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*Using dispersal guilds to assess connectivity
at the landscape scale:
a case study in the Tasmanian Midlands*



Report by:

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Using dispersal guilds to assess connectivity at the landscape scale: a case study in the Tasmanian

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Purpose of Report

The report presents findings of the project *Applying the Principles of the National Wildlife Corridors Plan to Regional Sustainability Planning*. The project is developing a framework for regional planners to use best practice science in their regional-scale planning of wildlife connectivity networks. The planning tool provides for ecological connectivity within a whole-of-landscape and cooperative approach to biodiversity conservation. This report describes the application of the GAP CLoSR tool developed in the Lower Hunter to the Tasmanian Midlands. The report extends the previous research through developing an approach for modelling dispersal guilds.

The report is an output of the Landscapes and Policy Research Hub.

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Executive Summary

Focal targets for connectivity conservation range can be applied to species or ecological communities. In the previous GAP CLoSR study in the Lower Hunter region of New South Wales (Lechner & Lefroy 2014), we modelled functional connectivity between patches of remnant woody vegetation, with the assumption that these patches provide habitat for many woodland or forest-dependent fauna species and the plant species that depend or benefit from these fauna for dispersal. In this study, we build on the previous approach by developing the concept of connectivity-based dispersal guilds. The guild concept groups species based on their shared properties. In this report, we group Tasmanian mammal fauna species into guilds on the basis of shared dispersal and habitat characteristics.

The objective of this study is to explore the potential for using dispersal guilds with connectivity modelling to characterise connectivity for conservation planning. By using dispersal guilds as the focal conservation target, we can capture a range of responses to fragmentation without having to resort to time-consuming single species modelling. This approach can identify those groups of species that are most impacted by fragmentation and are likely to benefit most from restoring links within a landscape. As well as developing the dispersal guild concept, we describe a process for engaging experts in eliciting the ecological and dispersal characteristics of target species, and identifying dispersal groups through cluster analysis of these characteristics.

The connectivity dispersal guild approach was used in conjunction with a regional scale analysis based on the GAP CLoSR framework with the Graphab graph theoretic connectivity model (Foltête et al 2012). Connectivity is characterised using the GAP CLoSR framework (Lechner & Lefroy 2014; Lechner et al 2015b) based on the following ecological parameters:

1. **Minimum patch size;** the smallest area that can support a viable population of a species,
2. **Gap-crossing distance;** the longest distance between connectivity elements (for example, scattered trees or shrubs) that a species can cross over non-habitat, and,
3. **Interpatch-crossing distance;** the longest distance that a species can move between patches (see 1 above) irrespective of the intervening habitat features.

These parameters, along with the graph theoretic approach allows for the characterisation of patch isolation, optimal least-cost pathways between patches, and the calculation of graph metrics describing landscape-scale connectivity patterns.

Our study area was the Northern Midlands of Tasmania, Australia, a flat, low-lying basin where native vegetation has been highly fragmented by historical agricultural development. The expert workshop identified 12 ground-based mammal species that are likely to be impacted by fragmentation in the Tasmanian Midlands. Using a cluster analysis, these twelve species were grouped into five dispersal guilds; two guilds consisted of a single large carnivore species and the other three included groups of small mammals. The dispersal guilds were; Large Carnivore -

Tasmanian Devil; Large Carnivore - Spotted-tail Quoll; Not Woodland dependent and/or riparian; Dense ground cover dependent; and Arboreal. We also compared connectivity models; one using mammal dispersal guilds (and dispersal distances), the other using vegetation mapping following Lechner & Lefroy (2014).

Our study found that there were large differences in the response to fragmentation between the dispersal guilds. The two large carnivore dispersal guilds were apparently unaffected by fragmentation, whereas the three guilds of smaller mammals were disconnected in the fragmented Tasmanian Midlands landscape. For the 'Not Woodland dependent and/or riparian' and 'Dense ground cover dependent' guilds, the presence or absence of connectivity elements such as wildlife corridors had very little influence on connectivity as patches within the landscape were found at distances from each other greater than their interpatch-crossing distance threshold. For these groups without broad-scale restoration of new habitat patches, connectivity for some mammal species will be poor. The Arboreal mammal guild were found to be sensitive to the inclusion of connectivity elements such as stepping stones and wildlife corridors, indicating that connectivity could be improved through moderate amounts of restoration of these connectivity elements. The sensitivity analysis found that at interpatch-crossing distances less than ~1000m, the Tasmanian Midlands appears highly disconnected. Species with dispersal distances at this threshold such as the Southern Brown Bandicoot and Eastern Barred Bandicoot are likely to benefit most from restoration of habitat or connectivity elements in the Tasmanian Midlands.

The outputs from this research indicate which mammal species are likely to be most impacted by fragmentation in the Tasmanian Midlands. These methods have potential application in conservation planning elsewhere, providing a novel connectivity approach that uses focal conservation targets that is an intermediate between single species connectivity model and a general approach which link landscape features. This approach provides a broad picture of connectivity for all species in the region, and applies multiple methods for testing the sensitivity of the dispersal parameters. The outputs give a preliminary indication of areas where restoration might be most effective for improving connectivity of some mammal fauna. More complex analytical methods could be applied, along with site-based knowledge, to best provide guidance on the location of conservation actions, as described in the previous study of the Lower Hunter region.



Contents

Executive Summary	1
Glossary of Terms	4
Frequently Used Abbreviations	5
1.0 Introduction	7
1.1. Connectivity modelling background.....	7
1.2. Ecological characteristics of dispersal	7
1.3. Dispersal guilds as a focal conservation target.....	8
1.4. Objectives.....	9
2.0 Methods.....	11
2.1. Study area	11
2.2. Stakeholder and expert engagement	13
2.3. Modelling fine-scale connectivity	14
2.4. Focal conservation target	15
2.5. General approach	16
2.6. Dispersal guild approach	18
2.7. Characterise habitat and structural connectivity elements using spatial data	22
2.8. Dispersal resistance surface	24
2.9. Regional connectivity model using Graphab.....	27
3.0 Results.....	29
3.1. General approach with TASVEG 3.0 Communities	29
3.2. Dispersal guild approach	33
4.0 Discussion	45
4.1. Overview	45
4.2. Applying this approach to conservation planning.	45
4.3. Next steps for the connectivity modelling in the Tasmanian Midlands	46
4.1. Applying the dispersal guild approach using expert opinion.....	46
4.2. Limitations.....	47
4.3. Conclusions	47
References.....	48
Appendix	51
R code for cluster analysis	51
Classification of Landuse classes into dispersal classes	52

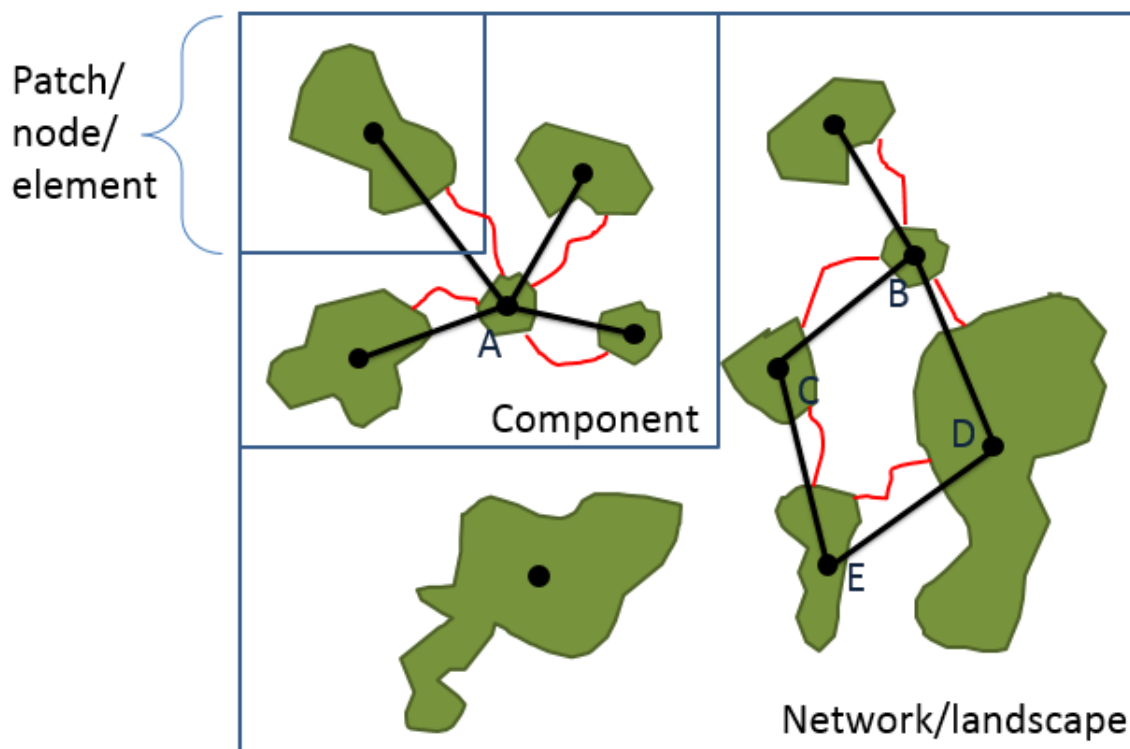
Glossary of Terms

Throughout the report, certain commonly used terms are used in a very specific sense to describe aspects of connectivity and its mathematical representation in the landscape. The glossary is divided into these commonly used terms and other terms used.

<i>Commonly Used Modelling Terms</i>	
Component	A group of nodes or patches that are linked to each other but isolated from other components, also made of groups of patches (landscape or network>component> node or patch).
Connectivity dispersal guild	A group of animals that share similar dispersal behaviour and dispersal thresholds that describe limitations to their movement through a landscape
Dispersal-cost	A value assigned to each land cover type in a landscape that reflects the ecological costs for individuals to move through it.
Dispersal-cost surface	A raster surface where each pixel's value represents dispersal cost. Also sometimes referred to as a resistance-cost surface.
Graph	A set of linked nodes/patches. Applied to landscape ecology a graph is a set of patches within a landscape linked by movement pathways.
Graph theory	The graph theoretic perspective applied to landscape ecology represents landscapes as a graph. Graph theory uses mathematical structures to describe pairwise relations between nodes.
Graph metrics	Metrics used to describe connectivity at the landscape (= network) scale, component scale, or patch (=node) scale.
Landscape-scale graph metric	A graph metric that describe a connectivity network with a single value for the entire landscape.
Least-cost path	The shortest pathway between two patches as a function of land cover resistance.
Local-scale model	This specifically refers to the use of the Circuitscape analysis for modelling connectivity for a subset of the Lower Hunter region.
Link	An element of a network/graph that connects nodes.
Network/Graph	A graph theory term describing a collection of nodes connected by links. In landscape ecology, nodes and links represent patches and pathways within a landscape.
Node	An element of a network/graph that is represented by patches in landscape ecology.
Patch	A relatively homogeneous area, often habitat, which differs from its surroundings. In this study, patches are defined as an area of woody vegetation greater with a minimum patch size between 10 and 20ha, depending on the scenario.
Patch-scale graph metric	A graph metric value calculated for each patch.
Raster	A rectangular grid of pixels commonly used in a GIS to represent land cover.
Resistance	A value assigned to each land cover type in a landscape that reflects the ecological costs for individuals to move through it. Also sometimes referred to as dispersal-cost. High resistance means high dispersal costs.
Regional-scale Model	This specifically refers to modelling connectivity with the Graphab software for the entire Lower Hunter region.



Schematic representation of the different levels of analysis within a connectivity network



Schematic representation of the different levels of analysis within a connectivity network in which patches (green) are connected by multiple links (black lines) represented by least-cost-pathways (red lines) that incorporate information about the matrix (white area). Graph metrics can be considered at three levels: patch-scale, component or landscape-scale. Using the language of graph theory, these patches are considered as nodes (black dots) linked within a graph (or graph-network) (black lines).

Frequently Used Abbreviations

DPIPWE	Department of Primary Industries, Parks, Water and Environment, Tasmania
GIS	Geographic Information system
IIC	Index of Connectivity
LULC	Land cover/land use
GAP CLoSR	General Approach to Planning Connectivity from Local Scales to Regional
NERP	National Environmental Research Program
NGO	Non-Government Organisations
TLC	Tasmanian Land Conservancy

Other Terms	
Circuit theory	Electronic circuit theory based on voltage, current and resistance. Applied to ecology it characterises landscapes as a graph where each cell of a raster grid is considered as a node (see McRae et al 2008).
Circuitscape	Connectivity modelling software that uses circuit theory (see McRae et al 2008).
Connectivity	The degree to which the landscape facilitates or impedes the movement of individuals between habitat patches. Maximising connectivity is often an objective of conservation planning.
Connectivity elements	Landscape features, which do not provide habitat in themselves, but can be used for dispersal. It includes wildlife corridors (linear links between patches), disconnected linear elements and stepping-stones (paddock trees, shrubs, rocky outcrops or small clusters of these features).
Connectivity model	A modelling method for assessing dispersal.
Connectivity network	A network of habitat patches at the landscape-scale or regional-scale.
Gap-crossing distance threshold	Maximum (average) distance an individual will move between two structural connectivity elements.
Graphab	A software for modelling ecological networks using landscape graphs and least-cost paths (see Foltête et al. 2012)
Interpatch-crossing distance threshold	The maximum distance that individuals would move between patches provided there is some kind of structural connectivity element such as stepping-stones (for example, scattered paddock trees) or corridors.
Multi-criteria decision analyses	A method for explicitly considering the multiple criteria associated with decision-making.
General Approach to Planning Connectivity from Local Scales to Regional (GAP CLoSR) Framework	The name coined to the framework developed in this report that integrates Multi-Criteria Decision Analysis with connectivity modelling at local and regional scales.
Wildlife Corridor	At the regional scale this term commonly refers to connectivity between isolated patches of habitat supporting the dispersal of species along major ecological gradients (for example, latitudinal, mountains to ocean). It is analogous to connectivity network. At the landscape or site-scale it is used to refer to a specific type of linear structural connectivity element. To avoid confusion we have only use this term in the former case.

