

Phylogenetic Analyses + Conservation Assessment and Planning In Australia – an ACEAS project*

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Key policy contexts

The Heritage group within the Department of Sustainability, Environment, Water, Population and Communities is interested in identification of sites of documentable significance for biodiversity conservation. This parallels other strategies, including efforts to identify global 'Key Biodiversity Areas'. The CBD Strategic Plan for Biodiversity and Aichi Biodiversity Targets also highlight this goal: "Target 11: By 2020, at least 17 per cent of terrestrial and inland water areas and 10 per cent of coastal and marine areas, especially areas of particular importance for biodiversity and ecosystem services, are conserved ..." (see: <http://www.cbd.int/sp/targets/rationale/target-11/>) Sites of particular importance for biodiversity include important places for phylogenetic diversity or "evolutionary heritage". GEO BON (Global Biodiversity Observation Network) includes phylogenetic diversity in its framework for monitoring biodiversity change. Our study provides an exemplar for GEO BON, through strategies to integrate phylogenetic diversity over multiple taxonomic groups, and development of useful indices relating to phylogenetic diversity conservation and change.

Our approach

Our study integrated data, derived from the Australian Natural Heritage Assessment Tool (ANHAT) database, for multiple taxonomic groups, including *Acacia*, *Daviesia* ("Bitter Peas"), Camaenid Land Snails, Myobatrachid and Hylid Frogs, Passerine Birds, and Mammals. Distribution information was summarized for a set of 9 adjacent sub planning units (a 30x30km square). For each taxonomic group, we derived PD indices using distribution data combined with recent phylogeny estimates from the literature. We used PD-based indices to capture the phylogenetic aspects of richness, endemism, complementarity and irreplaceability. Some indices are designed for grid-cell information, where values are inversely weighted by total number of cells sharing a given property. Questions included e.g.: "how much of Australia's unique evolutionary history is found only in Cape York?"

Supplementary sections below provide more background information

Study sites

The study areas are the Cape York Peninsula (red boundary) and South West Western Australia (green boundary). Parts of Cape York Peninsula are currently undergoing assessment for listing as a World Heritage Area and South West Western Australia has been recognized as a global biodiversity hotspot.



The Australian Natural Heritage Assessment Tool

The Australian Natural Heritage Assessment Tool (ANHAT) spatial database provides information for the conservation of Australia's unique biota. Species location data within ANHAT is sourced and updated from State and Territory Governments, Museums, Herbaria, and CSIRO. By analysing the distributions of numerous species, ANHAT provides a coherent picture of the spatial patterns in Australia's biodiversity and biogeography, for scientists and decision-makers. (see <http://www.environment.gov.au/heritage/anhath/index.html>)

Key policy challenges

Biodiversity option value is the value of maintaining living variation in order to retain possible future uses and benefits. A challenge is to include these option values of biodiversity in planning and decision-making.

One big problem:

Much recent conservation policy work wrongly characterises biodiversity as linked only to vaguely defined intrinsic (biocentric) values, with ecosystem services then providing the links to human well-being. Effective biodiversity policy will seek trade-offs and synergies between among biodiversity option values, ecosystem services and other needs of society.

Another big problem:

We need useful biodiversity option value measures for decision-makers. Phylogenetic diversity (through the PD measure) provides one widely accepted way to quantify option values, at the level of "features" of species. However, we need practical indices derived from PD for mapping and decision-making (e.g., gains and losses, endemism, expected loss).

