

# Taxonomy and biosystematics decadal plan 2018–2027

# Strategic Action 1.1:

Report on a national meeting held in April and May 2020 to scope and plan a mission to discover and document all remaining Australian species in a generation

Taxonomy Australia
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# Acknowledgment of Country

Taxonomy Australia respectfully acknowledges the First Peoples of Australia, their deep relationships and inherent connections to Country including biodiversity, and we recognise Elders past, present and emerging.

We acknowledge and respect Indigenous knowledge and stewardship of Country and Indigenous ways of being on Country.

The word 'discovery' is used extensively by Taxonomy Australia, including in this document. We acknowledge that the continent of Australia and its teeming biodiversity were discovered by its First Peoples many millennia ago, when the first human footsteps were made on an Australian shore. We use 'discovery' in the specific context of the Western scientific tradition, while acknowledging that there remain unresolved and important conversations to be had about the Western notion of discovery and the recognition of First Nations peoples and their knowledge.

We value different knowledge systems and perspectives and welcome all opportunities for First Peoples and Western scientific taxonomists to work together to better understand and care for the plants, animals, fungi and other organisms of this vast continent.

# Context

The decadal plan for taxonomy and biosystematics in Australia and New Zealand 2018–2027<sup>1</sup> outlines the foundational importance, impact and relevance of species discovery and other aspects of taxonomy and biosystematics for science, society, industry and government, and presents an agreed vision for the sector for the next decade.

The vision focuses on creating a step change in species discovery and biodiversity documentation, and through this a step change in understanding, protecting, managing and sustainably using Australia's and New Zealand's biodiversity.

The vision is supported by 22 strategic actions based on six key initiatives: accelerating discovery; enhancing services; engaging with Indigenous knowledge; improving infrastructure; educating for the future; and building strategic capabilities. These strategic actions were developed through extensive community consultations, both within the taxonomy and biosystematics sector and with key stakeholders.

The strategic actions in the decadal plan are outlined briefly but are not developed or discussed in detail: the plan provides a vision and destination, but not a roadmap to build the vision and get to the destination.

For that reason, a series of implementation plans is being developed to underpin the decadal plan. Each implementation plan will be relevant to one or more of the decadal plan's strategic actions and will set out in detail the strategic action's outcomes and objectives, analyse its dependencies and risks, and establish a timeline and budget for its implementation.

Because of substantial governmental, structural, biological and social differences between Australia and New Zealand, parallel and complementary implementation plans will be developed for each country.

This document provides background towards the development of an Australian implementation plan for the decadal plan's Strategic Action 1.1:

We will significantly increase the rate at which new species in Australia and New Zealand are discovered, resolved, named and documented.

This strategic action is part of the key initiative to enhance services for end-users of the knowledge provided by the taxonomy and biosystematics community. It will be directly relevant to any individual or agency with a need to identify an organism in Australia. This includes users in biosecurity, agriculture, fisheries, aquaculture, conservation, resource industries, ecology and other biological sciences, and members of the public who identify organisms for interest or enjoyment.

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<sup>&</sup>lt;sup>1</sup> https://www.science.org.au/support/analysis/decadal-plans-science/diversity-decadal-plan-taxonomy

# Background

Taxonomic knowledge of Australia's biodiversity is foundational to a wide range of activities in Australian society, industry and government, including conducting ecological, environmental and genetic research, planning for conservation and development, ensuring biosecurity and sustainable agriculture, managing environmental threats, and facilitating enjoyable and meaningful interactions with the natural world.

Best estimates are that only around 30% of Australia's species have been discovered, named and documented in more than 300 years of Western scientific taxonomic research – that is, 70% of Australia's biodiversity remains undocumented and effectively invisible to all the activities above. This severely compromises our ability to understand, manage, conserve and have responsible stewardship for the globally significant biological diversity of Australia.

An estimate was made in the decadal plan that, at current rate, it will take more than four centuries to complete a first-pass documentation of Australia's biodiversity. Given the accelerating threats to biodiversity, this time frame is substantially too long – that is, the current rate of discovery and documentation of species is not commensurate with the need for building knowledge of Australia's biodiversity.

This problem is the core of the decadal plan's Strategic Action 1.1. While in the decadal plan no firm target was specified for the quantum of acceleration, the Australian taxonomy sector has since settled on a vision to launch an ambitious mission to discover and document all remaining Australian species in a generation (25 years). If achieved, this would better align effort and activity with the urgency of the need.

Three key questions need to be answered before such an ambitious mission can be effectively advocated and launched: how exactly will we achieve such an ambitious goal, how much will it cost, and how much will it benefit Australia's society, environment and economy?

In April and May 2020, a national meeting of the taxonomy sector was convened by Taxonomy Australia, with funding from the Ian Potter Foundation and the University of Melbourne, to address the first question. More than 230 people from throughout the sector, both in Australia and overseas, engaged in an online conference and workshop to explore, discuss, and propose solutions for the many technical and logistical challenges of a mission to discover and document all remaining Australian species in a generation. The core of the meeting was a series of ten roundtables each dealing with an aspect of the mission.

This report is a summary and synthesis of the national meeting, both as a record and as a launchpad for actions and next steps.

# The National Meeting

The national meeting to scope and develop a roadmap for a mission to discover and document all remaining Australian species in a generation was conducted online between 20 April and 6 May 2020, structured around three core activities.

In the first week, after a short introduction, registrants were asked to view and consider a series of online presentations exploring aspects of a species discovery mission in different taxonomic contexts. Presenters and presentations were as follows:

Erinn Fagan-Jeffries (University of Adelaide). 'How will we discover and document the remaining hyperdiverse insects?'

Tom May (Royal Botanic Gardens Melbourne). 'How on earth will we discover and document all of the fungi in Australia'

Katharina Nargar (CSIRO and Australian Tropical Herbarium). 'How to describe the remaining Australian plants'

Zoe Richards (Western Australian Museum and Curtin University). 'The status of marine invertebrate taxonomy'

Mark Harvey (Western Australian Museum). 'How will we discover and document Australia's remaining arachnids and myriapods?'

Bryan Lessard (CSIRO Australian National Insect Collection). 'How will we discover and document the remaining non-hyperdiverse invertebrates?'

All presentations are available at <a href="https://www.taxonomyaustralia.org.au/national-meeting-2020-presentations">https://www.taxonomyaustralia.org.au/national-meeting-2020-presentations</a>.

In the second week, with the presentations as context, participants took part in a series of roundtable workshops, each dealing with a specific aspect of a mission to discover and document all remaining Australian species in a generation. Roundtables, and the topic and questions assigned to them, were as follows:

### Roundtable 1: What field campaigns are we likely to need to support our mission?

Many un-named species are already represented in our collections, but others will not be, or still need more specimens. This roundtable will consider issues around field work, including:

- Do we need to plan a field work campaign as part of this mission, or will field work be conducted on an as-needs basis?
- What role could there be for the public and citizen science in field collecting?
- If field work needs to be ramped up, should this happen early or late in the mission?

 What types of support structures and programs should we build to support field collecting for our mission?

This roundtable was led by Ben Parslow (South Australian Museum).

#### Roundtable 2: How can we most effectively use morphology for our mission?

Morphology obviously has a long history in species delimitation and discovery, but is being challenged now by DNA sequencing as a primary tool in some taxonomic groups. Some taxonomists support morphological-only taxonomy while other support DNA-only taxonomy. This roundtable will consider issues around morphology, including:

- Why exactly does morphology remain important in this age of genetics and genomics?
- Are we able to identify any taxonomic groups where we can say that morphology basically doesn't matter?
- How can we improve the capture, handling and use of morphological (trait) information in the service of our mission?

This roundtable was led by Gerry Cassis (University of New South Wales).

# Roundtable 3: How do we most effectively use DNA sequencing for rapid and robust species delimitation?

DNA sequencing will clearly play an important role in this mission - indeed, the mission would be impossible without it. Currently, some taxonomists have access to sequencing facilities while others do not, and some are skilled in all aspects of sequencing, bioinformatics and phylogenetics while others are not. This roundtable will consider issues around sequencing, including:

- How can we ensure that sequencing speeds up, rather than slows down, species discovery and delimitation?
- Should sequencing and bioinformatics support be more centralised or more dispersed than at present?
- Should all taxonomists be trained in every step along the sequencing->bioinfoirmatics->phylogeny->species delimitation pipeline, or should we specialise more?
- How do we best balance the roles of short, cheap, universal sequences (barcodes) versus longer, more expensive but more informative sequences (up to and including complete genomes)?

This roundtable was led by Michelle Waycott (University of Adelaide and State Herbarium of South Australia).