Chapter 1: Introduction

1.1. Connectivity modelling background

Human driven land-use changes have modified the extent and structure of native vegetation, resulting in fragmentation of native species habitat. Species movement through landscapes declines as habitat fragmentation increases. Decreased connectivity reduces population viability and increases extinction risk beyond that caused by habitat loss alone (Caughley 1994; Fischer & Lindenmayer 2006; Brook et al 2008). Land-use type in the matrix of land between habitat patches can strongly influence connectivity for species.

Current approaches to connectivity modelling include least-cost path analysis, circuit theory and graph theory, each of which model different aspects of connectivity in diverse ways (Urban and Keitt 2001; Adriaensen et al 2003; McRae et al 2008; Foltête et al 2012). Least-cost path analysis characterise non-habitat using dispersal costs which are intended to represent the energetic costs, difficulty, or mortality risk of moving across these areas (Adriaensen et al 2003; Sawyer et al 2011). Dispersal cost is determined by land cover characteristics, such as urbanisation, combined with species-specific dispersal probability over various distances. Least-cost pathways between patches of suitable habitat can be identified using cost-weighted distance analysis. The significance of patches within a connectivity network can be quantified using the graph theoretic approach and the calculation of network measures (Minor & Urban 2008; Rayfield et al 2011). In contrast, circuit theory conceptualises the landscape as a conductive surface within an electrical circuit, characterising 'resistance' to movement for every raster grid cell, considering current flow as analogous to individual movement probabilities (McRae et al 2008).

1.2. Ecological characteristics of dispersal

Our approach to characterising connectivity is based on a conceptual model of the ecology of dispersal outlined in a review by Doerr et al. (2010), which synthesised all available evidence on the relationship between structural connectivity and landscape-scale dispersal of Australian native faunal species. It identified three key important parameters, which can be used to characterise dispersal and are used in the GAP CLoSR framework (Lechner & Lefroy 2014; Lechner et al 2015b) (Figure 1):

1. Minimum patch size: The minimum area of habitat that can support a population.
2. Gap-crossing distance threshold: The maximum distance a species will cross between connectivity elements (such as scattered trees), which limit the distances of open ground (gaps) which individuals will move across.
3. Interpatch-crossing distance: The maximum distance that a species can move between patches as long as connectivity elements are within the gap-crossing distance (see minimum patch size).

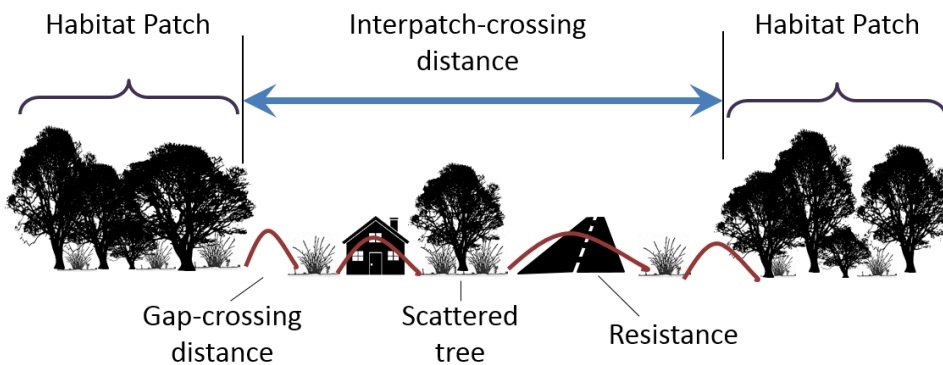


Figure 1: Conceptual model of fine connectivity behaviour where the likelihood of individuals moving between two patches is a property of two thresholds - the Interpatch-crossing distance and gap-crossing distance - as well as the dispersal cost of landcover features (such as roads).

A critical component of the GAP CLoSR framework is the inclusion of fine-scale dispersal behaviour that is often absent from many common connectivity modelling approaches. In order for species to move long distances between patches there is a need for structural connectivity elements such as corridors, or stepping stones to facilitate movement (Fischer & Lindenmayer 2002; Van Der Ree et al 2004).

1.3. Dispersal guilds as a focal conservation target

The choice of connectivity model and method for model analysis will depend on the focal conservation targets identified. Targets may include species, ecological communities or ecological systems. Targets might be selected because they represent biological diversity in decline, or entities protected by legislation (see The Nature Conservancy 2007).

Here, connectivity was modelled for groups of species (that is guilds), based on shared habitat and behavioural features, that is in terms of patch size, vegetation structure, dispersal characteristics. Our approach contrasts previous work in the Lower Hunter, where woody vegetation was treated equally for all species (Lechner et al; Lechner & Lefroy 2014) which was similar to the land-facet concept that has been used internationally (Alagador et al 2012; Brost and Beier 2012). It also contrasts approaches using single species models.

A guild is defined as a 'group of species whose members exploit similar resources in a similar manner' (Park & Allaby 2013). In this project, we are extending the guild concept to include species with similar dispersal characteristics as well as those that exploit similar resources in a similar manner. Using the guild approach we can integrate knowledge of single species into common groups providing greater generalisability of the results (Blaum et al 2011). Adopting single species approaches to understand many species' needs can be practically impossible to implement within a reasonable time frame and at a reasonable cost (Blaum et al 2011; Rudnick et al 2012).



In this study, we grouped species based on their dispersal characteristics defined by the conceptual model (Figure 1) and their habitat characteristics (Figure 2). The guild concept assumes that species can be grouped on their shared properties and it is likely that only certain combinations of attributes exist in nature. For example, it is unlikely that there are many species, which have both long interpatch-crossing dispersal thresholds and short gap-crossing distances.

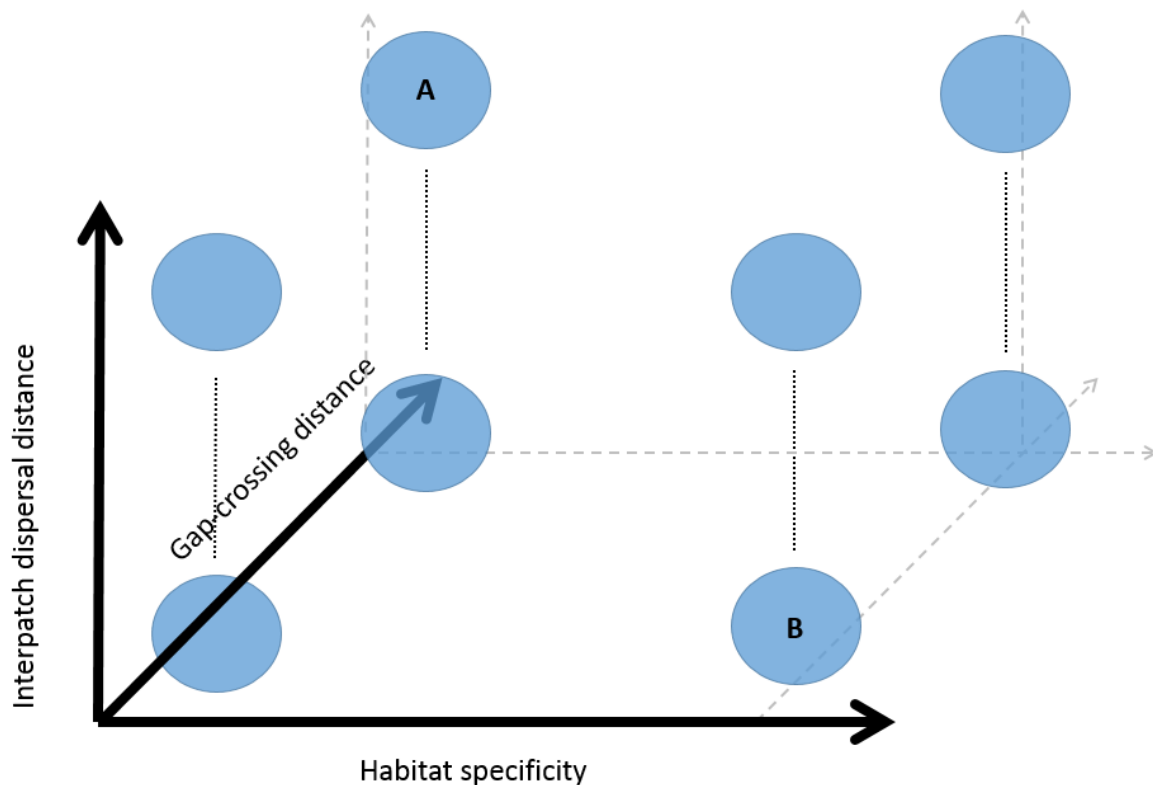


Figure 2: Extremes in dispersal behaviour and habitat suitability that may potentially be represented by the 'Dispersal guild' concept. A) species with narrow habitat requirements and thus little available habitat (habitat specialists), long-distance dispersers. B) Species with general habitat requirements, short maximum dispersal distances.

1.4. Objectives

The objective of this study is to understand connectivity for mammal fauna in the Tasmanian Midlands, to assist conservation planning. A secondary goal is to identify the combinations of mammal habitat/dispersal types that occur, and to identify species' connectivity networks that are based on characteristics of the dispersal guilds.

By modelling dispersal guilds we can capture a range of responses to fragmentation and thus identify those groups of species that are most impacted by fragmentation by different species types, and those that might benefit from habitat restoration. In addition to developing the

dispersal guild concept, we describe a process for engaging experts in characterising species' habitat needs and dispersal distances, to classify dispersal guilds.

Finally, connectivity mapping based on the dispersal guild concept was compared with general connectivity modelling where connectivity was assessed between native vegetation and between woody vegetation as in the previous Lower Hunter study without considering habitat requirements or dispersal distances for local species (Lechner & Lefroy 2014). This study focuses only on the dispersal guild concept as a conservation planning target. Tools and techniques that could be applied to landuse planning based on dispersal guilds are not explored in this report, but can be found in the report and publications on connectivity in the Lower Hunter region (Lechner & Lefroy 2014; Lechner et al 2015b; Lechner et al 2015a)

2.0 Methods

2.1. Study area

The Tasmanian Northern Midlands is an agricultural region located in a flat low-lying basin (Figure 3). It has a long history of agriculture and is one of the oldest livestock-grazed regions in Australia (Gadsby et al 2013). Wool continues to be the largest industry in the region, however agricultural production has diversified in recent decades to intensive agricultural crops such as peas, cereal, potato and poppies (Mooney et al 2010; Gadsby et al 2013). A planned expansion of irrigation schemes in the region will likely lead to greater agricultural intensification across the landscape (Gadsby et al 2013).

The Tasmanian Midlands is one of fifteen designated Australian Biodiversity Hotspots (Figure 3), including numerous endemic plants and nationally and state listed threatened plants and animals (Department of Environment 2014). However, widespread land clearing has left native vegetation highly fragmented with mostly small and scattered remnants remaining. The region's biodiversity faces many other threatening processes including weed invasion, salinity, rural tree decline and degradation of native grassland due to inappropriate grazing (Mooney et al 2010).

Our study area includes the Tasmanian Northern Midlands IBRA with some adjoining areas that have ecological affiliation with the midlands area according to the Tasmanian Land Conservancy (TLC) (see Figure 3).

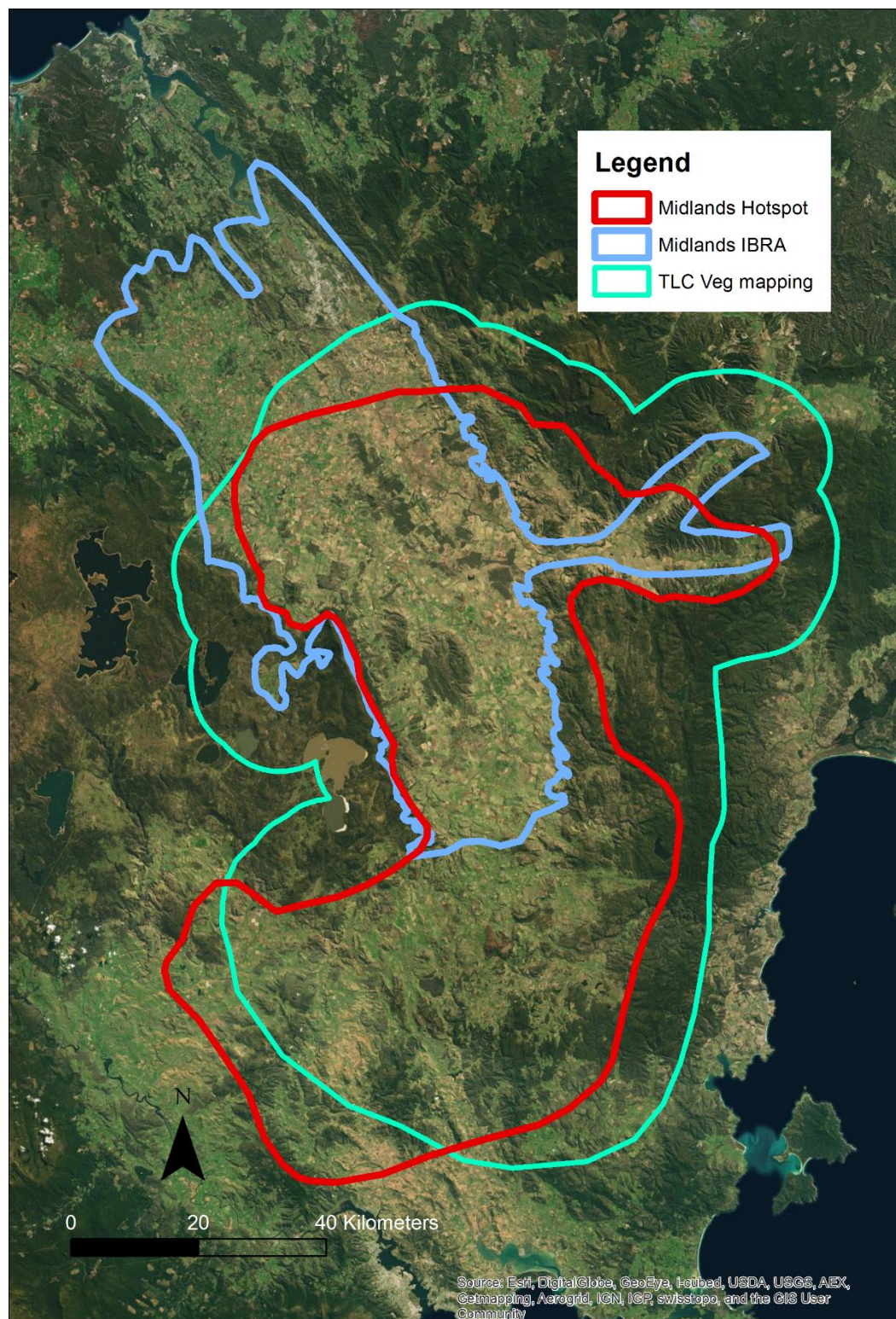


Figure 3: True colour remote sensed imagery with midlands biodiversity hotspot region, new the Tasmanian Northern Midlands Interim Biogeographic Regionalisation for Australia (IBRA) region and Tasmanian Land Conservancy (TLC) vegetation structure layer. The TLC vegetation structure layer was uses in this study.