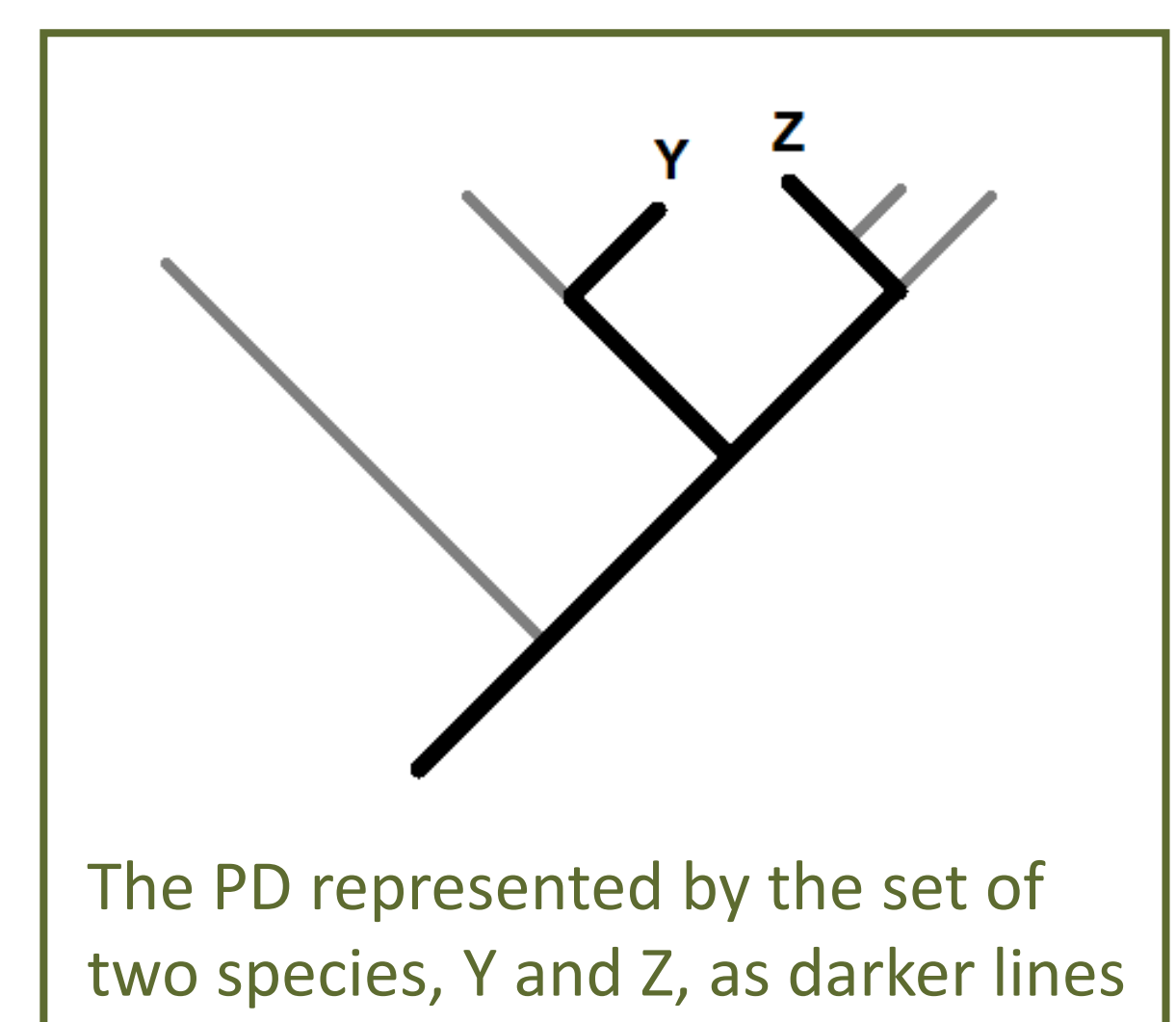
Discussion and future work

Results using simple existing PD indices suggest that further development of practical informative indices is needed, in order to better indicate key biodiversity areas and unique evolutionary heritage. For example, weighted PD indices based on grid cell counts may be unduly influenced by the species richness of the cell. Probabilistic approaches may help.

Future work will explore robust, policy relevant, measures for Phylogenetic Key Biodiversity Areas (KBAs) – identifying places with a high concentration of vulnerable PD. These indices build on weighted PD irreplaceability, which values places with branches that are non-existent within protected areas, and rare or non-existent among all other places that are not part of the protected set.

Key terms and ideas

The phylogenetic diversity measure, "PD" (Faith 1992), helps us to quantify current and potential future benefits derived from the tree of life. The PD of a given set of species is the minimum total length of all the phylogenetic branches required to connect all those species on the tree. PD provides a natural way to talk about future uses and benefits provided by species because the counting-up of branch lengths links sets of species to their expected relative diversity of features.