# Roundtable 4: How can we most effectively use phylogenetics for our species discovery mission?

Phylogenetics and species delimitation are becoming more and more closely integrated. Placing specimens of a potentially new species into a phylogeny is a great start in any taxonomic project. However, for this to be maximally effective for an all-species mission such as we envisage, we really need a phylogeny of all known species. This roundtable will consider issues around phylogenetics and species discovery, including:

- Is a phylogeny that includes all Australian species achievable in the medium term?
- How would we best go about constructing such a phylogeny?
- What systems would we need to have in place to manage a comprehensive phylogeny and allow it to be used effectively for species discovery and delimitation?

This roundtable was led by Michelle Guzik (The University of Adelaide) & Darren Crayn (James Cook University and Australian Tropical Herbarium).

# Roundtable 5: What informatics structures, processes and programs do we need to support our mission?

Taxonomy and informatics are no longer separable. Almost all traxonomists now use a wide range of informatics tools in their day-to-day work, including online taxonomic checklists and nomenclators such as are provided by ABRS, occurrence records in the ALA and GBIF, online repositories of type images and information, and online sequence repsoitories and analysis tools. This workshop will examine the informatics toolkit available to taxonomists and ask the questions:

- What more do we need?
- Are our exisiting tools comprehensive enough, and integrated enough?
- What's the next big thing we need to be aware of (or perhaps build)?

This roundtable was led by Ely Wallis (Atlas of Living Australia).

# Roundtable 6: What new technologies (other than genetics and genomics) will we need to deploy for our mission?

New technologies are available now that can help in our mission, including machine learning, high-end imaging, supercomputing and more. This roundtable will consider issues around new technologies, including:

 How exactly could machine learning be used in species discovery, delimitation and documentation?  What support structures do we need to be able to effectively use new imaging technologies?

This roundtable was led by Jane Melville (Museums Victoria).

#### Roundtable 7: What can (and should) change in current practice to enable our mission?

Taxonomy has a rich history and tradition. A downside of this is that some practices that may once have been strengths may now be weaknesses. This roundtable will critically examine all aspects of current taxonomic business-as-usual and try to identify those practices that remain valuable and those that we should consider changing to help with this mission. Issues examined will include:

- Is the traditional taxonomic revision fit-for-purpose for an all-species mission?
- What publication practices serve us well and which do not?

This roundtable was led by Mark Harvey (Western Australian Museum).

### Roundtable 8: What role can citizen science play in our mission?

Citizen science is increasingly important and popular, for a range of reasons. Many programs use citizen scientists to record aspects of biodiversity, usually observation records and images. But while these have some relevance to taxonomy (by adding new observations for known species, and occasionally serendipitously finding new species), on the whole they are fairly peripheral to taxonomy *per se*. This roundtable will consider issues around citizen science and taxonomy, including:

• Can we make better use of citizen science for species discovery, delimitation and documentation, and if so, how?

This roundtable was led by Tom May (Royal Botanic Gardens Melbourne and National Herbarium of Victoria).

#### Roundtable 9: How can we best build the required workforce for our mission?

Taxonomy clearly needs skilled people (at least until AI puts us all out of a job and we can go on a permanent field trip or holiday). And this mission clearly needs more skilled people than we have at present. This roundtable will consider issues around the taxonomic workforce, including:

- What type of workforce will we need over the 25 years if this mission?
- How will we train and build this workforce?
- What important skills are currently in shortest supply, and how will we redress this?

This roundtable was led by Mike Bayly (The University of Melbourne) & Andy Austin (The University of Adelaide).

#### **Roundtable 10: Collections**

There will be many implications of an accelerated species discovery mission for biodiversity collections - think of all the extra specimens collected in the field, loans and exchanges, management of DNA vouchers, samples and sequences, and management of collection databases and information systems. This roundtable will explore these issues, including:

- How will collections cope with a significantly expanded role and workload?
- Could some aspects of current collections practices become more efficient? If so, which, and how?
- What will a collection even look like in 20 years' time?

This roundtable was led by Shelley James (Western Australian Herbarium).

Wrap-up presentations from these roundtables are available at <a href="https://www.taxonomyaustralia.org.au/national-meeting-2020-roundtables">https://www.taxonomyaustralia.org.au/national-meeting-2020-roundtables</a>.

Finally, the roundtables were synthesised into a set of actionable items. Items were categorised into:

- (1) those that can be actioned now, with minimal requirements for extra resourcing
- (2) those that could be actioned with modest extra resourcing, and
- (3) those that would require substantial funding and investment to action.

Participants were asked to prioritise all actionable items into High (score 3), Medium (score 2) and Low (score 1) priority. Finally, scores for all items were averaged, and the items ranked within the three funding categories above.

Items ranked by their averaged priority scores are as follows. (The maximum possible averaged priority is 3; the minimum is 1; averaged priorities >2.3 are considered high priority (green), between 1.6 and 2.3 are considered medium (yellow), and <1.6 are considered low priority (blue). It should be noted that, despite the prioritisation, all items listed below are important and should be actioned.

# 1. Items that can be actioned now, with minimal requirements for extra resourcing:

Item	Priority	Idea
1.1	2.45	We need to start including funding for collections activities in grant applications
1.2	2.37	We need to build a collaboration space that combines an expertise directory (online register of taxonomists), a portal for shared field work, and a clearing-house mechanism to connect citizen scientists and scientists for taxonomic projects and a coordinated recognition system for citizen science contributions to taxonomy
1.3	2.29	We need to streamline the permitting process in every state to reduce the burden on collectors applying for permits
1.4	2.18	We need to design collections now for years 5, 10 and 25 of our mission
1.5	2.14	We need to increase the number of joint appointments between collections institutions and universities
1.6	2.06	We need to start writing shorter, faster morphological descriptions
1.7	2.06	We need to create a new specialised journal for rapid taxonomic description and publication
1.8	1.98	We need to agree on a controlled name-space for informal species (OTUs)
1.9	1.98	We need to measure the economic value of our collections (independently from their replacement cost)
1.10	1.94	We need to agree a community consensus on how to integrate molecular and morphological data, especially when they conflict

# 2. Items that could be actioned with modest extra resourcing:

Item	Priorit	y Idea
2.1	2.59	We need to establish regular entry-level and advanced training programs and internships for students and others in morphology, genomics, bioinformatics, nomenclature and collection management.
2.2	2.51	We need to establish a professional exchange program between institutions to deal with the backlog of unidentified specimens
2.3	2.33	We need to co-design Indigenous engagement opportunities for taxonomy
2.4	2.33	We need to attract undergraduates to study taxonomy and systematics by offering more learning opportunities
2.5	2.20	We need to build the architecture for a sequence reference library (including non-types)
2.6	2.10	We need to start including collection professionals on field expeditions to help handle collecting
2.7	2.06	We need to build a platform for recording traits and semi- automatically producing descriptions
2.8	1.96	We need to develop a national program to use citizen science opportunities to ramp up digitisation of our collections
2.9	1.86	We need to start building a super-phylogeny for the Australian biota and a workable, functional, comprehensive and curated database of phylogenies, with national protocols for adding species, sequences and trees
2.10	1.86	We need to hold a series of national workshops to develop standard ontologies/descriptors for taxonomic groups
2.11	1.71	We need to build a national repository for expedition metadata

# 3. Items that require substantial funding and investment to action:

Item	Priorit	ty Idea
3.1	2.69	We need to locate, database, image and sequence all Australian types, both here and overseas
3.2	2.53	We need increase the number of specialised and generalised technicians in institutions
3.3	2.46	We need to fund targeted PhD and post-doctoral positions, especially in hyperdiverse groups, and fellowships for senior researchers
3.4	2.43	We need to complete the National Species Lists and develop efficient and timely mechanisms to curate it
3.5	2.39	We need to complete an inventory of our collections (including both museum/herbarium and biosecurity etc. collections)
3.6	2.29	We need to build more efficient data and collections management systems
3.7	2.18	We need to build a national repository to store high-resolution images both 2D and 3D
3.8	2.14	We need to build a high-performance, centralised (or decentralised) sequencing and bioinformatics services (with economies of scale)
3.9	2.08	We need build a national network of paid bioinformatics specialists to help with taxonomic projects
3.10	2.06	We need to plan and fund a targeted, stratified sampling fieldwork campaign to collect the many new specimens we still need
3.11	2.06	We need to establish paid positions to support volunteer programs
3.12	1.98	We need to build a system to enable enhanced access to the modern tools needed for morphology (SEM, micro-CAT etc)
3.13	1.67	We need to image all incompletely identified specimens
3.14	1.39	We need to establish robotic handling of specimens where sensible

# **Actions**

Actions needed to make progress on these actionable items are as follows.