2.2. Stakeholder and expert engagement

The application of the GAP CLoSR framework to the Tasmanian Midlands provided a greater opportunity for stakeholder engagement than was possible during the pilot study undertaken in the Lower Hunter. Stakeholders and experts were engaged in a series of four workshops and multiple one-on-one discussions to parameterise the model and identify mammal dispersal guilds (see below).

*Individuals and Groups Engaged**

The following individuals either participated in the workshops or provided expert opinion. We are grateful for their contributions.

Amy Koch – Forest Practices Authority
Bronwyn Fancourt - UTAS
Chris Johnson - UTAS LaP Hub
Daniel Sprod – Tasmanian Land Conservancy (TLC)
Erik Doerr – CSIRO
Felicity Faulkner - DPIPWE
Gareth Davies – UTAS
Kirsty Dixon– UTAS
Kirstin Proft– UTAS
Louise Gilfedder - Department of Primary Industries, Parks, Water and Environment (DPIPWE) and UTAS LaP Hub
Mat Appleby – Bush Heritage
Menna Jones (UTAS LaP Hub)
Neil Davidson – Greening Australia
Nick Fitzgerald – Greening Australia
Oberon Carter - DPIPWE and UTAS LaP Hub
Rebecca Harris - UTAS LaP Hub
Sarah Maclagan - Deakin University
Shannon Troy - DPIPWE
Stewart Nicol - UTAS
Veronica Doerr - CSIRO

* This report represents the viewpoint of the report authors only and not those of the stakeholders or experts engaged.

2.3. Modelling fine-scale connectivity

In this paper we use the General Approach to Planning Connectivity from LOcal Scales to Regional (GAP CLoSR) framework (Lechner & Lefroy 2014). The GAP CLoSR framework describes how, through scenario analysis, connectivity models can support land-use planning. The framework characterises connectivity based on dispersal behaviour of species (or species groups) and includes:

- i) A workflow that starts with identification of key habitat needs and dispersal parameters and describes how to pre-process spatial data (Figure 4);
- ii) GIS tools for pre-processing spatial data based on these parameters; and
- iii) A method for running these spatial data within existing connectivity modelling software, and for interpreting outputs for conservation planning.

The connectivity model used depends on the spatial scale of investigation. The regional scale model is based on Graphab (Foltête et al. 2012), a graph-network connectivity model that uses least-cost paths, and incorporates dispersal behaviour. The local scale model uses Circuitscape, a model that uses circuit theory to characterise connectivity for all pixels within the region of interest (McRae et al 2008). Graphab is used to characterise connectivity between patches based on a threshold distance between adjacent patches. Where connectivity exists between patches a single optimal least cost path is identified between patches. In contrast, Circuitscape characterises connectivity for all pixels in the area of interest between all dispersal sources (patches or groups of patches) but does not allow dispersal thresholds to be used. Details of the modelling method can be found in (Lechner & Lefroy 2014; Lechner et al 2015b). In this report, we do not include Circuitscape outputs, however, we recognise that it is an important part of the GAP CLoSR method.

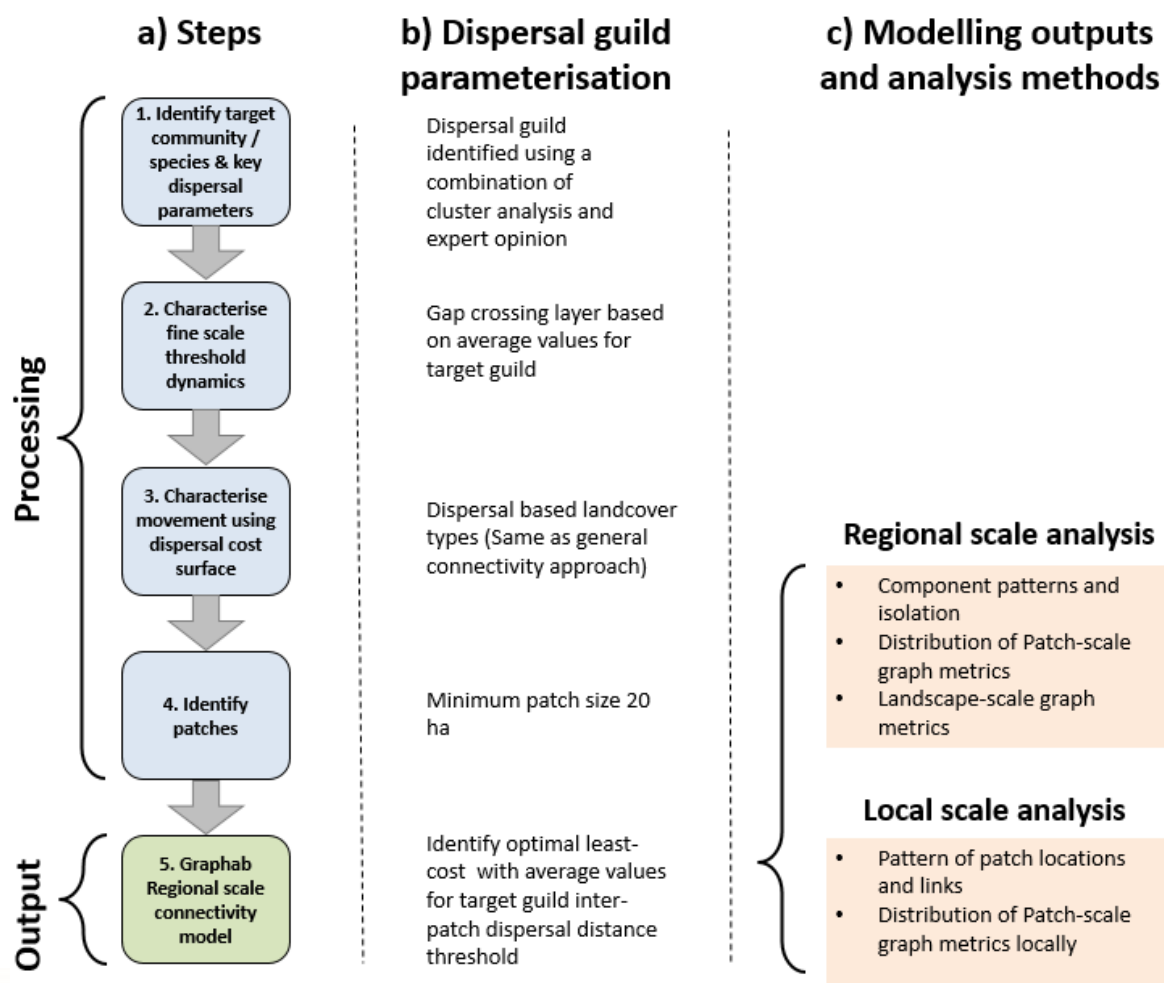


Figure 4: Flow diagram describing the steps used in parameterising the general connectivity model. These steps can be adapted for any focal conservation target.

2.4. Focal conservation target

For this study, we mapped connectivity for the following focal targets:

1. A general approach connecting vegetation groups based on TASVEG 3.0 communities as opposed to individual species – similar to the original method proposed and assessed in the Lower Hunter.
2. A new dispersal guild approach mapping connectivity for a range of ground dwelling mammals grouped into dispersal guilds.

The next two sections (Sections 2.5 and 2.6) describe the parameterisation of the general approach and the dispersal guild approach. Section 2.7 then describes the parameterisation of the landcover map in order to create the resistance surface for both methods and finally Section 2.8 summarises the analysis method. The final two sections (Sections 2.7 and 2.8) are common to the general approach and the dispersal guild approach.

2.5. General approach

2.5.1. Identify TASVEG 3.0 communities

We modelled connectivity for TASVEG 3.0 (DPIPWE 2013) vegetation communities for three subsets of the TASVEG 3.0 data: All vegetation including exotics, All Native vegetation and All woody vegetation (Table 1).

The subsets describe a range of ways of representing habitat relevant to fauna:

All vegetation including exotics: Species dependent on any form of vegetation including gorse, not found in predominantly cleared areas such as urban or agricultural areas.

All Native vegetation: Species dependent on any form of native vegetation, not found in disturbed areas such as plantation forest or cleared areas such as urban or agricultural.

All woody vegetation: Species found within woody vegetation areas only such as woodlands and forests including exotic plantations. Similar to the conservation target used in the Lower Hunter.

TASVEG 3.0 is a digital map of Tasmania's vegetation, including sub-Antarctic Macquarie Island. The map characterises the extent of more than 156 vegetation communities captured at a nominal scale of 1:25,000. Mapping was conducted primarily using photographic interpretation of aerial photography along with field verification of representative polygons undertaken where practicable.

Table 1: TASVEG 3.0 vegetation communities for three different subsets based on a general approach. Where 'n' means exclude and 'y' means include. All TASVEG 3.0 communities not described in this Table are included.

Landcover	TASVEG 3.0 code	All vegetation including exotics	All Native vegetation	All woody vegetation
Cleared	FAG	n	n	n
Plantation	FPL	y	n	y
Weeds	FWU	y	n	y
Easements	FPE	n	n	n
	FPU	y	n	y
Miscellaneous	FUM	n	n	n
Urban	FUR	n	n	n
Water	OAQ	n	n	n
Marram (Exotic grass sp. - Not in midlands)	FMG	n	n	n
Spartina (Exotic grass sp. - Not in midlands)	FSM	n	n	n
All grassland	G**	y	y	n
All wetland	A**	y	y	n



2.5.2. General approach parameterisation

For each of the TASVEG 3.0 subsets we modelled connectivity using the default interpatch-crossing distance threshold of 1100 m identified by Doerr et al. (2010), and used previously in the Lower Hunter GAP CLoSR analysis (Table 2). The gap-crossing threshold distance was not modelled as suitable fine-scale data that was conceptually accurate and provided a reasonable representation for modelling structural connectivity elements that correspond to TASVEG 3.0 communities such as grasslands was not available (Table 2). Both patch size and resistance was modelled based on a parameterisation by experts described in Section 2.7.

Table 2: Parameterisation of dispersal characteristics using TASVEG communities

Parameters	Values	Source
Patch size	30ha	Workshop
Inter-patch distance threshold	1100 m	Doerr et al. 2010
Gap crossing distance	Not included	-
Resistance	Default	Workshop

2.6. Dispersal guild approach

2.6.1. Workshop flow

The dispersal guild approach was parameterised using expert assessment in conjunction with information from the literature and a cluster analysis. All aspects of the parameterisation and the validation the cluster analysis were driven by expert judgement from ecologists with site and species expertise (Figure 5). As well as performing the analysis the role of the modeller was to ensure that the expert judgments match GAP CLoSR conceptual model of connectivity through facilitating workshop discussions. This process was conducted over a series four workshops, where each workshop was followed by desktop analysis.

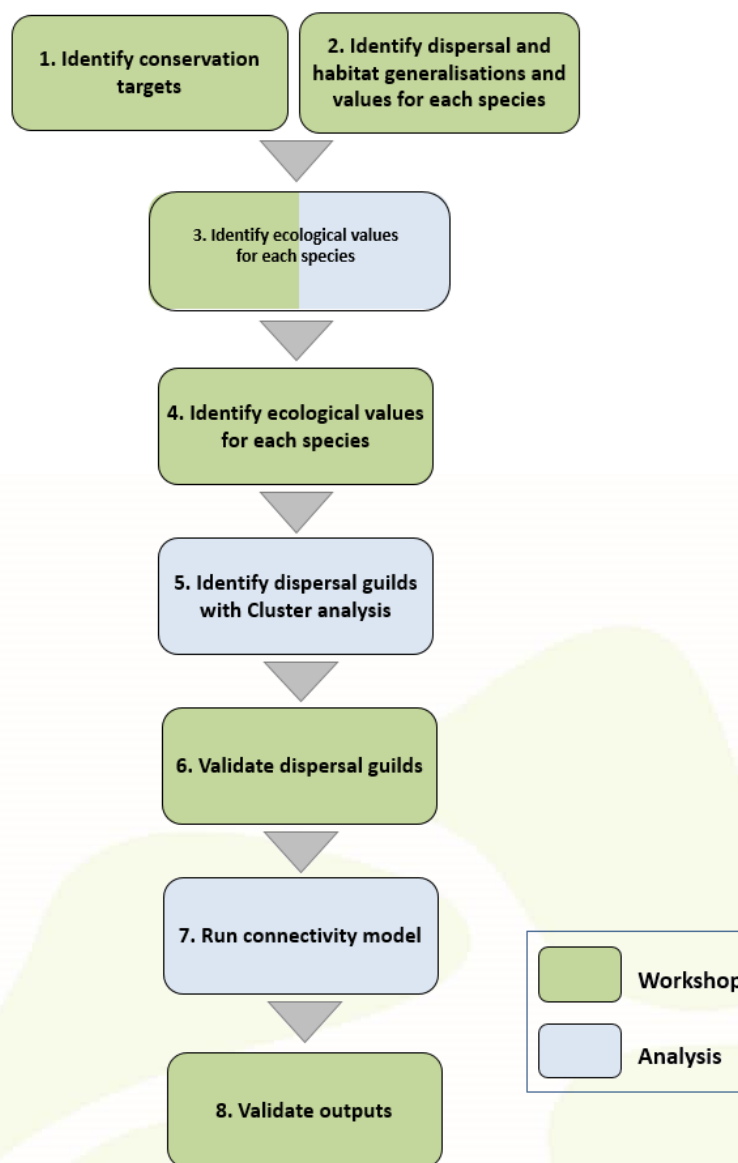


Figure 5: Sequence of workshops and desktop analysis for deriving and modelling dispersal guilds.