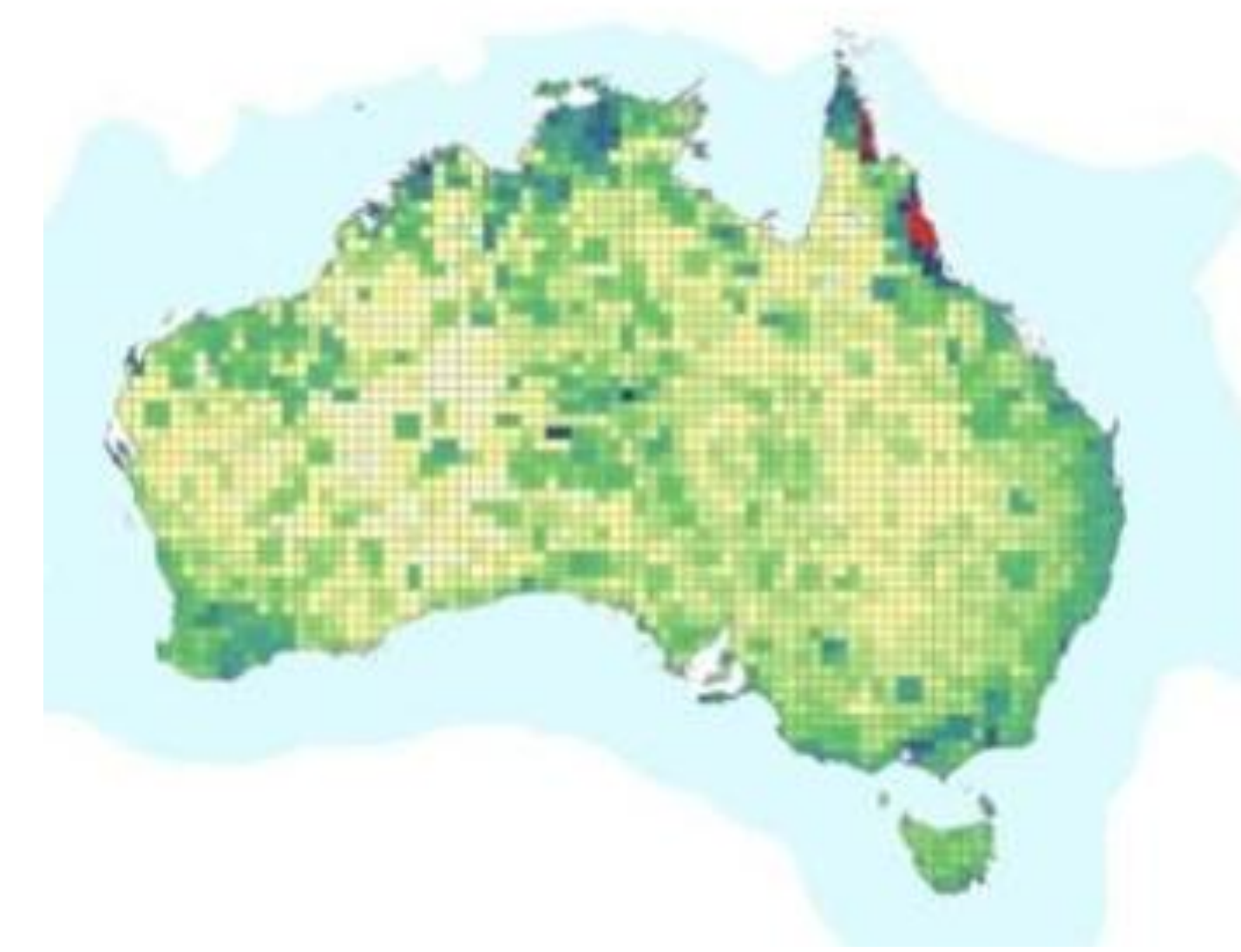


A family of PD calculations is derived from the interpretation of PD as counting-up features. These extend conventional species-level indices such as complementarity to the features level. Indices include PD endemism and PD complementarity. High PD irreplaceability indicates that a place offers vulnerable PD, and there are few if any substitute places offering these potential conservation gains.

Example maps for mammals showing scores for grid cells:



Red, blue = high PD



Red, blue = high PD-endemism, using "PE"

* We thank ACEAS and the Dept. of Sustainability, Environment, Water, Population and Communities for support.

Our ACEAS workshop was held in Brisbane with 17 participants with experience in conservation assessment and planning, phylogenetic methods and applications, and government policy setting. Participants were from government agencies, CSIRO, universities and museums. Participants included Margaret Byrne, Craig Costion, Darren Crayn, Dan Faith, Simon Ferrier, Carlos Gonzalez-Orozco, Shawn Laffan, Joe Miller, Craig Moritz, Dan Rosauer and six SEWPAC Staff – Brian Prince, Tania Laity, Jane Ambrose, Karl Newport, Jonathan Face and Annie Sharrock. Also involved in the workshop but unable to attend due to other commitments were Alaric Fisher, Frank Koehler, Andrew Hugall and Edward Biffin.