- 1. Items that can be actioned now, with minimal requirements for extra resourcing.
- 1.1: We need to start including funding for collections activities in grant applications

This item deals with problems that arise when grants are applied for, and awarded for, research projects that involve the collection of voucher specimens, but the grant funding does not include resources for those vouchers to be processed and curated in collections institutions. All biodiversity institutions are highly resource-limited, and cannot readily take on the burden of curating substantial numbers of specimens without resourcing to do it.

ACTION 1.1: Request guidelines from CHAH and CHAFC with estimates of the costs of specimen processing and curation, then distribute widely in the biodiversity and grant funding sector with an expectation that it will be used to include indicative and agreed costs in all research funding proposals.

1.2: We need to build a collaboration space that combines an expertise directory (online register of taxonomists), a portal for shared field work, and a clearing-house mechanism to connect citizen scientists and scientists for taxonomic projects and a coordinated recognition system for citizen science contributions to taxonomy

The taxonomy and biosystematics sector comprises a relatively tight-knit community. However, options are always available to enhance connections between taxonomists, and between the taxonomy sector and related groups. A print version Directory of Australian Taxonomists was previously maintained by the Australian Biological Resources Study, but was last released in 1981.

An online Directory could readily fulfil three functions: it could connect taxonomists with each other; connect users needed taxonomic expertise with relevant taxonomists; and connect citizen scientists with taxonomists for project work

In addition, a shared social space such as an online Directory could be used to share plans for field work, to meet needs for collections of specific taxa and to plan joint field trips.

ACTION 1.2: Develop an online Australian Taxonomic Community Directory on the Taxonomy Australia website. In the first instance, work to get all Australian taxonomists to register with the directory, then expand its scope to fill the other functions listed above.

ACTIONED: see the Australian Taxonomy Community Directory at <a href="https://www.taxonomyaustralia.org.au/tcd-search">https://www.taxonomyaustralia.org.au/tcd-search</a>

1.3: We need to streamline the permitting process in every state to reduce the burden on collectors applying for permits

In most jurisdictions in Australia, obtaining required permits for the collection of scientific specimens is frustratingly time-consuming, both due to onerous application processes and delays in the processing of applications. Some states and territories are better than others, but all are frustrating, especially for interstate visitors who are often unfamiliar with the required processes.

It would be a significant outcome if negotiations could result in a shared system across states and territories for the straightforward granting of permits to *bona fide* taxonomic researchers and collectors. Taxonomists collecting specimens to improve our knowledge of Australia's biodiversity is of substantial benefit to all, but this is often not recognised. Improving this would save substantial time for taxonomists and taxonomy-associated collectors.

ACTION 1.3: Establish a working group for Taxonomy Collecting Permits, with one or more representatives from each state and territory, to (1) scope a proposal for a shared or streamlined permitting system for recognised, *bona fide* collectors and (2) negotiate with relevant state and territory agencies to try to implement such a system.

### 1.4: We need to design collections now for years 5, 10 and 25 of our mission

Biodiversity collections – the collections of scientific specimens in museums and herbaria – are the backbone of taxonomy and of the mission to discover and document all remaining Australian species in a generation. An important question is – are they fit for purpose for the mission, or do we need to rethink collections and collection processes to ensure that collections contribute to, and do not get overwhelmed by, the substantial acceleration in all aspects of taxonomy if we are to achieve the mission.

ACTION 1.4: Request a report from organisations such as the Society for the Preservation of Natural History Collections (SPNCH) and from Australian institutions through CHAH and CHAFC, on issues that are likely to arise from the mission that will impact collections, and ways that collections may adapt.

# 1.5: We need to increase the number of joint appointments between collections institutions and universities

State- and Commonwealth-based collections institutions (museums and herbaria) and universities play distinct and complementary roles in taxonomy and biosystematics in Australia. Traditionally, and in many cases still, the institutions and universities have been relatively separate, and their activities in taxonomy and biosystematics have not been closely integrated. In some cases, however, close relationships including joint appointments have proven very productive and effective for both partners. Such close relationships and joint appointments will become more important with the launch of the mission, particularly for the students and PhD candidates who will need to be trained for the mission to succeed.

ACTION 1.5: Institutions and universities should consider joint appointments for any new hires and strengthen partnerships for existing appointments by establishing formal adjunct appointments for all or most staff.

### 1.6: We need to start writing shorter, faster morphological descriptions

Descriptions of new taxa are mandated by the Codes of Nomenclature. However, the Codes do not mandate how long, detailed or adequate a description needs to be. Over time, in many sectors of taxonomy, the length and depth of detail of descriptions has been steadily increasing until in some sectors descriptions may now perhaps be excessive (the fact that this issue arose from several of the national meeting roundtables indicates that this is a widespread view). The trend towards writing longer and longer descriptions appears to be largely driven by referees and editors of scientific papers requiring it. While writing a description is only one part of the process of erecting a new description and may not be the longest part (compared with delimiting the new taxon in the first place) nevertheless excessive descriptions take up time that could be better spent discovering more species. It is acknowledged that any move towards shorter descriptions must be balanced against continuing to ensure taxonomic adequacy and rigour.

ACTION 1.6: Establish a working group to develop and propose, to all Australian taxonomic journals, guidelines for what constitutes a minimal, effective, adequate and acceptable taxonomic description.

# 1.7: We need to create a new specialised journal for rapid taxonomic description and publication

Australia is well-served by taxonomic journals, with a combination of institutional house journals, the CSIRO suite of journals that accept taxonomic papers, and international journals such as Zootaxa, Phytotaxa, Zookeys and Phytokeys.

However, participants at the national meeting felt that there is still room for a dedicated, specialised, rapid-turn-around journal specifically to deal with the no-fuss publication of taxonomic novelties, and that such a journal is an important to support the substantial acceleration of taxonomic discovery and documentation envisaged under the mission. The ideal for such a journal will be that it is diamond open access (that is, with no paywalls for either authors or readers), fully-online, community-owned and operated, and taxon-blind.

ACTION 1.7: Establish a diamond open access, fully online, community-owned and operated, taxon-blind new journal for the rapid and no-fuss publication of new Australian taxa

#### 1.8: We need to agree on a controlled name-space for informal species (OTUs)

Controlled name-spaces are crucial in many sciences, and particularly for biology. Our key controlled name-space for biodiversity is the Linnaean naming system, as controlled by the

Codes of Nomenclature. However, in Australia we also have a second controlled name-space for plant names, the formal phrase-naming system controlled through APC. In this system, putative new species of vascular plants that have not yet been given a Linnaean name are given a 'formal' informal name, such as 'Banksia sp. Coleraine (A.B.Smith 224)'. In some ways, this system is more sophisticated than the Linnaean naming system. The APC-controlled phrase-naming system is used by all herbaria in Australia, ensuring common usage of such names throughout Australian botany.

No such agreed system has been adopted for the formal phrase-naming in Australian zoology, and this means that names are applied (and coined) somewhat haphazardly. In several respects, phrase-naming in zoology is more difficult than in botany due to the wider taxonomic scope of zoology and the fact that many informally recognised species cannot be adequately assigned to a genus or even family in some cases. Nevertheless, suggestions have been made in the past for the adoption of a formal phrase-naming system for Australian zoology, but these suggestions have not been formally adopted.

ACTION 1.8: Request that CHAFC and CHAH develop or adopt and endorse a universal phrase-naming system for Australian taxonomy, and/or for CHAFC to develop or adopt and endorse a phrase-naming system for Australian zoology

1.9: We need to measure the economic value of our collections (independently from their replacement cost)

Economic value matters, to governments and society. While the biodiversity collections in Australia are literally priceless assets, they also need to be valued as economic assets. For the decadal plan, an estimate was made that the *replacement value* of c. 70M specimens in the aggregated biodiversity collection in Australia is \$7B. Their actual economic value is greater than their replacement value. It is important to determine this value, in order to make the case that our biodiversity collections are science infrastructure on a par with space telescopes, particle accelerators and other more conventionally recognised science assets.

ACTION 1.9: Request that CHAH and CHAFC conduct an asset valuation of the Australian national biodiversity collection.

1.10: We need to agree a community consensus on how to integrate molecular and morphological data, especially when they conflict

In earlier decades and centuries taxonomy was largely a morphology-based discipline. Since the genetics and genomics revolutions, molecular (DNA) data plays an increasingly important role. However, there is currently no consensus on (1) how to handle incongruence between morphological and molecular patterns of variation and (2) in what circumstances molecular evidence is now effectively mandatory for good taxonomy, and in what circumstances it is an optional extra.