2.6.2. Identify focal conservation targets

An initial workshop was run to identify species of importance for conservation in the Tasmanian Midlands. This workshop identified ground-based mammals as a key target group for conservation (

Table 3). The final list of species was then limited to those that depend only on non-grassland, mainly woody or shrubby vegetation. In the Tasmanian Midlands, native grasslands and the original woody vegetation communities have been fragmented by clearance from agriculture and conversion to non-native pastures or degraded native vegetation. Addressing this type of fragmentation is the goal of the dispersal guild approach in the Tasmanian Midlands. Consequently, species such as the Eastern Quoll that appear to readily utilise cleared areas such as non-native pastures were not included in this approach as addressing a lack of connectivity is likely not to be an important factor for the conservation of these species.

Table 3: Key ground-based mammal species identified by workshop participants.

Common name	Species name	Weight (kg)
Brush tailed possum	<i>Trichosurus vulpecula</i>	3
Eastern Pygmy Possum	<i>Cercartetus nanus</i>	0.04
Eastern-Barred Bandicoot	<i>Perameles gunnii</i>	0.6
Little Pygmy Possum	<i>Cercartetus lepidus</i>	0.01
Long-tailed Mouse	<i>Pseudomys higginsii</i>	0.08
Ring tailed possum	<i>Pseudocheirus peregrinus</i>	1.1
Southern Brown Bandicoot	<i>Isodon obesulus</i>	1.05
Spotted-tail Quoll	<i>Dasyurus maculatus</i>	4
Swamp rat	<i>Rattus lutreolus</i>	0.1
Tasmanian Bettong	<i>Bettongia gaimardi</i>	2
Tasmanian Devil	<i>Sarcophilus harrisii</i>	12
Water Rat	<i>Hydromys chrysogaster</i>	0.6

2.6.3. Identify dispersal and habitat generalisations and values for each species

After the target species was identified the next step was to qualitatively assess what generalisation can be made in terms of habitat and dispersal behaviour. At the time of this report species distribution modelling did not exist within the Tasmanian Midlands at a suitable resolution. Instead, an expert based approach was used to identify the type of habitat that each species uses. This approach was used to identify commonalities between species rather than

accurately identifying suitable habitat for each species as the final dispersal guilds were intended to represent a group of species rather than a single species (in most cases).

Through an expert engagement process at workshops, we determined that we could summarise habitat and connectivity elements as either above 1 m (for example, trees) or below 1 m (for example, undergrowth) (Table 5). Furthermore, vegetation for habitat and vegetation for connectivity needed to be differentiated. This choice was also guided by readily available TLC vegetation mapping data. We then used a combination of information from the literature and expert opinion to identify ecological information for each species identified in the previous step (Table 4).

Table 5: Parameterisations identified by expert workshop

Habitat (patches)	
Habitat cover over 1 metre	Smaller and larger trees with suitable nesting/perching/resting places.
Habitat cover under 1 metre	Smaller trees and shrubs/large graminoids with suitable nesting/hiding/resting places.
Rule-set	AND function for example, If Habitat cover over 1 metre = Yes and Habitat cover under 1 metre = Yes, species require both and won't be found where one exists in isolation.
Minimum patch size	Minimum area of patch with suitable cover, for species to commonly breed and raise young. Patch size can be thought of in simple terms of 'in what patch sizes would this species not be commonly found?'. We do not consider the multiple ecological issues that may affect this value such as habitat quality or emigration. If the species uses native vegetation and the matrix, patch size should be considered in terms of what area of native vegetation is required.
Connectivity elements (for example, Stepping stones and corridors that provide cover)	
Stepping stones and corridors with cover over 1 metre	Trees or even man-made structures with suitable perching/resting places.
Stepping stones and corridors with cover under 1 metre	Shrubs/large graminoids or even man-made structures with suitable hiding/resting places.
Rule-set	OR function for example, Stepping stones and corridors with cover over 1 metre = Yes and Stepping stones and corridors with cover under 1 metre = Yes, species will use either, whatever is available, it is not necessary that both occur together.
Minimum size	There is no minimum area.
Dispersal distances	
Interpatch-crossing distance threshold	Distances between patches
Gap crossing distance threshold	Distance between structural connectivity elements

2.6.4. Identify dispersal guilds using cluster analysis and expert workshop

In this step, the dispersal guilds were identified using cluster analyses to explore patterns in dispersal and habitat parameters associated with each species and their relationship between each other. The two cluster analysis methods were a hierarchical clustering analysis in R using the *pvcust* package version 1.2-2 (Suzuki 2013) and Partitioning Around Medoids (PAM) algorithm (Kaufman & Rousseeuw 1990) in the *Cluster* package for R 2.15.2 (See appendix for R code). A hierarchical cluster analysis is based on an agglomerative algorithm and produces a dendrogram or tree diagram used to illustrate the arrangement of the clusters. The PAM cluster analysis method groups objects into clusters based on the number of clusters need to be specified *a priori*. In our study a range of cluster numbers were tested. To determine the stability of the clustering, for each number of clusters the average silhouette width was calculated –a standard measure of cluster isolation. High values of average silhouette width is one way to identify the appropriate number of clusters within which the data naturally falls. PAM uses a medoid as its measure of cluster centre as opposed to a centroid based on mean values. This method is more robust in the presence of noise and outliers than mean-based approaches (for example, k-mean). The two cluster analysis methods have very different approaches and different graphical outputs. Using two approaches allowed us to test the consistency of the clustering.

Before the cluster analysis could be conducted, categorical variables such as habitat above and below 1 m needed to be converted to a matrix of zeros and ones as all inputs had to be numerical. The categorical data were then combined, and singular value decomposition (SVN) was applied to create new continuous variables (as both cluster analysis methods require all variables to be continuous), each of which represents a composite of the original datasets.

The outputs from both cluster analysis methods were then presented at an expert workshop and these clusters were refined manually into the final dispersal guilds. The cluster analysis provides a sensible graphical way of summarising the complex similarity and dissimilarity of ecological parameters between species that may be difficult to identify from an expert panel looking only at the raw data.

2.7. Characterise habitat and structural connectivity elements using spatial data

The TLC vegetation mapping data was used to characterise vegetation for habitat and connectivity elements. This unpublished spatial data was derived through photographic interpretation, with the aid of TASVEG 3.0 mapping (Figure 6). The resolution was much greater than the spatial resolution of 1:25000 for the TASVEG 3.0 mapping. The data describes vegetation over 1 m at a range of tree densities and vegetation under 1 m (Table 6).

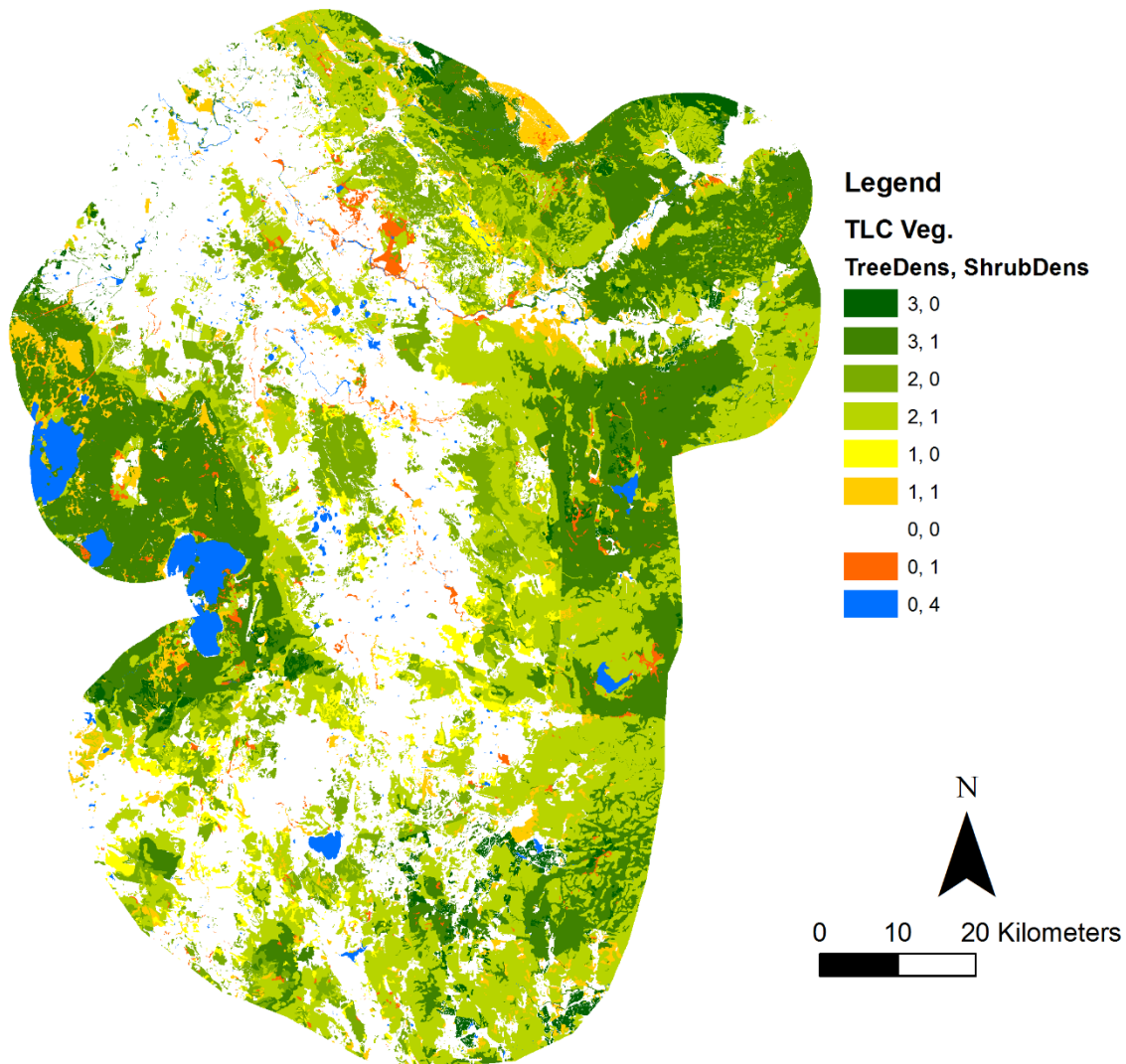


Figure 6: Tasmanian Land Conservancy (TLC) vegetation structure layer used for characterising habitat and structural connectivity elements with Tree and Shrub combinations identified.

Table 6: Tasmanian Land Conservancy (TLC) vegetation mapping classes and reclassification according to dispersal guild approach.

Vegetation over 1 m	Reclassification	Vegetation under 1 m	Reclassification
<i>Tree density</i>		<i>Shrub Density</i>	
<2%	Absent	None	Absent
1 = 2- 10%	Present	None	Present
2= 10-30%	Present		
3=>30%	Present		

The above and below 1 m vegetation classes were then converted into two binary layers (Table 6). These binary layer were combined characterise cover for habitat and for connectivity (Figure 7):

Vegetation over 1 m

Vegetation under 1 m

Vegetation over 1 m AND Vegetation under 1 m – overlap of both vegetation layers

Vegetation over 1 m OR Vegetation under 1 m – union of both vegetation layers

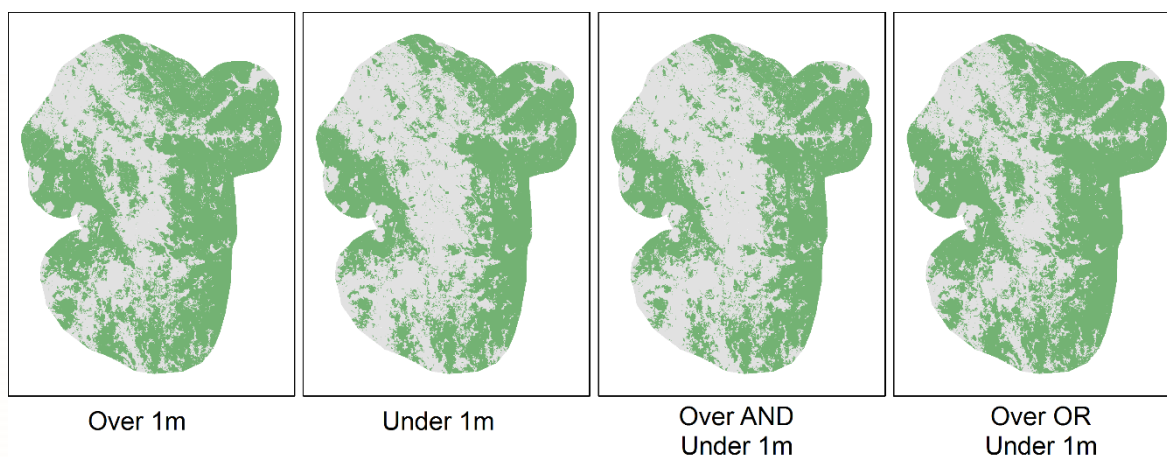


Figure 7: Four combinations of the TLC vegetation structure layer used for characterising habitat and structural connectivity elements.

