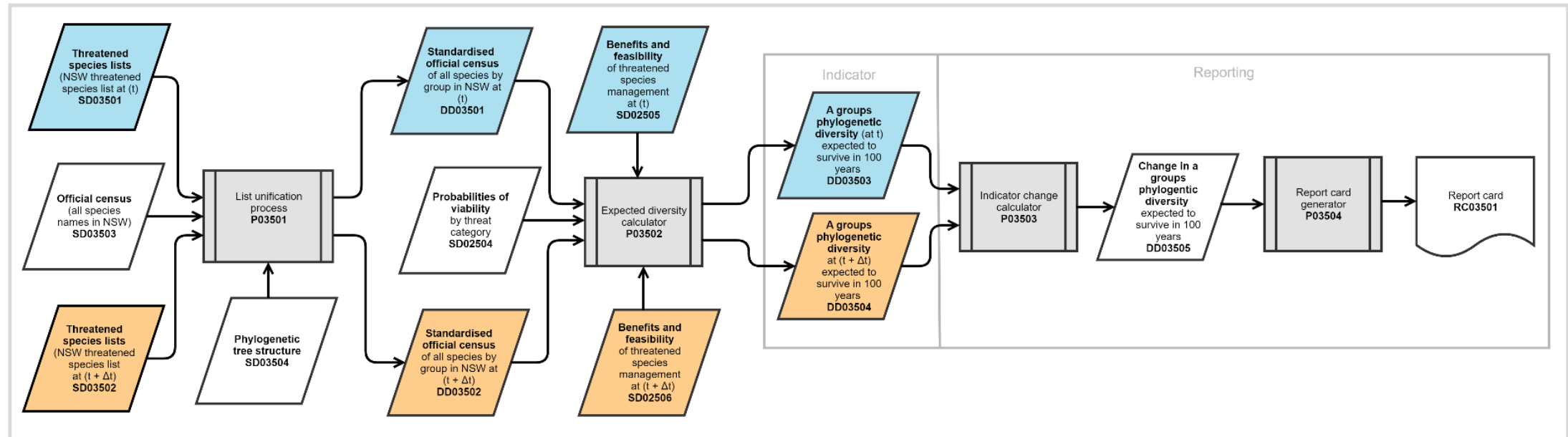
Object id range

02501-03000

Workflow for indicator: Expected existence of listed threatened ecological communities



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



Legend

Shapes



Process (with unique identifier starting with 'P')



Dataset (with unique identifier starting with 'DD' for derived dataset and 'SD' for source datasets)



Document (with unique identifier starting with 'RC' for report cards)



Decision variable (treated like a source data set but separately defined in the workflow)

Colours



Time t



user defined number of years after time t

Object id range

03501-04000

Glossary

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), which includes genetic diversity, species diversity and ecosystem diversity.

Biogeographic: pertaining to the study of the distribution of species and ecosystems in geographic space and geological time.

Bioregion: relatively large land area characterised by broad, landscape-scale natural features and environmental processes that influence the functions of entire ecosystems and capture large-scale biophysical patterns. These patterns in the landscape are linked to fauna and flora assemblages and processes at the ecosystem scale. There are 18 bioregions represented in New South Wales.

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.

Confidence interval: a range of possible values for some parameter with upper and lower limits. The interval is associated with a level of confidence (usually 95%) which is interpreted broadly as the probability that the true value of the parameter lies within the interval.

Conservation: in relation to biodiversity, conservation is the protection, maintenance, management, sustainable use, restoration and improvement of the natural environment. In relation to natural and cultural heritage, conservation generally refers to the safekeeping or preservation of the existing state of a heritage resource from destruction or change.

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

Ecological integrity: maintaining the diversity and quality of ecosystems and enhancing their capacity to adapt to change and provide for the needs of future generations.

Ecosystem: a dynamic complex of vegetable, animal and microorganism communities and their non-living 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 in tropical seas.

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 (expected survival): the number of features (species, genes, ecosystems) that are expected to be extant in 100 years' time, estimated from survival probabilities. Can be reported as a proportion of either original (ie. pre-industrial) or current diversity. The remainder is expected loss.

Extant: still in existence, surviving.

Extent: the area covered by something.

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 (i.e. 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.

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

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.

Index (plural indices): a metric used to quantify the information represented by an indicator.

Indicator: provides information on the condition of the environment. It may also include information on pressures on the environment, environmental conditions and societal responses.

IUCN: International Union for the Conservation of Nature, a union of government and non-government organisations that provides public, private and non-governmental organisations with the knowledge and tools that enable human progress, economic development and nature conservation to take place together.

Landscape: a heterogeneous area of local ecosystems and land uses that is of sufficient size to achieve long-term outcomes in the maintenance and recovery of species or ecological communities, or in the protection and enhancement of ecological and evolutionary processes.

Listed ecological communities: ecological communities listed as threatened in the *Biodiversity Conservation Act 2016*.

Listed threatened species: species and subspecific taxa listed as threatened or extinct in the *Biodiversity Conservation Act 2016*.

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

Monitoring: in this context, activities to collect new biophysical data.

Permutation: a statistical procedure where the original data are randomly re-ordered. 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 (PD): 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: (Ecology) a group of individuals of the same species or subspecific taxon occurring together in a particular area at a particular time.

Pre-industrial era: A baseline epoch at which a region's habitat is expected to be in an intact state with no significant anthropogenic degradation or resultant loss of biodiversity. The Biodiversity Indicator Program estimates this to be c. 1750.

Red List of Ecosystems: a global standard for how to assess the risk of extinction status of ecosystems, applicable at local, national, regional and global levels. Under the auspices of the IUCN.

Red List of Threatened Species: a global standard for how to assess the risk of extinction status of species, applicable at local, national, regional and global levels. Under the auspices of the IUCN.

Sensitivity analysis: a technique used to determine how different assumptions or other inputs affect the outcome of an analysis.

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).

Status: the condition or 'health' of a species, population, community, habitat or ecosystem, scaled relative to predetermined minimum and maximum potentials.

Surrogate, biodiversity: a species, group of species or ecosystem that can be used as a substitute for wider biological groups.

Synonym: (Biology) a scientific name for a taxon that is no longer the accepted name.

Taxon (plural 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.

Threatening process: a process that threatens, or that may threaten, the survival or evolutionary development of species or ecological communities.

Trends: directions of significant change in the environment, as shown by the changing values of measures (like essential variables, indicators or indices).

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