On one hand, the powerful evidentiary base provided by molecular data is important for high-quality taxonomy; on the other hand, the aim of the mission is to accelerate the discovery and documentation of Australia's species, and a requirement for molecular evidence may in some cases slow taxonomy down rather than speed it up.

ACTION 1.10: Taxonomy Australia to bring together a symposium on the balance between morphological and molecular taxonomy, as a step to gaining community consensus on these issues.

### 2. Items that could be actioned with modest extra resourcing:

2.1: We need to establish regular entry-level and advanced training programs and internships for students and others in morphology, genomics, bioinformatics, nomenclature and collection management.

Training in taxonomy and biosystematics is clearly a necessary precondition for the mission to discover and document all remaining species in a generation – it cannot be done without a new generation. There is a reciprocating problem here – the relatively low status of taxonomy and biosystematics as a career means that training in these fields is not well-serviced at universities, and the relative scarcity of well-trained graduates further limits the ability of the sector to increase its standing. Another way to express this is that there are both push and pull factors – there is not enough pull (positions for graduates opening up) to encourage universities to increase their investment in courses, and not enough push (taxonomy graduates from universities) to service the relatively few positions that do open up.

A partial solution is to create resources from within the sector that make it easier for universities to offer taxonomy and systematics training. This, however, will require resourcing to develop and promote those resources and to package them in ways that work in the university sector.

The 'others' in this item ('students and others') is an important issue. A well-designed solution to the problem of university training will be one that can also provide opportunities for training and up-skilling outside the university sector. This can be used as a way to raise the profile of taxonomy and biosystematics in the community, a necessary precondition to gaining traction in advocacy to governments.

ACTION 2.1: Establish a working group to plan a package of training programs in morphology, genomics, bioinformatics, nomenclature and collection management, and to cost the resources required to roll this out.

2.2: We need to establish a professional exchange program between institutions to deal with the backlog of unidentified specimens

All biodiversity collections hold moderate to large numbers of unidentified specimens. In many cases, an expert with the right domain knowledge can quite quickly deal with identifications in that backlog (in other cases identifications are impossible because the taxonomy of the group in question is too unresolved).

As taxonomic revisions are conducted, specimens are often loaned and dealt with, then returned. This is often a time-consuming process, and may be risky (to the specimens). An alternative might be to establish a mechanism to support travel and accommodation to bring the experts to the collection to work through backlogs of unidentified specimens. It is not clear whether an expanded and more effective loans program or the establishment of a professional exchange program will be the more efficient way to deal with backlogs of unidentified specimens.

ACTION 2.2: Establish a working group to consider the merits of alternative approaches of an expanded loans program and the establishment of a professional exchange program, and to develop an indicative budget for both

### 2.3: We need to co-design Indigenous engagement opportunities for taxonomy

Indigenous knowledge systems, including knowledge of the biodiversity of Australia, and Western scientific knowledge systems, including formal Linnaean taxonomy, are complementary and can be mutually supportive if approached with mutual respect and trust. Important issues centre on the unresolved conversations to be had about the Western notion of 'discovery' and the recognition of First Nations peoples and their knowledge.

Mutual respect means respecting difference in approach as well as similarities. Within this context, there are important opportunities to co-design and implement collaborative taxonomic projects and programs.

ACTION 2.3: Establish a standing working group to discuss the co-design of the mission to discover and document all remaining species in a generation, in the context of both Indigenous and Western traditions and perspectives

# 2.4: We need to attract undergraduates to study taxonomy and systematics by offering more learning opportunities

Undergraduates in modern universities often face a difficult choice: take a course of study that they are interested in or take a course of study that will lead to a good job and career. Currently, for those students with an interest or passion for biodiversity, this is a particularly difficult choice, given the very sparse and infrequent jobs in taxonomy and biosystematics.

The aim of the mission to discover and document all Australian taxa in a generation is to change this dynamic. If taxonomy can become a high-profile occupation, and if career paths for taxonomists can be re-established through investment in the mission, then keen students with a passion for biodiversity will not face such a difficult choice and are likely to be very attracted to such courses.

In the meantime, the erosion of courses and course content in taxonomy and biosystematics at many universities needs to be addressed. One way to do this is to build online content that can be used to develop low-bar-to-entry courses or units in taxonomy and biosystematics at more universities.

ACTION 2.4: Establish a standing working group to develop a plan for online course material in taxonomy and biosystematics, developed and managed by the taxonomy and biosystematics community and offered to students through universities

2.5: We need to build the architecture for a sequence reference library (including non-types)

DNA sequences are core data in taxonomy. In some taxonomic groups, taxonomy in practice is no longer done in the absence of sequences. However, the management of existing DNA sequence libraries is imperfect, and can be improved.

A DNA sequence library for all Australian taxa would be an immensely important resource, supporting not only taxonomy but also biodiversity diagnostics, evolutionary studies and meta-analyses, ecology and conservation, biomonitoring, bioprospecting and much more.

Issues around managing a DNA sequence library are complex, partly because sequencing technologies are in a state of rapid development, with new sequencing opportunities, markers and methods rolled out every year.

Given this, and because there are well-established resources in this space such as Genbank and BOLD, it would be inefficient to build and maintain a new DNA sequence reference library in Australia. A better approach may be to develop an Australian sequence curation layer on top of global resources such as Genbank and BOLD. It would be sensible to build the architecture for this before the mission to discover and document all remaining Australian species commences.

ACTION 2.5: Establish a working group to scope and design the architecture for an Australian sequence reference library

2.6: We need to start including collection professionals on field expeditions to help handle collecting

Collecting specimens for vouchering, and dealing with the curation of specimens in collections, are both skilled tasks. Inefficiencies arise when the tasks (collection of specimens in the field and curation of specimens into the collection) are handled separately. These inefficiencies can be ameliorated if collection professionals are, as a matter of course, including in field expeditions. Specimens and their associated data can then be collected in a form that automates their accession, or can perhaps even be accessioned directly in the field.

A good opportunity to explore the advantages of including collections professionals on field expeditions would be on BushBlitz expeditions, where large numbers of specimens are collected specifically for accessioning into collections by teams of taxonomists.

ACTION 2.6: BushBlitz to consider opportunities for including collections professionals directly on BushBlitz expeditions, and accessioning specimens directly or semi-directly at the time of field processing

# 2.7: We need to build a platform for recording traits and semi-automatically producing descriptions

Several systems have been built in Australia (DELTA, Lucid) for recording traits from taxa or specimens and creating descriptions. These have been used extensively by some taxonomists, for creating trait-based interactive keys or descriptions for taxonomic treatments. These however are desktop applications that have never been adequately implemented in a collaborative, online environment. Other custom online systems have been built for specific taxonomic projects (e.g. for the goblin spiders Oonopidae), but these have not been generalised for use outside their individual project scope.

There is a need to solve this problem and to develop an online, generalised system for recording taxonomic traits for a wide range of taxonomic projects, and generating automated or semi-automated descriptions and identification systems. This could substantially increase the rate of description of new taxa in some taxonomic groups.

ACTION 2.7: Seek funding for the development of an online, generalised trait-scoring and description generation system

# 2.8: We need to develop a national program to use citizen science opportunities to ramp up digitisation of our collections

Digitising the national collection of voucher specimens is a key task for increasing the accessibility of biodiversity information. While most Australian herbaria are fully digitised (at least for Australian specimens), less than 10% of the much larger collection in Australian museums is digitised. Museum collections are more difficult to digitise, as specimen labels are usually less readily transcribed than on herbarium specimens, and are physically more diverse.

A number of examples of large-scale digitisation programs have been successful in Australia and overseas, including the Australian DigiVol and the US iDigBio programs. Databasing the complete biodiversity collection in Australia would bring substantial opportunities and is an important component of the mission to discover and document all remaining Austraian species. Citizen science will need to play a part on this digitisation effort.

ACTION 2.8: Establish a working group to develop a strategy for substantially ramping up digitisation efforts by citizen scientists and to budget a program to do so.

2.9: We need to start building a super-phylogeny for the Australian biota and a workable, functional, comprehensive and curated database of phylogenies, with national protocols for adding species, sequences and trees

Phylogenetic relationships are key to our understanding of biodiversity. The project of taxonomy since the advent of 'natural' classifications in the late 18<sup>th</sup> Century has been to discover and document species and to classify them by their evolutionary relationships. With the formalisation of phylogenetics by Hennig in the mid-20<sup>th</sup> Century, the intersection between phylogenetics and classification has grown, resulting in broad agreement that all classifications should reflect monophyletic groups.

