

Integrating Measures of Phylogenetic and Taxonomic Diversity and Endemism into National Conservation Assessment

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Project Objectives

The increasing availability of information on phylogenetic and taxonomic diversity and endemism that takes into account the evolutionary history of organisms provides a more sophisticated understanding of biodiversity and an improved foundation for conservation assessment and planning than was previously possible. Integrated spatial and phylogenetic data for the whole of Australia, combined with guidelines for their application, will contribute to the inclusion of this important aspect of biodiversity into conservation planning and natural resource management.

The spatial database underpinning the Australian Natural Heritage Assessment Tool (ANHAT) represents an important source of information for improving evolutionary understanding of Australia's biodiversity, and for incorporating this knowledge into biodiversity assessment for policy development, planning and scientific purposes. Species location data within ANHAT is predominantly sourced and updated from State and Territory Governments, Museums, Herbaria and CSIRO.

By analysing the distributions of numerous species together, ANHAT seeks to give a coherent picture of the spatial patterns in Australia's biodiversity and biogeography. The availability of taxonomic as well as phylogenetic data in ANHAT means that sophisticated analyses of phylogenetic diversity and endemism can now be undertaken. Additional expertise was required to maximise the application and interpretation of these analyses to enable effective and innovative use of these data in biodiversity assessment and conservation planning. This workshop brought together several biodiversity scientists and practitioners to evaluate the capacity of phylogenetic data currently held in ANHAT to support biodiversity assessment, identify appropriate analytical and interpretive approaches to working with these data, and explore potential applications of these approaches in biodiversity science and conservation practice throughout Australia. The workshop also identified an integrated set of phylogenetic approaches for biodiversity assessment, for both species and localities.

Methods

The following analyses were conducted for each of a set of taxon groups, comprising Camaenid Land Snails, Mammals, Passerine Birds, Hylid and Myobatrachid Frogs, *Acacia* and *Daviesia*:

- Phylogenetic Diversity (PD) and Phylogenetic Endemism (PE) complementarity
- Comparison of phylogenetic measures with traditional species measures (such as species richness and endemism) at a national and regional level (pilot / exemplar regions – Cape York Peninsula and South West Western Australia)
- Residual PE and PD
- PD of the national reserve system within Australia with the whole of each exemplar region.
- Species and PD turnover analyses within each region.
- Basic complementarity maps of species richness, endemism, PD and PE.

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Major Findings

The preliminary findings of our workshop were:

For some groups analyses there is not much difference between phylogenetic measures and standard measures, but for others there appears to be opportunities for assessment of conservation values and conservation planning. An example of one of these analyses for turnover in *Daviesia* is shown in Figure 1 to the right.

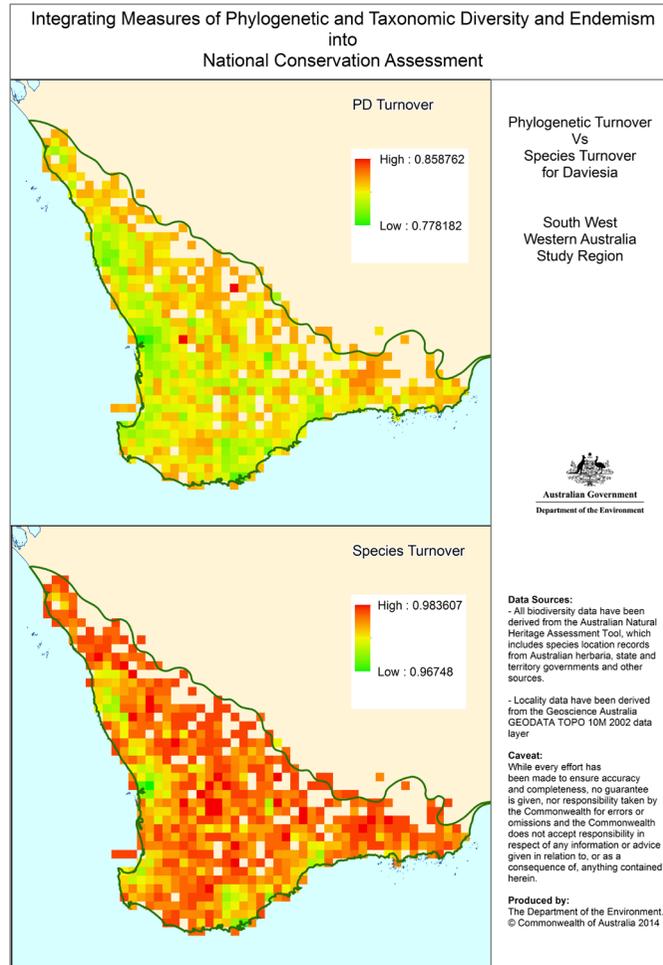


Figure 1: Phylogenetic turnover analyses and traditional species turnover analyses of the National Reserve System in comparison with reserves in the rest of Australia for *Daviesia* in South West Western Australia region.

How will this affect Australian ecosystem science and management?

Future applications of these analyses include conservation priority setting at state and commonwealth level through understanding the comparative biogeography of a diverse range of plant, vertebrate and invertebrate taxa. Other applications may include providing a regional context for assessment of the potential impact of proposed development action on biodiversity.

Phylogenetic measures will provide important information regarding the evolutionary history and heritage value of an area, adding an extra dimension to heritage stories for significant natural heritage sites in Australia.

Another application may be the national scale analysis of the existing reserve system to evaluate how much PD and PE are currently reserved to get a sense of how the current reserves are protecting phylogenetic diversity and endemism.

Key papers or products resulting from your work

A journal paper is currently in preparation “Environmental phylogenetics to inform conservation policy: the Australian Case”. This paper looks at current policy frameworks for biodiversity conservation in Australia and traditional species based measures. It examines how various phylogenetic analyses can be used to supplement the information gathered for conservation assessments and management of biodiversity.

As a result of this work, several new phylogenies have been incorporated into ANHAT and a number of phylogenetic analyses are now available in this program.

It is planned that a protocol and guidelines targeted at government agencies and conservation groups to use and interpret phylogenetic analyses in conservation assessments will be developed from this work.

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