2.8. Dispersal resistance surface

The dispersal resistance surface characterises how landcover between habitat patches reduces or prevents movement. It is a result of combining the gap crossing layer and the landcover resistance surface.

2.8.1. Gap crossing layer

The gap-crossing distance threshold distance layer is simulated through the creation of the gap-crossing layer. The gap-crossing layer identifies distances between structural connectivity elements and patches beyond the movement threshold that then act as barriers to dispersal. The input vegetation layers are buffered by half of the gap-crossing distance threshold (Figure 8). If structural connectivity elements or patches are within the gap-crossing distance threshold, it is possible that buffers will touch or overlap connectivity between patches. Areas mapped outside the buffer area describe areas in which dispersal cannot take place.

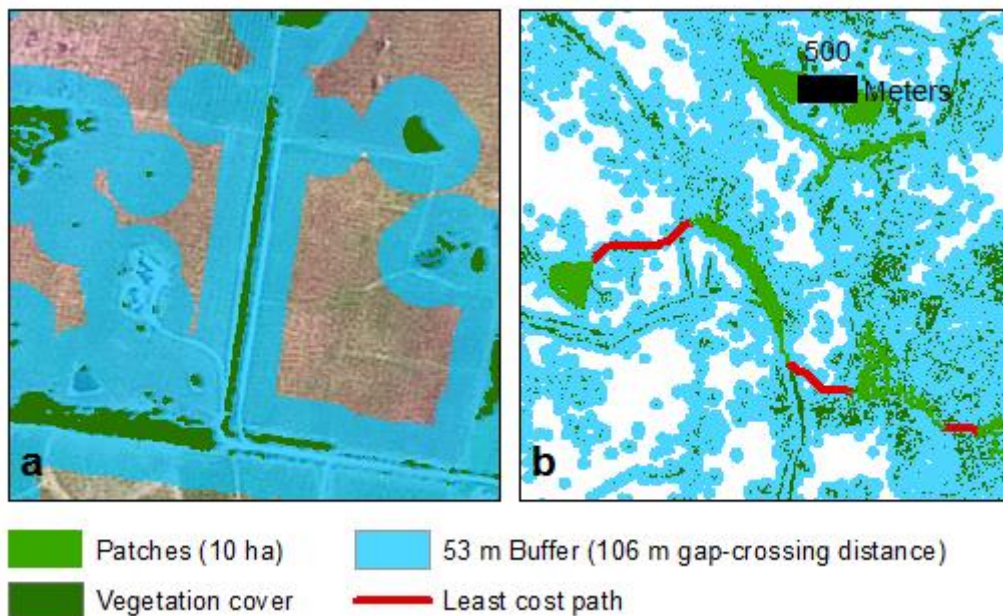


Figure 8: Example of the gap crossing layer (adapted from Lechner et al. 2015b). Vegetation is buffered by half the gap-crossing distance threshold. a) 53m buffer around vegetation to simulate 105 m gap-crossing distance. b) gap-crossing layer with example of how least-costs paths are modelled.

2.8.2. Landcover resistance surface

Resistance to dispersal between patches is characterised by increasing the movement costs based associated with land cover. For example, if land cover with high dispersal resistance doubled the movement cost, the interpatch-crossing distance threshold would be reduced from 1.1 km to 550 m. In the Tasmanian Midlands, we used generic land cover classes with dispersal costs assigned to each pixel based on expert opinion for small and large mammals (Table 7).

Table 7: Land cover dispersal costs and corresponding pixel value for a resistance surface with a 50 m pixel size for small and land mammals.

Landuse Category	Large mammals dispersal cost	Small mammals dispersal cost	Large mammals Resistance layer pixel values (m)	Small mammals Resistance layer pixel values (m)
Hydrology	200%	200%	100	100
Intensive agriculture	200%	200%	100	100
Intensive landuse	333%	333%	166	166
Railways	167%	500%	84	250
Roads	167%	500%	84	250
Urban - CBD	500%	500%	250	250
Urban - Suburban	333%	333%	166	166
No resistance	100%	100%	50	50

We used the 1:50 000 Land Use Tasmania spatial dataset for the spatial characterisation of resistance (see appendix). The Land Use Tasmania maps was attributed to ALUM 7 standards as at summer 2009/2010. It was created from fieldwork, consultation with local experts, current 1:25000 vector datasets and 2009/2010 RapidEye imagery. The minimum mappable area was 10ha. An update to the landcover map was supplied by DPIPW, which identified changes to irrigation (especially farms with pivot irrigation) that have occurred since the previous official version in 2013. The ALUM 7 landcover classes were then converted into landcover classes that correspond to general land cover classes identified at the expert workshop (Figure 9).

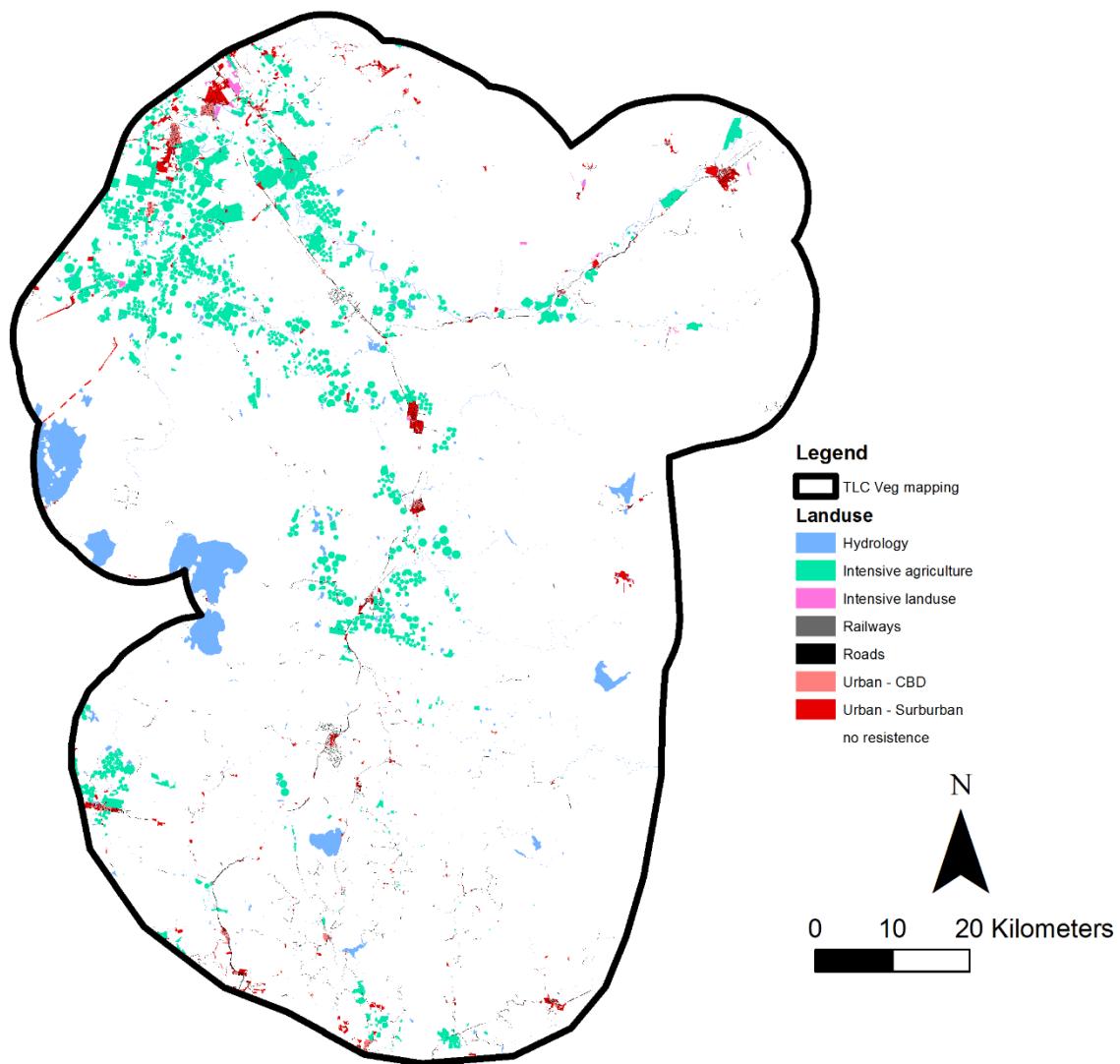


Figure 9: Tasmanian Land use layer used to derive the resistance surface.

2.8.3. Calculating dispersal resistance surface

In the final step, the dispersal cost surface was created by combining the binary gap-crossing layer with the resistance surface based on land cover. The dispersal cost pixel values assigned is a function of: a) pixel size (for example, if the pixel size is 30 m and there is no resistance the cost should be 30 m); b) land cover resistance (200% resistance means a pixel size with of 30 m will have a value of 60 m); and c) the presence of structural connectivity elements identified with the gap-crossing layer.

A summary of the processing rule-set is:

- Structural connectivity elements take precedence over all other land cover classes, because dispersal cannot occur in the absence of structural connectivity;
- Barriers due to land cover will have infinite cost regardless of their physical size in relation to the aggregated pixel size - this processing step is important to ensure linear features that represent barriers are actually modelled as barriers and there are no discontinuities as a result of the aggregation process. In the current modelling for the Tasmanian Midlands there were no landcovers that formed a barrier. However, such scenario testing is possible.
- Barriers due to areas outside of the gap-crossing threshold shall be assigned to a pixel where they are in the majority.
- The dispersal cost for a single aggregated pixel is calculated as an average of all land covers except if a barrier due to land cover or gap-crossing distance is present as described in the above steps.

The result is a layer that recognises threshold dynamics by ensuring there is no dispersal where gaps are too large between connectivity elements, but still models cumulative costs where dispersal is considered possible but may be impeded by land use.

2.9. Regional connectivity model using Graphab

The graph theoretic approach is used within the Graphab software (Foltête et al 2012) to represent the landscape as a set of patches within a network connected by least-cost analysis which identifies the single most optimal link between patches based on cumulative cost in relation to land cover resistance (Minor & Urban 2007; Dale and Fortin 2010; Etherington and Penelope Holland 2013). Patches that are connected to each other but isolated from other patches can be considered as components, or groups of interconnected patches. Whether a patch is linked to another patch will depend on:

Distances between patches

Interpatch-crossing distance threshold

The resistance of the landcover

Presence of structural connectivity at the gap-crossing distance thresholds.

The two inputs into the Graphab software were the habitat and the dispersal cost surface. The original pixel size were aggregated to 50 m. We found that 50 m was the finest pixel size that could be processed by the Graphab connectivity software in the Tasmanian Midlands.

A range of methods can be used to interpret the outputs of the connectivity model (Figure 10). They include visual methods based on the patterns of connections and components to quantitative methods using graph metrics (Rayfield et al 2011). Patch-scale graph metrics can be calculated for each patch to describe the role of a patch in providing connectivity for a whole network. In contrast, landscape-scale graph metrics are calculated as a single value intended to

describe connectivity for the whole landscape and are useful for comparisons between landscapes or scenarios (see Lechner & Lefroy 2014 for more detail).

For this report, we have focused on patch isolation by identifying groups of patches that are linked to each other but isolated from other groups of patches. These groups of interlinked patches are known as components. The patterns in the size and shape of the components can be used to characterise fragmentation and locate barriers to connectivity and isolation. At the regional scale, large components represent areas where dispersal is possible, while smaller components characterise highly fragmented areas that act as dispersal barriers.

Regional scale analysis

- Component patterns and isolation
- Distribution of Patch-scale graph metrics
- Landscape-scale graph metrics

Local scale analysis

- Pattern of patch locations and links
- Distribution of Patch-scale graph metrics locally

Figure 10: Regional and local scale analysis using the graph theoretic approach available with the Graphab software.

We also calculated a number of landscape-scale graph-metrics describing component characteristics: mean size of components (km²), size of the largest component (km²) and number of components and graph-theoretic dispersal metrics (Minor & Urban 2008; Rayfield et al 2011). Patch-scale were not processed or analysed for this report.

3.0 Results

3.1. General approach with TASVEG 3.0 Communities

The assessment using the general approach based only on patch size and the interpatch-crossing distance found that the majority of the vegetation within the Tasmanian Midlands is connected with the exception of areas to the north and a small part of the central region. Visually connectivity was greatest for 'All vegetation including exotics' and least for 'All woody vegetation'. The total amount of vegetation was the greatest for the former at 6294 km² and the least for the latter at 5681 km² (Table 8). The visual differences in connectivity patterns between the three TASVEG 3.0 subsets were also reflected in the total number of patches and components and the graph metrics (Class Coincidence Probability, Expected Cluster Size and IIC). For example, 'All vegetation including exotics' had an IIC of 0.120 versus 'All native vegetation' with 0.105 and 'All woody vegetation' with an IIC of 0.082. The IIC metric is defined as the probability that two points randomly placed within a landscape fall into habitat areas that can be reached. Values for this metric increase with greater connectivity from zero to one. The definitions of all the graph metric values can be found in the previous Lower Hunter report (Lechner & Lefroy 2014).