A super-phylogeny of all Australian organisms would be a key resource for our understanding of Australia's biodiversity and for research into its ecology, conservation and evolution. Building a super-phylogeny is non-trivial, but achievable given the genetics revolution and the amount of phylogenetic work being conducted as a matter of course in taxonomy. It will be made easier if a curated database of phylogenies is developed, and national protocols agreed for curating the database and the summary super-phylogeny that will result.

ACTION 2.9: Establish a national symposium and workshop to begin scoping the work required to create a super-phylogeny of all Australian organisms.

2.10: We need to hold a series of national workshops to develop standard ontologies/descriptors for taxonomic groups

Action 2.7 in this report outlines the need for a generalised, online platform for recording traits and producing standardised descriptions from them. Such a system will be substantially more efficient and effective if standard descriptors are agreed for different taxonomic groups.

It will be inefficient to develop such standard descriptors until the online platform is developed. This action is thus contingent on Action 2.7 being implemented.

ACTION 2.10: Following Action 2.7, establish a series of workshops to standardise descriptors for different taxonomic groups

#### 2.11: We need to build a national repository for expedition metadata

Field work often takes taxonomists to remote and relatively inaccessible areas, either for general or targeted collecting. In some cases, shared collecting trips may be efficient and cost-effective; in other cases, a trip to collect specimens for one taxonomic project could also, with relatively little effort, collect specimens for others. For example, botanists visiting a remote area to collect plant specimens may also be able to set up malaise traps to collect insects, or a taxonomist on one trip could be asked to collect, if found, specimens for another taxonomist.

A limitation in all these cases is that individual taxonomists are often unaware when other taxonomists plan to visit an area, and hence are unable to consider joint field work or make requests for specific collections. A national clearing house of expeditions could help make field work more effective and efficient for the entire taxonomy sector.

ACTION 2.11: Develop a national clearing house where taxonomists share information about planned field work.

### 3. Items that require substantial funding and investment to action:

3.1: We need to locate, database, image and sequence all Australian types, both here and overseas

Taxonomy cannot proceed without access to type specimens. In any taxonomic revision, substantial time is spent locating types, particularly of species named in the 18<sup>th</sup> and 19<sup>th</sup> centuries, most of which are in overseas museums and herbaria.

A significant milestone in a mission to discover and document all remaining Australian species, and a necessary early step, is to locate, database, image and, if possible, sequence all Australian types. This step is necessary to ensure that, if a putative new taxon is recognised, it can be straightforwardly determined if it has already been named (that is, if a type matches the taxon). Many putative Australian species cannot yet be named because this limiting step cannot readily be achieved.

There is currently no central repository that lists all known types for named species, or conversely lists all named species for which the location of the type is currently unknown. The first step in dealing with this action then is to database all known types for all Australian taxon names. A second step will be to locate all currently un-located types. Many of these will be in overseas institutions. An effective way to do this may be to build a network of retired taxonomists who live close to key European and North America institutions, and develop a program for them to access the collections and locate the types for databasing etc.

ACTION 3.1: Establish a working group to plan and cost a program to locate and database all Australian types starting with located types and working towards current unlocated ones.

3.2: We need to increase the number of specialised and generalised technicians in institutions

Technical positions, ranging from specialised positions such as high-end imaging, informatics and bioinformatics positions to generalised technical positions to augment curation staff, will be as important as research positions for the success of the mission. Over recent decades the ratio of technical to research positions has declined in many institutions including herbaria, museums and universities, and this decline needs to be reversed. Training programs, both entry-level and professional development training, will also be

necessary to ensure good career paths for technical positions and to ensure the mission can encompass and effectively utilise new and emerging technologies.

ACTION 3.2: Include specific funding for specialised and generalised technical positions and their training in any budgets developed during advocacy for the mission

3.3: We need to fund targeted PhD and post-doctoral positions, especially in hyperdiverse groups, and fellowships for senior researchers

A mission to discover and document all remaining Australian species in a generation will require substantial new capacity in taxonomy and biosystematics, particularly in the taxonomy of hyperdiverse including many invertebrate groups, fungi etc. This capability will need to be built over time, and needs to include enhanced undergraduate taxonomy teaching, the provision of targeted, funded PhD and post-doctoral fellowship programs, and a career path to permanent positions. As well, funded fellowships for senior researchers will be needed to ensure that the deep knowledge of Australia's biodiversity in existing researchers is brought to bear on the mission and that new entrants to the sector are appropriately mentored.

The ABRS NTRGP grants program currently provides modest funding for PhD and post-doctoral programs and for senior researchers, but due to the limited pool of funding this is insufficient for capacity-building. An appropriate vehicle for funding PhD and post-doctoral programs is through reinvestment in the NTRGP.

ACTION 3.3: Advocate for a substantial increase in funding available through the ABRS NTRGP program, and target the funding for capacity building across taxonomy with a weighting towards the taxonomy of hyperdiverse groups

3.4: We need to complete the National Species Lists and develop efficient and timely mechanisms to curate it

The National Species Lists is foundational infrastructure not only for taxonomy and biosystematics but also for many other activities including conservation policy, ecological research, biosecurity, compliance with international treaty obligations, and as a basis for much of our understanding of the biodiversity of Australia.

While much progress has been made, the National Species Lists are not yet complete. Gaps exist for some groups. Equally importantly, there is frequently a lag of several years before a new taxon is included in the list of accepted taxa in Australia. Both the incompleteness and the lag have negative consequences for all uses and users of the National Species Lists.

There are two reasons why the National Species Lists remain incomplete. The major reason is that there is limited support for the management of the lists, and most existing support comes from a narrow set of institutions which have competing priorities. A secondary reason is that the mechanisms for governance and curation of the lists have built-in time delays

from publication of a name to inclusion as an accepted name on the lists. These factors are inter-related.

It is important that the National Species Lists be complete, and mechanisms for their timely maintenance be in place and working effectively, before the mission to discover and document all remaining Australian species in a generation is launched. Otherwise the substantial acceleration in taxonomy necessary for the mission is likely to overwhelm the maintenance of the lists, which will in turn have a negative impact on the mission.

ACTION 3.4: Seek funding to complete the National Species Lists and develop the most timely possible mechanism for their maintenance and curation

3.5: We need to complete an inventory of our collections (including both museum/herbarium and biosecurity etc. collections)

The national biodiversity collection comprises an estimated >70M specimens of animals, fungi, plants and algae. This is a priceless national asset and infrastructure that underpins our understanding of Australia's biodiversity.

Digital specimen records are becoming almost as valuable as the specimens themselves for many applications, but most of these specimens are not databased, and are increasingly inaccessible for analysis and study. This is both a wasted resource and a threat to our proper understanding of Australia's biodiversity.

ACTION 3.5: Establish a working group to develop and cost a program of work to digitise all remaining specimens in the Australian national biodiversity collection.

### 3.6: We need to build more efficient data and collections management systems

Biodiversity collections (museums, herbaria and other special-purpose collections) underpin our understanding of Australia's biodiversity and provide the key infrastructure of taxonomy and biosystematics. The curation and management of all aspects of these collections needs to be as efficient as possible before the mission to discover and document all remaining species in a generation is launched. Otherwise, they are likely to be overwhelmed, with negative consequences for the mission.

A key part of collection management is the management of specimen data. Effective, interoperable collections management systems across the national biodiversity collection will enable much-needed efficiencies, both within and between institutions, that will be key enablers of the mission.

Currently, most biodiversity institutions hold specimen records in standalone relational databases. Records are then aggregated into the Atlas of Living Australia. This effectively duplicates records at several levels (duplicate records in multiple institutional databases when specimens are duplicated across institutions, and duplication between the normative records in the institution and the aggregated records in the ALA). Deduplication of records

within the ALA and managing information flows between the ALA back to the institutions are both currently relatively inefficient.

A better model may be to develop an integrated national biodiversity knowledge graph, in which all records (and other biodiversity records) are managed as part of a single graph (at the core of which are the National Species Lists). Management of the national collection of specimen records can then be achieved in a more integrated manner, bringing efficiencies in data management that will be critical when taxonomy is ramped up to achieve the mission.

ACTION 3.6: Establish a working group to plan and cost the development of a national biodiversity knowledge graph that includes both specimen records and other biodiversity information in a flexible, comprehensive and unitary graph

3.7: We need to build a national repository to store high-resolution images both 2D and 3D

High-resolution imagery, both 2D and 3D, is becoming increasingly important in taxonomy and biosystematics. High-resolution images of specimens available online allows them to be studied remotely by taxonomists in other institutions without the need for borrowing of the physical specimens (with associated costs and risks). Similarly, technologies such as 3D microCT scanning is allowing taxonomists to study non-destructively specimens in exquisite detail.

Both 2D and 3D high-resolution images comprise very large files (up to many Gb per image). Both disk storage and online access to such large image files is problematic, and both need to be solved if high-resolution imagery is to contribute its full potential to the mission. Highly scalable solutions need to be implemented for both storage and online access to these images.

Fortunately, this problem is shared with other sectors including medical diagnostic imagery, and solutions found in these other sectors should be readily implemented for taxonomy.

ACTION 3.7: Establish a working group to plan and cost a highly scalable storage and online delivery platform for high-resolution 2D and 3D images for taxonomy, using where possible solutions developed or under development in other sectors

3.8: We need to build a high-performance, centralised (or decentralised) sequencing and bioinformatics services (with economies of scale)

DNA sequencing, along with morphology, plays a central role in modern taxonomy, species discovery and delimitation, and biosystematics. It will play an equally central role in the mission to discover and document all remaining species in a generation, and will need to scale to very-high-throughout to meet the needs of the mission.

Currently, DNA sequencing facilities and capability for taxonomy are highly dispersed and fragmented. Most biodiversity institutions have labs and other facilities for extraction and preparation of DNA for sequencing, and some have the bioinformatics expertise to process

and analyse gene and genome sequence data. Many, though by no means all, taxonomists have developed the expertise to analyse and interpret the resultant data.

However, there are two major inefficiencies in this dispersed approach. Firstly, many institutional DNA labs are used only part of the time at less than full capacity, creating downtime expenses and overall inefficiencies in the aggregate system. Secondly, genetic and genomic methods, particularly bioinformatics and analysis, is a fast-moving field. The challenges for taxonomists to keep abreast of relevant new developments and methods is a large one, and arguably is inefficient given that their core business is the end-stage interpretation of genetic and genomic patterns into a taxonomy, which in its own right is a skilled discipline.

The necessary scaling-up of genetic and genomic capability at all stages of the pipeline from DNA extraction to analysis and taxonomy may be more efficient and effective if some or many components of the pipeline were managed as an integrated national facility. It is likely that this will best operate as a virtual facility encompassing existing and new lab resources across multiple institutions, with technical bioinformatics staff equally dispersed across locations to ensure close collaboration between practicing taxonomists and facility staff.

A suitable model and budget for such a facility needs to be developed. Given the expense of genetic and genomic methods, the budget will be necessarily high if these methods are to be deployed at scale. A model that incorporates cost offsets (such as provision of commercial user-pays services for external clients that cross-subsidise the core taxonomic work of the facility) will need to be explored to ensure that a national sequencing and bioinformatics facility is achievable and effective.

Action 3.8: Establish a working group to plan and cost a scalable, national DNA sequencing and bioinformatics facility or capability in Australia that will adequately service the mission to discover and document all remaining Australian species in a generation.

3.9: We need build a national network of paid bioinformatics specialists to help with taxonomic projects

Bioinformatics is a specialised and fast-moving field, which is closely allied to but distinct from taxonomy (which increasingly uses bioinformatics to hep analyse patterns of genetic and genomic variation, then integrates these patterns with others to discover, delimit and classify taxa.

As noted under Action Item 3.8, it is relatively inefficient and ineffective to require taxonomists to keep abreast of all new developments in bioinformatics. A better model would be the close collaboration between taxonomy specialists and bioinformatics specialists, each working over multiple projects.

This requires dedicated funding and the appointment in all institutions, as part of the national DNA sequencing and bioinformatics facility discussed above, of bioinformatics specialists.

Action 3.9: In concert with Action 3.8, develop and cost a plan for building the specialised bioinformatics capability needed to support the mission

3.10: We need to plan and fund a targeted, stratified sampling fieldwork campaign to collect the many new specimens we still need

While many new species remain to be discovered in the existing national biodiversity collection, field collecting will be essential for the mission to discover and document all remaining Australian species. Many species have not yet been collected, particularly from more remote parts of Australia and among hyperdiverse groups, and many species already in collections will need further specimens and field observations to resolve and delimit.

An equally important opportunity arising from a targeted field sampling campaign is to stratify sampling to enable accurate estimates of the numbers of species that remain undiscovered in different taxonomic groups in Australia. The specimens in collections have been collected non-randomly (some taxonomic groups and some areas have been collected more extensively than others) and without stratification (many collections are more or less serendipitous and no overarching sampling strategy has been applied). This makes rigorous estimation of the numbers of species in Australia impossible.

One option for a stratified, targeted fieldwork campaign that would enable such as estimation would be to identify a set of sites across Australia that together evenly sample the Australian environment (taking into account climate, soils and vegetation), to sample each of these sites for all organisms, and to identify all collected specimens. If, once the first set of sites has been sampled, a second set is interpolated between the first and sampled, and the process repeated, then a species-area curve for the Australian continent could be estimated, the asymptote of which is the estimated number of species.

A fieldwork campaign will be most effective in the latter half of the mission, particularly if at this time most new species in the existing collections have been discovered and documented. However, some field work is also necessary early in the mission targeting specific groups under taxonomic revision and to sample other groups that are sufficiently well-known that stratified sampling is achievable.

ACTION 3.10: Establish a working group to develop a plan for a targeted, stratified sampling fieldwork campaign, and ensure that the costs of fieldwork (including costs of processing and accessioning collected specimens into the national collection) are included as the mission budget is developed

3.11: We need to establish paid positions to support volunteer and citizen science programs

There are many opportunities to use volunteers in a mission to discover and document all remaining species. Volunteers have important and meaningful roles in activities ranging from collection management and curation to digitising specimens, helping in or conducting field campaigns, and targeted help with specific taxonomic projects.

However, well-run volunteer programs including citizen science programs require close coordination and management. This cannot fall as an 'extra duty' for curation staff or taxonomists. Volunteer programs will be most effective, and volunteers most productive, if dedicated paid positions are established to coordinate and manage volunteer programs across the breadth of the mission.

ACTION 3.11: Ensure that the costs of dedicated positions to coordinate and manage volunteer programs are included in the mission budget

3.12: We need to build a system to enable enhanced access to the modern tools needed for morphology (SEM, micro-CT etc)

Modern imaging methods including SEM and micro-CT X-ray tomography are becoming increasingly important in taxonomy, enabling taxonomists to assess and analyse micromorphology in ever more powerful ways. Morphological analysis and DNA sequence analysis are the twin pillars of modern species discovery and taxonomy.

As with DNA sequencing, tools to enable these powerful methods are dispersed and scattered. Many institutions have no or only limited access to these technologies, limiting their utility across the breadth of taxonomy. Ensuring that every taxonomist has ready access to these tools when needed will be an important part of the capability-building needed to accelerate species discovery. At the very least, one institution in every capital city should have well-developed imaging capability, with formal arrangements to share the capability between other institutions in the same capital.

ACTION 3.12: Establish a working group to assess opportunities and gaps in modern imaging methods for the Australian taxonomy sector and advise on a strategy and budget to build capability.

### 3.13: We need to image all incompletely identified specimens

Many specimens in all biodiversity collections are unidentified. This is usually because the specimens have not been examined by relevant experts in other institutions (in some cases the relevant specialists are overseas). While some of these specimens will be of alreadynamed taxa, others will be of new taxa; all are invaluable in the documentation of Australia's biodiversity.

While the existing program of loaning specimens to specialists in other institutions is well-established and effective in some cases, it comes with risks and may not be adequately scalable for the mission. A cost-effective alternative may be to capture high-resolution images of all unidentified specimens and make these available online. At the very least, this will allow many specialists to assess the specimens, identify those that can be readily dealt with and request a loan of others that need closer scrutiny.

ACTION 3.13: Establish a working group to plan, scope and budget a campaign to image all unidentified specimens in the Australian national biodiversity collection

#### 3.14: We need to establish robotic handling of specimens where sensible

Biodiversity collections (museum and herbaria) store and handle specimens now in largely the same way as in past centuries, in shelving systems accessible by people. In modern collections there is a move towards dedicated, climate-controlled storage spaces to maintain the archival conditions necessary for specimen security, though still with full access and manual handling of specimens.

It will be necessary to build more collection space to support a mission to discover and document all remaining species in a generation, especially once fieldwork campaigns ramp up and many more specimens are accessioned into collections. There are potential opportunities when building this storage space to reconsider traditional collections and to explore robotic handling systems like the ones increasingly used by large supply-chain companies. The advantage of such systems is that they can be more compact (as human access and movement is not required) and climate-controlled to conditions that would be uncomfortable for people.