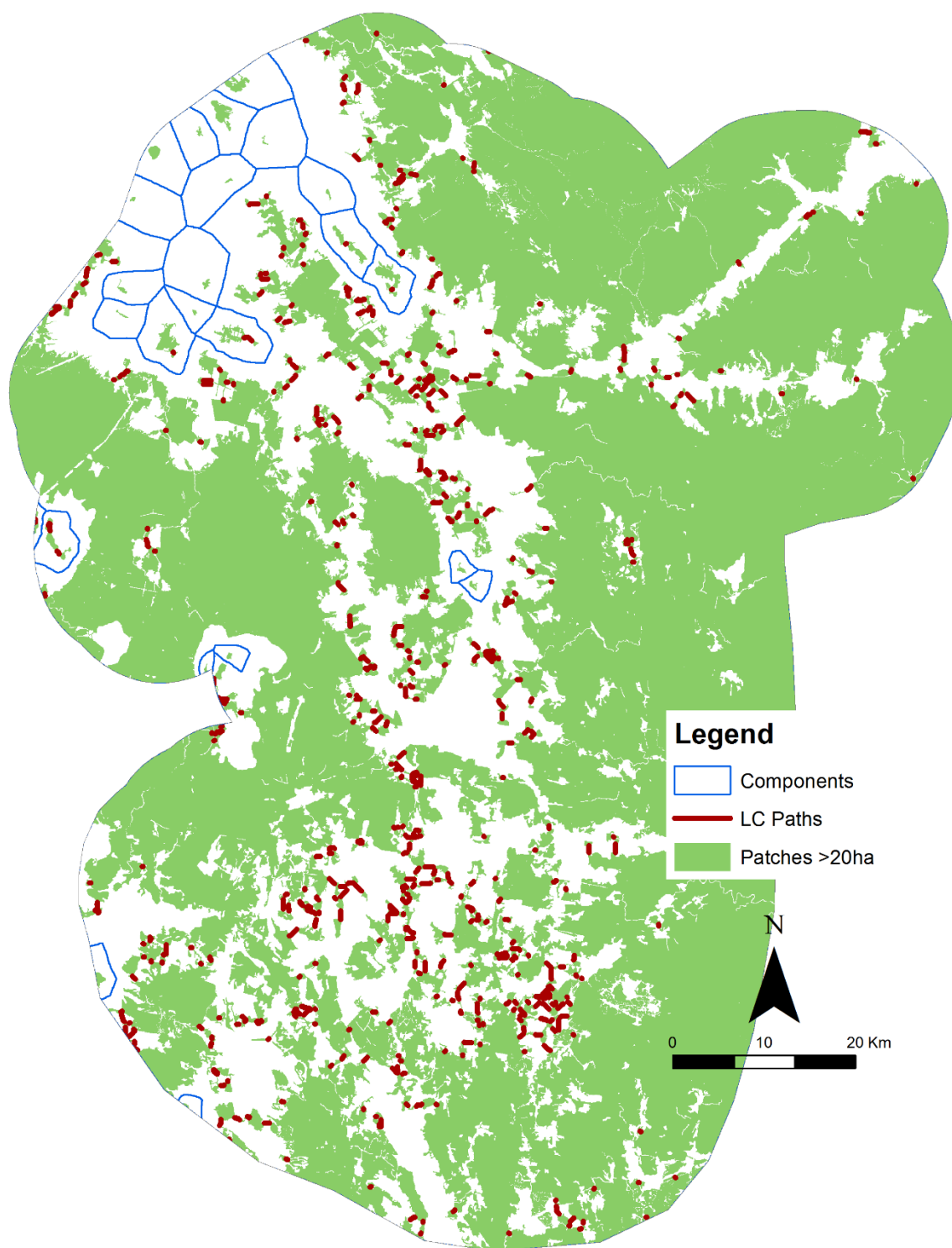


Figure 11: Regional-scale connectivity analyses of TASVEG 3.0 'All vegetation including exotics' based on least-cost (LC) paths for patches greater than 20 ha using Graphab software. Component boundaries in dark blue are located at the midpoint between patches.

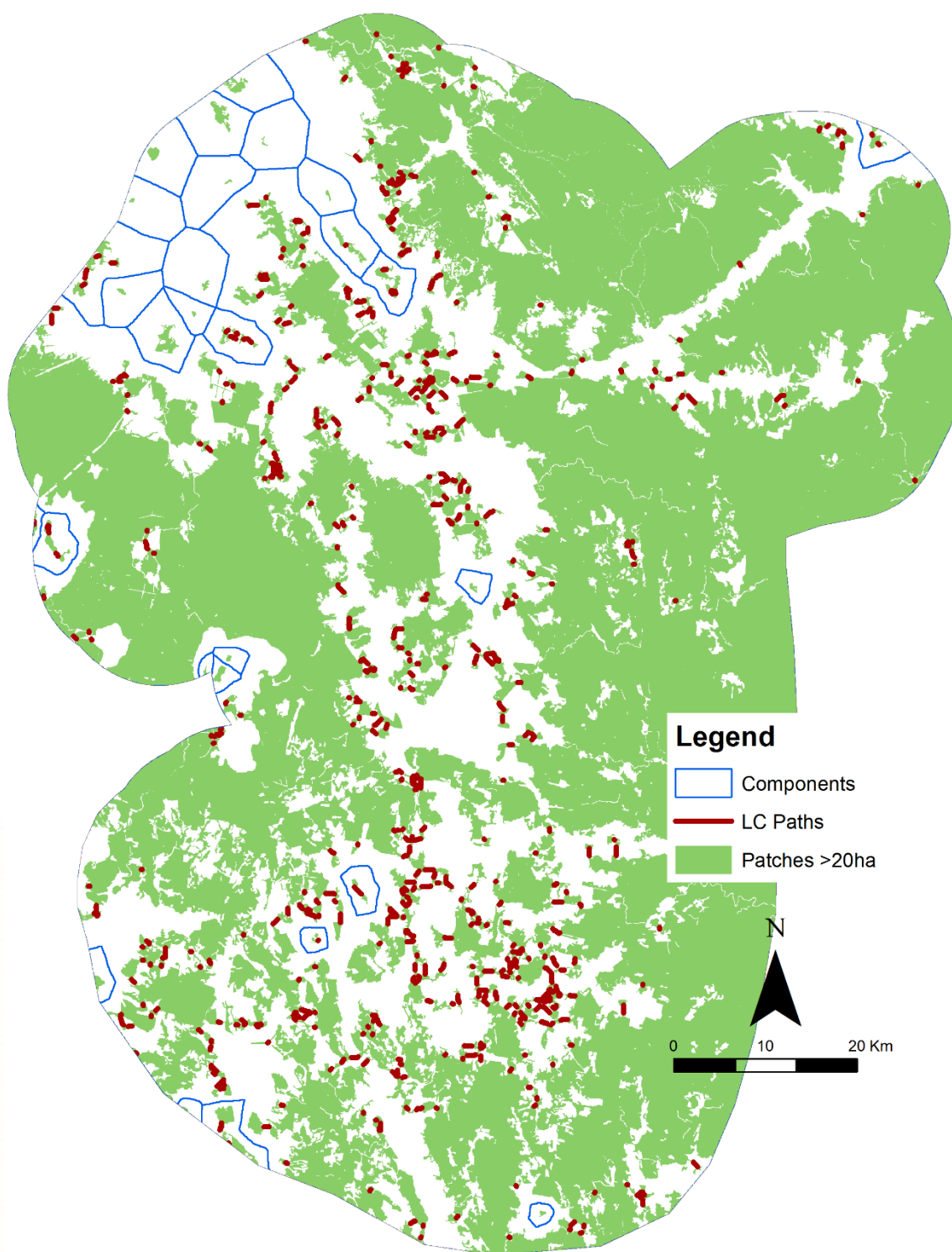


Figure 12: Regional-scale connectivity analyses of TASVEG 3.0 'All native vegetation' based on least-cost (LC) paths for patches greater than 20 ha using Graphab software. Component boundaries in dark blue are located at the midpoint between patches.

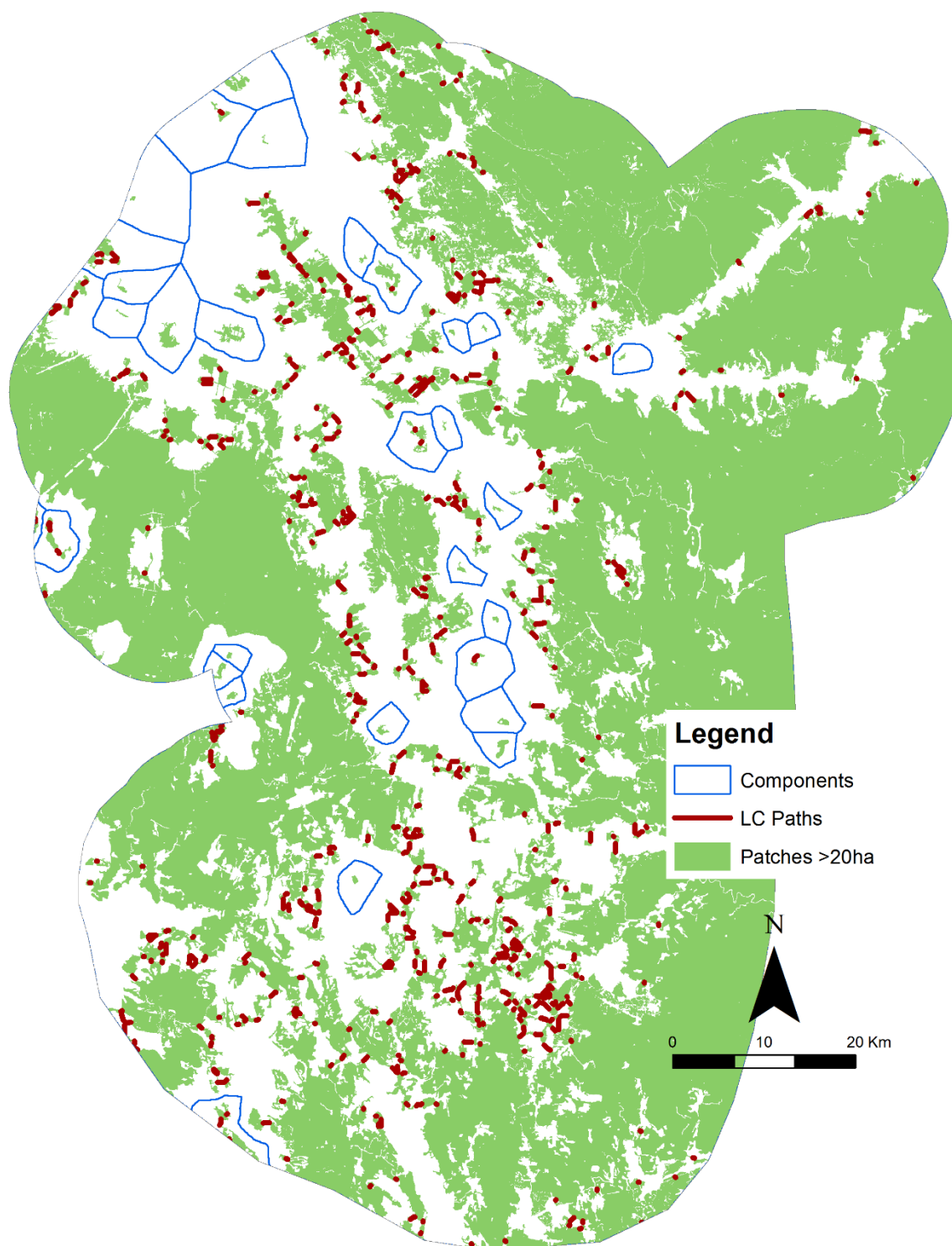


Figure 13: Regional-scale connectivity analyses of TASVEG 3.0 'All woody vegetation' based on least-cost (LC) paths for patches greater than 20 ha using Graphab software. Component boundaries in dark blue are located at the midpoint between patches.



Table 8: Landscape-scale characteristics for the three habitat parameterisation approaches and the five dispersal guilds.

Graph Metric	All vegetation including exotics	All Native vegetation	All woody vegetation	Large Carnivore Tasmanian Devil	Large Carnivore Spotted-tail Quoll	Not Woodland dependent and riparian	Dense ground cover dependent	Arboreal
Mean Size of Components (km ²)	253	206	184	5461	1411	22	28	20
Size of Largest Component (km ²)	6294	5943	5681	5461	5632	2583	2539	4089
Number of Components	25	29	31	1	4	221	166	297
Patches	372	394	397	21	76	448	278	1393
Total area (km ²)	6324	5983	5719	5461	5644	4810	4681	5876
Class Coincidence Probability	0.990	0.986	0.987	1.000	0.996	0.355	0.362	0.543
Expected Cluster Size	6263	5902	5644	5461	5620	1708	1694	3193
IIC	0.120	0.105	0.082	0.090	0.091	0.040	0.038	0.069

3.2. Dispersal guild approach

3.2.1. Identify dispersal and habitat values for each species

The values for the dispersal and habitat parameters for each species were derived by engaging experts in a workshop environment and consulting the literature. The literature review found very few examples of empirical studies that could be used to confidently characterise dispersal distances for single species. Thus, the final values presented in Table 9, were primarily driven by expert opinion. These values were only approximations and the relative values between species versus the absolute values are likely to be more accurate.

Table 9: Tasmanian Midlands fauna species (n=12) and their dispersal and habitat characteristics identified by experts and the literature.