While this will not be a solution sensibly deployed in all situations, it will be worth exploring, especially given the advances in these technologies likely in the next decades.

ACTION 3.14: Establish a working group to research and report on robotic handling systems in commercial use and the opportunities for adapting these to biodiversity collections.

# Summary of Actions

### **Working Groups**

The following actions begin with the establishment of a working group to consider and report on the action item (high-priority actions are shaded green, medium-priority actions yellow, and low-priority actions blue):

ACTION 1.3: Establish a working group for Taxonomy Collecting Permits, with one or more representatives from each state and territory, to (1) scope a proposal for a shared or streamlined permitting system for recognised, *bona fide* collectors and (2) negotiate with relevant state and territory agencies to try to implement such a system.

ACTION 1.6: Establish a working group to develop and propose, to all Australian taxonomic journals, guidelines for what constitutes a minimal, effective, adequate and acceptable taxonomic description.

ACTION 2.1: Establish a working group to plan a package of training programs in morphology, genomics, bioinformatics, nomenclature and collection management, and to cost the resources required to roll this out.

ACTION 2.2: Establish a working group to consider the merits of alternative approaches of an expanded loans program and the establishment of a professional exchange program, and to develop an indicative budget for both

ACTION 2.3: Establish a standing working group to discuss the co-design of the mission to discover and document all remaining species in a generation, in the context of both Indigenous and Western traditions and perspectives

ACTION 2.4: Establish a standing working group to develop a plan for online course material in taxonomy and biosystematics, developed and managed by the taxonomy and biosystematics community and offered to students through universities

ACTION 2.5: Establish a working group to scope and design the architecture for an Australian sequence reference library

ACTION 2.8: Establish a working group to develop a strategy for substantially ramping up digitisation efforts by citizen scientists and to budget a program to do so.

ACTION 3.1: Establish a working group to plan and cost a program to locate and database all Australian types starting with located types and working towards current unlocated ones.

ACTION 3.5: Establish a working group to develop and cost a program of work to digitise all remaining specimens in the Australian national biodiversity collection.

ACTION 3.6: Establish a working group to plan and cost the development of a national biodiversity knowledge graph that includes both specimen records and other biodiversity information in a flexible, comprehensive and unitary graph

ACTION 3.7: Establish a working group to plan and cost a highly scalable storage and online delivery platform for high-resolution 2D and 3D images for taxonomy, using where possible solutions developed or under development in other sectors

Action 3.8: Establish a working group to plan and cost a scalable, national DNA sequencing and bioinformatics facility or capability in Australia that will adequately service the mission to discover and document all remaining Australian species in a generation.

Action 3.9: In concert with Action 3.8, develop and cost a plan for building the specialised bioinformatics capability needed to support the mission

ACTION 3.10: Establish a working group to develop a plan for a targeted, stratified sampling fieldwork campaign, and ensure that the costs of fieldwork (including costs of processing and accessioning collected specimens into the national collection) are included as the mission budget is developed

ACTION 3.12: Establish a working group to assess opportunities and gaps in modern imaging methods for the Australian taxonomy sector and advise on a strategy and budget to build capability.

ACTION 3.13: Establish a working group to plan, scope and budget a campaign to image all unidentified specimens in the Australian national biodiversity collection

ACTION 3.14: Establish a working group to research and report on robotic handling systems in commercial use and the opportunities for adapting these to biodiversity collections.

### Requests for reports

The following actions are directed at organisations including CHAH, CHAFC, BushBlitz and SPNHC (high-priority actions are shaded green, medium-priority actions yellow, and low-priority actions blue):

ACTION 1.1: Request guidelines from CHAH and CHAFC with estimates of the costs of specimen processing and curation, then distribute widely in the biodiversity and grant funding sector with an expectation that it will be used to include indicative and agreed costs in all research funding proposals.

ACTION 1.4: Request a report from organisations such as the Society for the Preservation of Natural History Collections (SPNCH) and from Australian institutions through CHAH and CHAFC, on issues that are likely to arise from the mission that will impact collections, and ways that collections may adapt.

ACTION 1.8: Request that CHAFC and CHAH develop or adopt and endorse a universal phrase-naming system for Australian taxonomy, and/or for CHAFC to develop or adopt and endorse a phrase-naming system for Australian zoology

ACTION 1.9: Request that CHAH and CHAFC conduct an asset valuation of the Australian national biodiversity collection.

ACTION 2.6: BushBlitz to consider opportunities for including collections professionals directly on BushBlitz expeditions, and accessioning specimens directly or semi-directly at the time of field processing

#### Symposia

The following actions involve setting up a symposium or workshop (high-priority actions are shaded green, medium-priority actions yellow, and low-priority actions blue):

ACTION 1.10: Taxonomy Australia to bring together a symposium on the balance between morphological and molecular taxonomy, as a step to gaining community consensus on these issues.

ACTION 2.9: Establish a national symposium and workshop to begin scoping the work required to create a super-phylogeny of all Australian organisms.

ACTION 2.10: Following Action 2.7, establish a series of workshops to standardise descriptors for different taxonomic groups

#### Miscellaneous actions

The following are miscellaneous actions not covered by the categories above (high-priority actions are shaded green, medium-priority actions yellow, and low-priority actions blue):

ACTION 1.2: Develop an online Australian Taxonomic Community Directory on the Taxonomy Australia website. In the first instance, work to get all Australian taxonomists to register with the directory, then expand its scope to fill the other functions listed above.

ACTIONED: see the Australian Taxonomy Community Directory at <a href="https://www.taxonomyaustralia.org.au/tcd-search">https://www.taxonomyaustralia.org.au/tcd-search</a>

ACTION 1.5: Institutions and universities should consider joint appointments for any new hires, and strengthen partnerships for existing appointments by establishing formal adjunct appointments for all or most staff.

ACTION 1.7: Establish a diamond open access, fully online, community-owned and operated, taxon-blind new journal for the rapid and no-fuss publication of new Australian taxa

ACTION 2.7: Seek funding for the development of an online, generalised trait-scoring and description generation system

ACTION 2.11: Develop a national clearing house where taxonomists share information about planned field work.

ACTION 3.2: Include specific funding for specialised and generalised technical positions and their training in any budgets developed during advocacy for the mission

ACTION 3.3: Advocate for a substantial increase in funding available through the ABRS NTRGP program, and target the funding for capacity building across taxonomy with a weighting towards the taxonomy of hyperdiverse groups

ACTION 3.4: Seek funding to complete the National Species Lists and develop the most timely possible mechanism for their maintenance and curation

ACTION 3.11: Ensure that the costs of dedicated positions to coordinate and manage volunteer programs are included in the mission budget

# Limitations of this document

The ideas generated during the national meeting and the actions outlined in this document comprise an important set of ideas and actions to support the mission to discover and document all remaining Australian species in a generation.

However, even if all implemented, they will not alone make the mission a success. For that, these ideas and actions need to be (1) augmented by bigger-picture, bolder ideas that will provide the needed step-change acceleration in species discovery and documentation, and (2) be supported by substantial extra and sustainable investment in the sector.

This document is a report of the national meeting and is not the place to develop either of these components. Other aspects of Taxonomy Australia's work will address these.

# **Next Steps**

This report will form the basis of a broad-based national action plan as part of the implementation of the mission to discover and document all remaining Australian species in a generation.

Its actions need to be actioned, acknowledging the fact that some can be actioned immediately while others depend in obtaining significant funding. In parallel with actions that do not depend on extra funding, Taxonomy Australia is developing an advocacy campaign to bring about the substantial reinvestment needed to fulfil the goals of the mission.

A review of these action items will be undertaken in mid-2021 by the Taxonomy Australia Steering Committee.

# Appendix 1. Meeting participants

The following people registered and participated in the national meeting that is the subject of this report.

Name Institution

Alejandro Velasco C Department of Agriculture, Water and Environment

Alex Chapman Western Australian Herbarium

Alexander Schmidt-Lebuhn CSIRO

Alison Kellow La Trobe University

Alison Vaughan Royal Botanic Gardens Victoria

Andre Zerger Atlas of Living Australia
Andrea Crowther South Australian Museum

Andreas Zwick Australian National Insect Collection CSIRO

Andrew Drinnan The University of Melbourne
Andrew Pengelly Indigenous Plants for Health

Andrew Thornhill State Herbarium of South Australa/University of Adelaide

Andrew Young CSIRO

Andy Austin Biological Sciences, Adelaide University
Anna Monro Centre for Australian Biodiversity Research

Anne Fuchs CANBR/ABRS

Anthony Whalen Biodiversity Science, Dept of Agriculture, Water & the Environment

Arthur Georges Institute for Applied Ecology, University of Canberra

Ashley Field Queensland Herbarium, Department of Environment and Science

Barbara Baehr Queensland Museum

Barry Fordham

Beau Picking

Ben Parslow

Bevan Buirchell

Bill Barker

Australian National University

The University of Melbourne

South Australian Museum

Western Australian Herbarium

State Herbarium of South Australia

Bobbie Hitchcock Department of Agriculture Water and Environment

Braxton Jones The University of Sydney

Brian Looney Duke University

Bronwyn Collins Australian National Herbarium

Bryan Lessard CSIRO

Caine Barlow

Catharina Mees University of Western Australia
Catherine Gallagher Royal Botanic Gardens Victoria
Cathy Byrne Tasmanian Museum and Art Gallery

Cathy Car Western Australian Museum
Cecile Gueidan Australian National Herbarium
Chris Anderson Australian Academy of Science

Chris Cargill Australian National Herbarium
Corinna Paeper ALA / CSIRO

Craig Moritz ANU

Dan Murphy Royal Botanic Gardens Victoria

Daniel Huston University of Tasmania
Darren Crayn James Cook University
Dave Seldon University of Auckland

David Gopurenko NSW DPI

David Juszkiewicz Curtin University

David Yeates Australian National Insect Collection

Donald Hobern International Barcode of Life Consortium

Doug Palmer ALA

Dr Mallik MALIPATIL Agriculture Victoria, DJPR

Duncan Farquhar ecoconnect.me
Elaine Davison Curtin University

Elizabeth Sheedy

Ely Wallis Atlas of Living Australia (CSIRO)

Ema Corro RMIT

Emily Roycroft

Emma Toms

Australian National University

Australian National Herbarium

The University of Adelaide

Ethan Briggs

The University of Queensland

Ethan P. Beaver

South Australian Museum

Francesco Martoni Agriculture Victoria Research - AgriBio

Genefor Walker-Smith Museums Victoria
Georgina Binns Macquarie University

Gerry Cassis University of New South Wales

Gill Brown Queensland Herbarium
Giulia Perina Western Australian Museum

Grace Sun Department of Agriculture, Water and the Environment

Graeme Smith Australian Museum

Greg Whitbread Taxamatics

Hannah McPherson National Herbarium of NSW
Harvey Orel University of Melbourne

Haylee Weaver Department of Agriculture, Water and the Environment

Helen Kennedy University of New England
Heroen Verbruggen The University of Melbourne

Herve Sauguet Royal Botanic Gardens and Domain Trust

James Bickerstaff Western Sydney University

James Buxton La Trobe University
James Dorey Flinders University

James F. Wallman University of Technology Sydney
James K. Douch The University of Melbourne

James Tweed

Jason Alexander Curtin University

Jeffrey Skevington Canadian National Collection of Insects, Arachnids and Nematodes

Jeremy Bruhl University of New England

Jess Marsh Murdoch University/ SA Museum

Jo Palmer Australian National Herbarium

Joanna Sumner Museums Victoria

Joanne Birch The University of Melbourne

Joel Johnson CQ University
John Early Auckland Museum
Jon Lewis CSIRO (volunteer)
Joseph Schubert Museums Victoria

Juanita Rodriguez Australian National Insect Collection
Julia Haska Volunteer, South Australian Herbarium

Karl Magnacca Bishop Museum

Kate Sparks Department of Agriculture, Water and Environment

Kate Umbers Western Sydney University

Australian Tropical Herbarium & National Research Collections

Katharina Nargar Australia, CSIRO
Kathryn Hall Queensland Museum

Kathy Ebert The University of Queensland
Keith Maguire South Australian Museum

Ken Walker Museums Victoria
Kevin Kocot University of Alabama
Kevin Thiele Taxonomy Australia
Kingsley Dixon Curtin University

Kirrily Moore Tasmanian Museum and Art Gallery

Kit Prendergast Curtin University

University of Western Australia/ Dept of Water and Environmental

Kym Abrams Regulation

Laetitia Gunton Australian Museum

Lalita Simpson Australian tropical Herbarium

Lara Senior Department of Agriculture and Fisheries, QLD

Laura Fagan Department of Primary Industries and Regional Development

Lauren Hughes Natural History Museum London Leela Maya Rizal The University of Queensland

Leon Perrie Museum of New Zealand Te Papa Tongarewa

Levente Kiss University of Southern Queensland

Linda Broadhurst CANBR/CSIRO

Linda Semeraro Agriculture Victoria

Lindsay RJ Shelton University of Western Australia Lisa Kirkendale Western Australian Museum

Lizzy Joyce James Cook University
Luke Harmon University of Idaho
Lyn Cave Tasmanian Herbarium

Lyn Cook The University of Queensland

Madalene Giannotta University of Adelaide, ANU, and ANIC

Maggie Watson Charles Sturt University
Manu Saunders University of New England

Marco Duretto Royal Botanic Gardens & Domain Trust

Marco Girardello Joint Research Centre - European Commission

Marco Pellegrini Independent researcher
Margaret Brookes The University of Melbourne
Mark Harvey Western Australian Museum
Mark Stevens South Australia Museum
Martin Brummell University of New England

Matt Renner National Herbarium of New South Wales

Matt Shaw South Australian Museum Matthew Baker Tasmanian Herbarium

Matthew Barrett Australian Tropical Herbarium

Matthew Bulbert Macquarie University

Matthew Nimbs Southern Cross University, National Marine Science Centre

Matthew Watters **Deakin University Murdoch University** Michael Borowitzka Michael Hope Atlas of Living Australia Michael Shackleton Latrobe University Michela Mitchell Queensland Museum Michelle Guzik The University of Adelaide Michelle Guzik The University of Adelaide Mike Bayly The University of Melbourne

Mike Rix Queensland Museum

Min Pokhrel University of New England

Nerida Wilson Western Australian Museum

Nicole Fisher CSIRO Collections

Nicole Gunter The Cleveland Museum of Natural History

Nicole Kearney Biodiversity Heritage Library Australia (Museums Victoria)

Niels Klazenga Royal Botanic Gardens Victoria

Nigel Fechner Queensland Herbarium

Nik Tatarnic Western Australian Museum

Nikolas Johnston University of Wollongong

Nimal Karunajeewa Royal Botanic Gardens Victoria

Owen Seeman Queensland Museum

Paige Maroni The University of Western Australia

Pat Hutchings Australian Museum

Patrick Fahey The University of Melbourne

Paul Flemons Australian Museum

Paulo Baleeiro The University of Queensland Penelope Mills The University of Queensland

Peter Brenton Atlas of Living Australia
Peter Cowman James Cook University

Pina Milne Royal Botanic Gardens Victoria
Pratyaksh Singh University of Bonn, Germany
Rachael Fowler The University of Melbourne
Rachael King South Australian Museum

Rae Young Lewisham

Raees Khan The University of Adelaide

Renee Catullo ANU

Richard Jobson National Herbarium of New South Wales

Rod Page University of Glasgow

Roger Shivas University of Southern Queensland

Rose Andrew University of New England
Ryan Ellis Biologic Environmental Survey
Ryan O'Donnell University of New England

Sally Fryar Flinders University

Sally South
Samantha Ward
Samille Loch-Wilkinson
Samuel Brown
Sangay Dema
South Australian Museum
The University of Melbourne
Healthy Land and Water
Plant and Food Research
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Sapphire McMullan-Fisher Fungi4Land

Scott Cutmore The University of Queensland
Sergio Stampar Sao Paulo State University
Shelley James Western Australian Herbarium
Sherie Bruce Capricorn Conservation Council
Shirley Sorokin South Australian Museum

Hawkesbury Institute for the Environment, Western Sydney

Simon Tierney University

Stanislaw Wawrzyczek La Trobe University

Stephanie von Gavel CSIRO Stephen Jackson NSW DPI

Stephen Keable Australian Museum

Steve Cooper South Australian Museum/ The University of Adelaide

Susanna Bryceson La Trobe University
Tanya Latty University of Sydney
Tim Collins University of New England
Tim Hammer Western Australian Herbarium
Todd McLay Royal Botanic Gardens Victoria

Tom Bridge Queensland Museum

Tom Cribb The University of Queensland
Tom May Royal Botanic Gardens Victoria
Tom Saunders University of Auckland, NZ
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Volker Framenau Murdoch University

Wayne Gebert Royal Botanic Gardens Victoria
William Brockelsby Department of Conservation NZ

Australian National Insect Collection, CSIRO; Division of Ecology and Evolution, Research School of Biology, Australian National

Yun Hsiao University

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