Common name	Species name	Weight (kg)	Habitat - Over 1 m	Habitat - Under 1 m	Minimum Patch size (ha)	Interpatch distance (m)	Structural connectivity elements - Over 1 m	Structural connectivity elements - Under 1 m	Gap crossing (m)	Cluster group
Tasmanian Devil	<i>Sarcophilus harrisii</i>	12	Yes	No	800	10000	Yes	Yes	2000	Large Carnivore - Tasmanian Devil
Spotted-tail Quoll	<i>Dasyurus maculatus</i>	4	Yes	No	150	10000	Yes	Yes	750	Large Carnivore - Spotted-tail Quoll
Eastern-Barred Bandicoot	<i>Perameles gunnii</i>	0.64	No	Yes	30	1000	No	Yes	100	Not Woodland dependent and riparian
Water Rat	<i>Hydromys chrysogaster</i>	0.6	No	Yes	2	1000	No	Yes	200	Not Woodland dependent and riparian
Long-tailed Mouse	<i>Pseudomys higginsii</i>	0.08	Yes	Yes	1	400	No	Yes	100	Dense ground cover dependent
Southern Brown Bandicoot	<i>Isodon obesulus</i>	1.05	Yes	Yes	30	1000	No	Yes	100	Dense ground cover dependent
Swamp rat	<i>Rattus lutreolus</i>	0.108	Yes	Yes	1	200	No	Yes	30	Dense ground cover dependent
Tasmanian Bettong	<i>Bettongia gaimardi</i>	2	Yes	Yes	90	2000	No	Yes	200	Dense ground cover dependent
Brush tailed possum	<i>Trichosurus vulpecula</i>	3	Yes	No	5	4000	Yes	Yes	500	Arboreal
Eastern Pygmy Possum	<i>Cercartetus nanus</i>	0.043	Yes	No	3	200	Yes	Yes	50	Arboreal
Little Pygmy Possum	<i>Cercartetus lepidus</i>	0.01	Yes	No	1	400	Yes	Yes	50	Arboreal
Ring tailed possum	<i>Pseudocheirus peregrinus</i>	1.1	Yes	No	5	2000	Yes	No	200	Arboreal

3.2.2. Identify dispersal guilds using cluster analysis and expert workshop

The dispersal guilds were identified through a combination of the two cluster analysis methods (hierarchical and Partitioning Around Medoids or PAM) plus expert advice. The hierarchical cluster analysis dendrogram qualitatively identified six groups made up of groups and single species (Figure 14). The output from the PAM clustering method set at six clusters found exactly the same membership as the hierarchical cluster analysis (Table 10). The average silhouette widths (a method for assessing the strength of clustering) for six clusters was 0.591, which according to Kaufman and Rousseeuw (Kaufman & Rousseeuw 1990) indicates ‘reasonable structure has been found’. Average silhouette widths below 0.5 indicate weak structure that could be artificial or no structure at all. With five to seven clusters, all had greater than 0.5 average silhouette width (Figure 15), so assigning between five and seven dispersal guilds is supported by this statistical analysis.

The results from the cluster analysis were then presented to the expert group who agreed with the clustering except for the ring tailed possum. They recommended that the ring-tailed possum should be grouped with the other arboreal species. It was grouped in a class of its own due to the fact that it is the only species which used connectivity elements over 1 m and elements under 1 m (Table 9). The expert panel also agreed with the identification of the Tasmanian Devil and Spotted-Tail Quoll as separate single-species dispersal guilds as their characteristics were unique (for example, long dispersal distances). For each cluster group, the expert panel retrospectively determined the ecological characteristics that united group members and labelled them accordingly (Figure 14, Table 10).

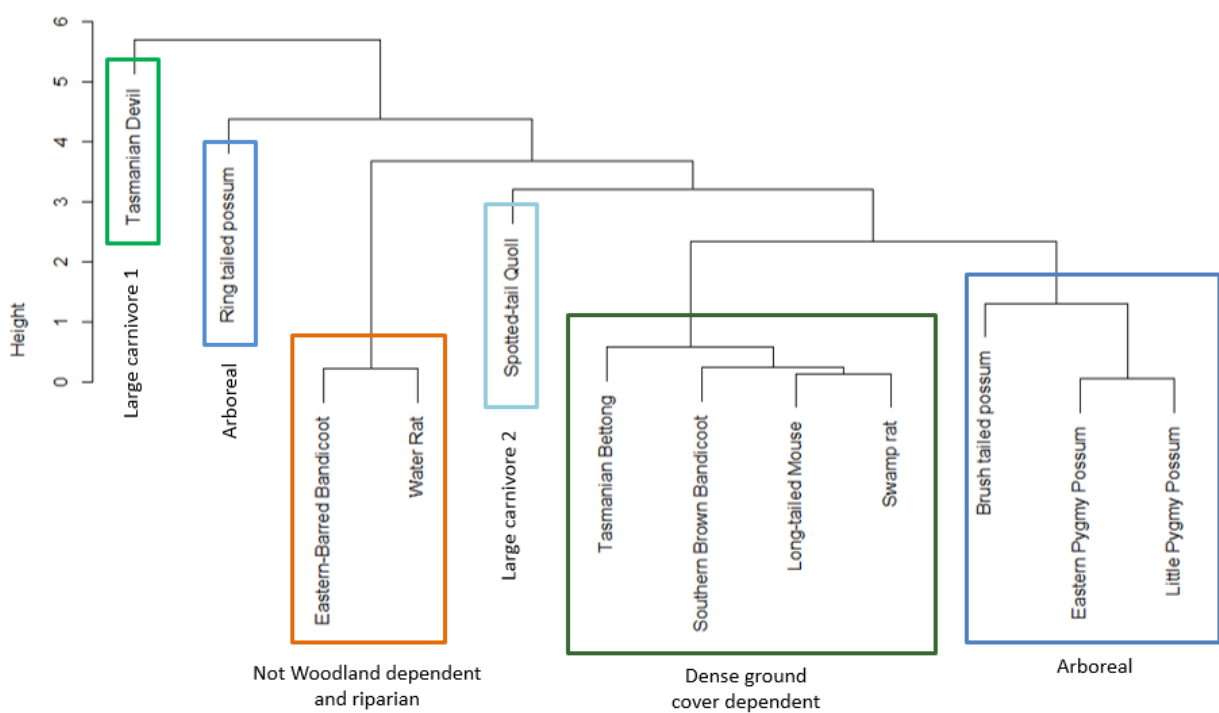


Figure 14: Hierarchical cluster analysis where height describes the similarity between individual species. Labelled dispersal guilds identified post-hoc through discussion with experts.

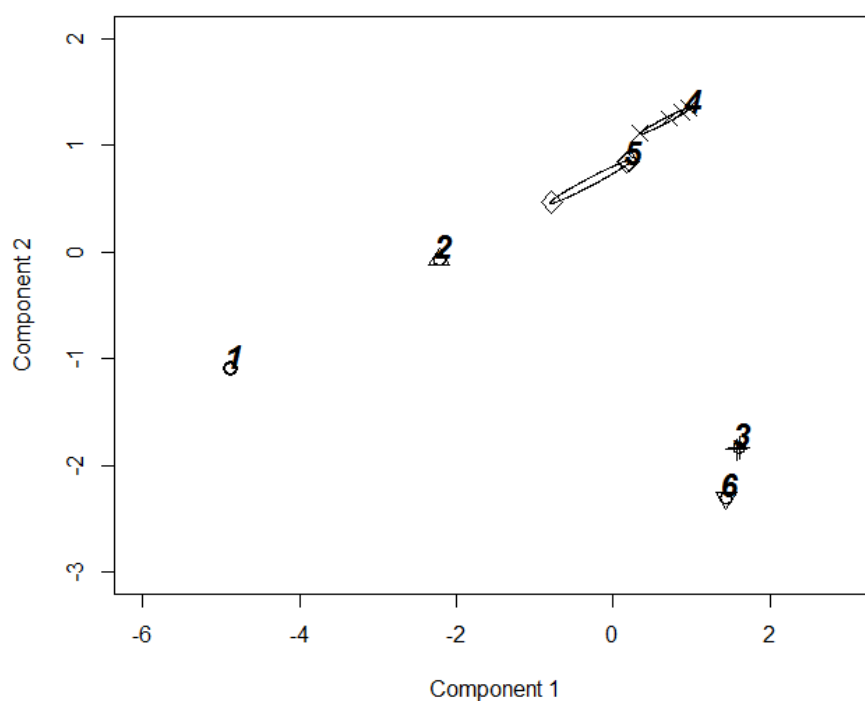


Figure 15: Cluster analysis using the Partitioning Around Medoids (PAM) method presented as Principle Components Analysis to reduce dimensionality of the data and in order to observe the similarities between clusters. Individuals belonging to each cluster group can be found in Table 9.

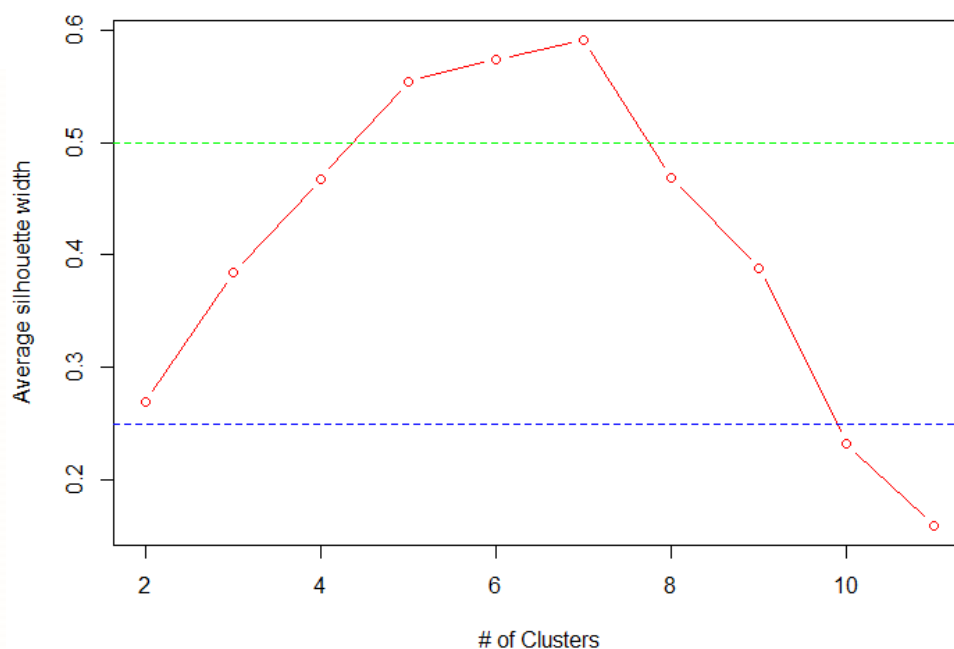


Figure 16: Average silhouette widths versus cluster number. Where values above 0.5 (green line) indicate a reasonable structure has been found, 0.25 – 0.5 indicate weak structure that could be artificial or no structure at all and values below 0.25 (red line) indicate no structure at all.

Table 10: Cluster analysis output using the PAM method compared with hierarchical cluster analysis.

Species	Cluster #	Same as hierarchical cluster analysis	Cluster analysis determined dispersal guild
Tasmanian Devil	1	Y	Large Carnivore - Tasmanian Devil
Spotted-tail Quoll	2	Y	Large Carnivore - Spotted-tail Quoll
Eastern-Barred Bandicoot	3	Y	Not Woodland dependent and/or riparian
Water Rat	3	Y	Not Woodland dependent and/or riparian
Long-tailed Mouse	4	Y	Dense ground cover dependent
Southern Brown Bandicoot	4	Y	Dense ground cover dependent
Swamp rat	4	Y	Dense ground cover dependent
Tasmanian Bettong	4	Y	Dense ground cover dependent
Brush tailed possum	5	Y	Arboreal
Eastern Pygmy Possum	5	Y	Arboreal
Little Pygmy Possum	5	Y	Arboreal
Ring tailed possum	6	Y	Arboreal

3.2.1. Identify connectivity model input parameters for dispersal guilds

For each of the dispersal guilds a single value for each of the habitat characteristics and dispersal thresholds is required for connectivity modelling. For the two large carnivore guilds their original values were used, while for the three other dispersal guilds the average values were used. In cases with categorical variables the combination of vegetation above and below 1 m that resulting in the majority was used (Table 11).

Table 11: Average and majority values for each dispersal guild.

Group Name	Hab. over 1 m	Hab. Under 1 m	Min Patch size (ha)	Interpatch distance (m)	Connectivity over 1 m	Connectivity Under 1 m	Gap crossing (m)
Large Carnivore - Tasmanian Devil	Yes	No	800	10000	Yes	Yes	2000
Large Carnivore - Spotted-tail Quoll	Yes	No	150	10000	Yes	No	750
Not Woodland dependent and riparian	No	Yes	16	1000	No	Yes	150
Dense ground cover dependent	Yes	Yes	30.5	900	No	Yes	107.5
Arboreal	Yes	No	3.5	1650	Yes	Yes	200

3.2.2. Dispersal guild final connectivity outputs

The connectivity analysis of the five dispersal guilds (Figure 17 - Figure 21) showed large differences in how each group was affected by fragmentation. For the two large carnivores the landscape essentially appears connected with all patches for the Tasmanian Devil connected directly or indirectly via other patches (Figure 17) and all patches for the Spotted-tail Quoll but four connected (Figure 18).

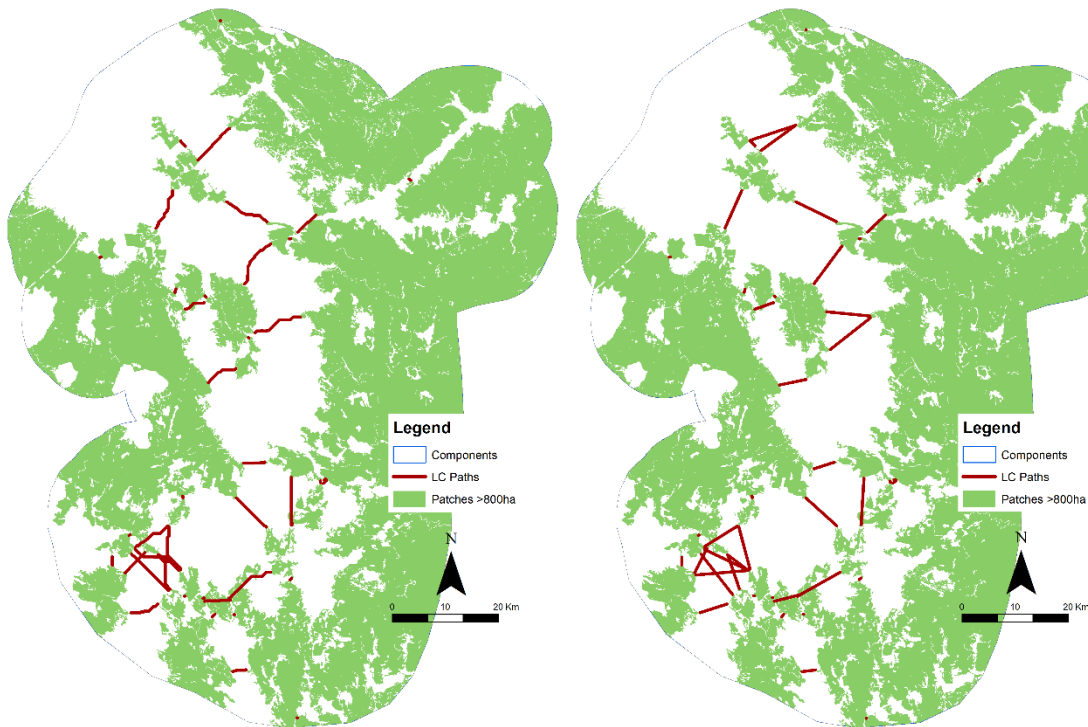


Figure 17: Connectivity analysis for 'Large Carnivore - Tasmanian Devil' dispersal guild with an interpatch-crossing distance threshold of 10,000m. Left) least-cost paths between patches based on gap-crossing layer and resistance. Right) least-cost paths between based only on interpatch-crossing distance threshold.

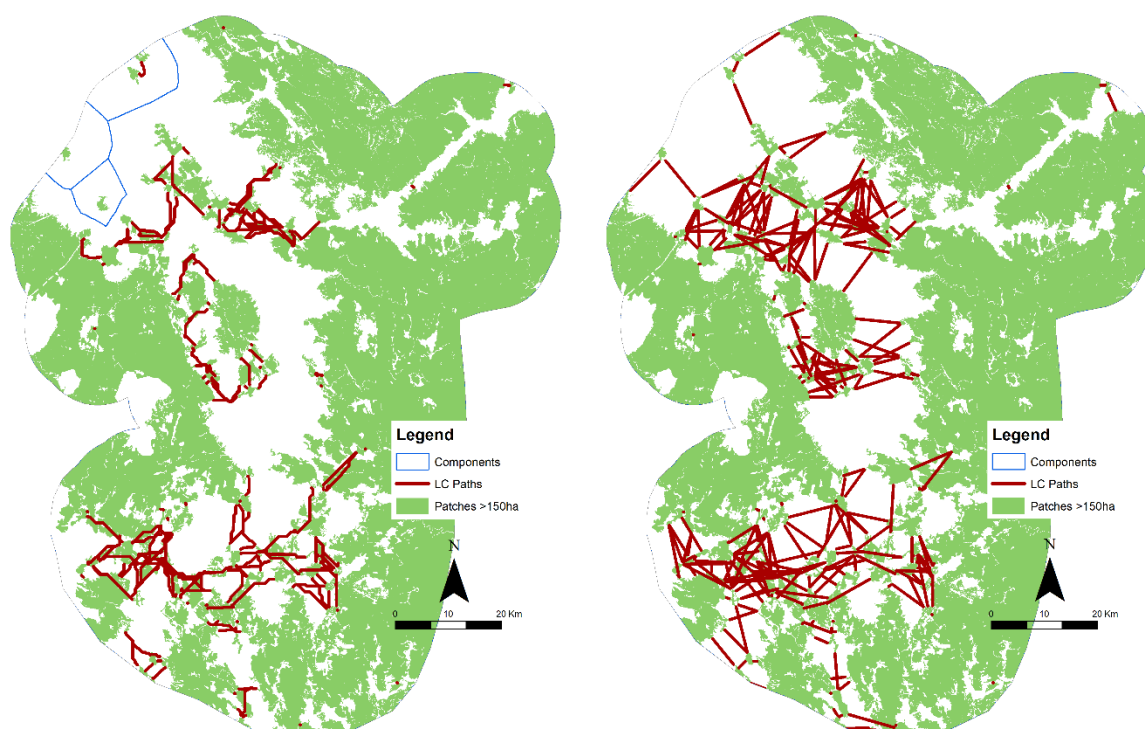


Figure 18: Connectivity analysis for ‘Large Carnivore - Spotted-tail Quoll’ dispersal guild with an interpatch-crossing distance threshold of 10,000m. Component boundaries from connectivity located at the midpoint between patches. Left) Analysis using gap-crossing layer and resistance. Right) Analysis using based only on interpatch-crossing distance threshold.

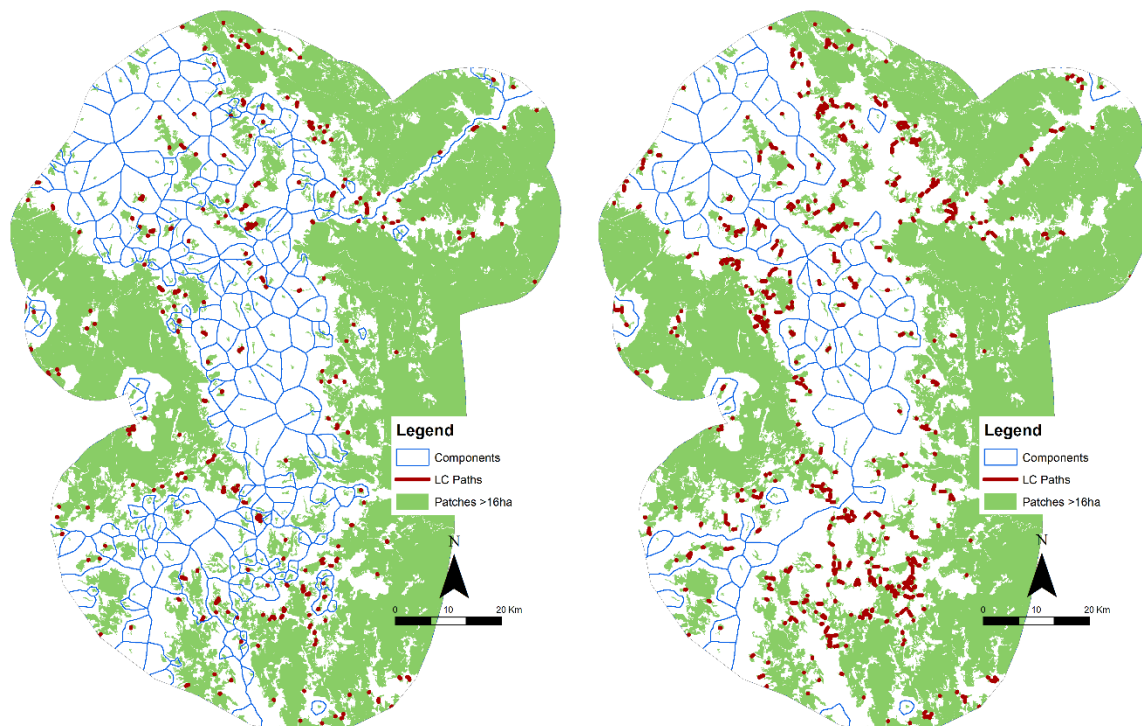


Figure 19: Connectivity analysis for ‘Not Woodland dependent and/or riparian’ dispersal guild with an interpatch-crossing distance threshold of 1,000m. Component boundaries from located at the midpoint between patches. Left) Analysis using gap-crossing layer and resistance. Right) Analysis using based only on interpatch-crossing distance threshold.

From the perspective of the three clusters of smaller mammals, the landscape appears highly fragmented with the majority of the connected areas in the east and west of the study area and most patches in the central region isolated or connected to relatively few patches (Figure 19 - Figure 21). The average component size was from 20 to 28 km² (Table 8). Class coincidence probability, Expected Cluster Size and IIC all had higher values for the large carnivores versus the small mammals indicate that at the landscape scale there is greater connectivity.

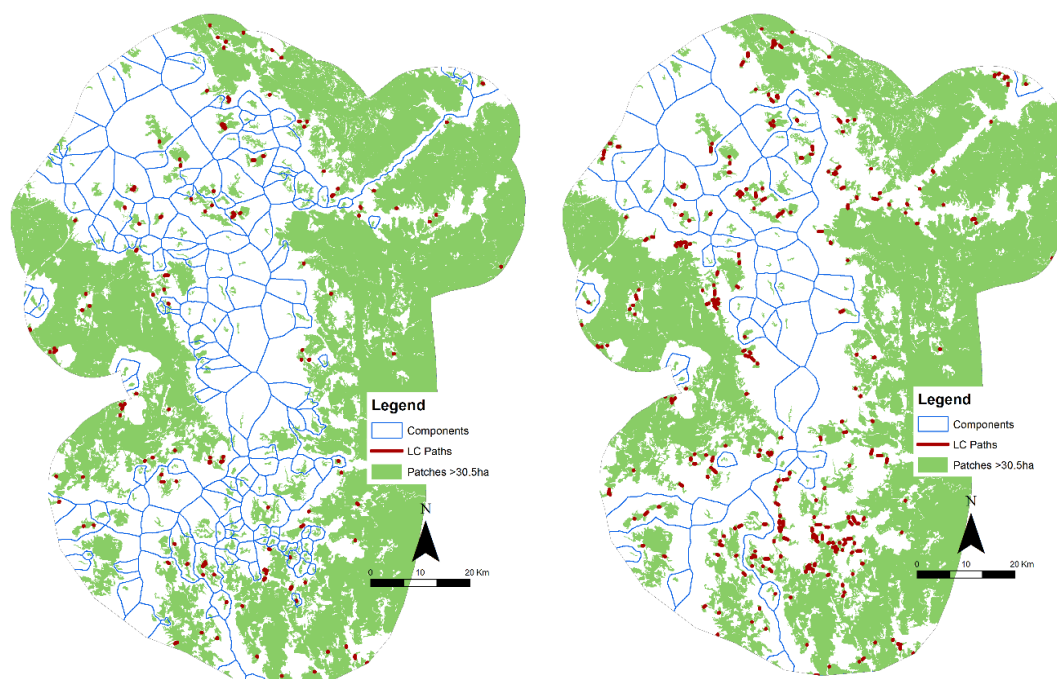


Figure 20: Connectivity analysis for 'Dense ground cover dependent' dispersal guild with an interpatch-crossing distance threshold of 1,000m. Component boundaries from located at the midpoint between patches. Left) Analysis using gap-crossing layer and resistance. Right) Analysis using based only on interpatch-crossing distance threshold.

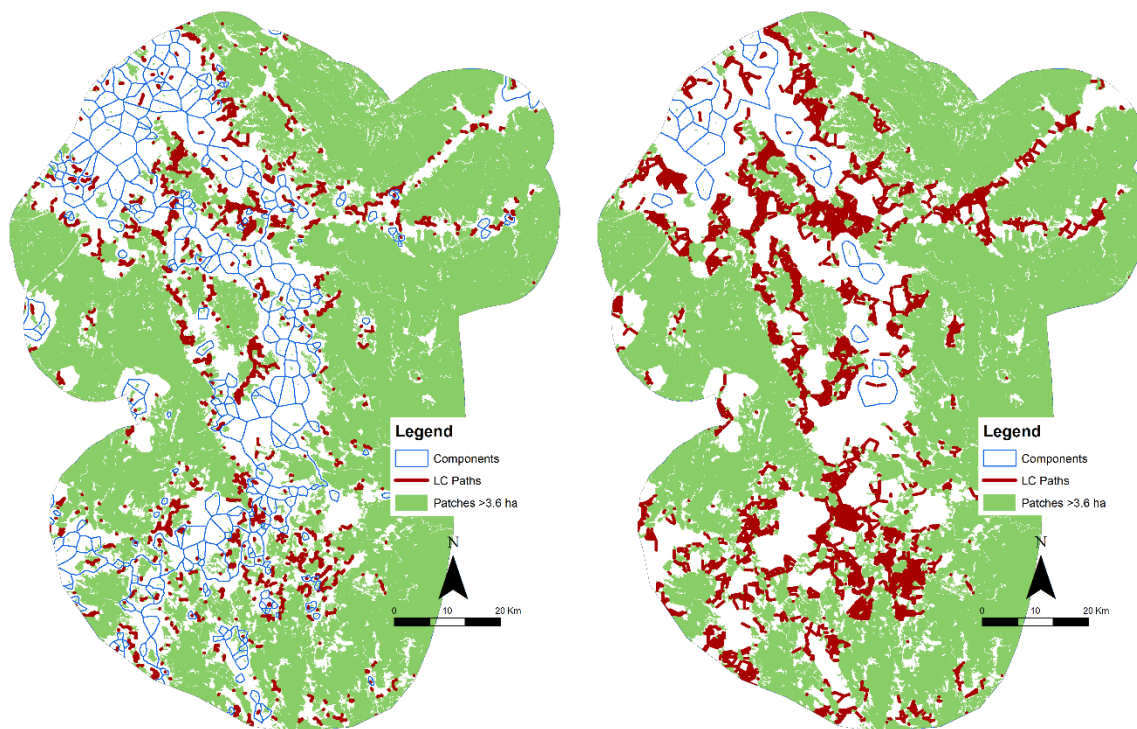


Figure 21: Connectivity analysis for 'Arboreal' dispersal guild with an interpatch-crossing distance threshold of 1,000m. Component boundaries from located at the midpoint between patches. Left) Analysis using gap-crossing layer and resistance. Right) Analysis using based only on interpatch-crossing distance threshold.

3.2.3. Sensitivity analysis

The connectivity outputs need to be assessed for the sensitivity of the input data and parameterisation. A comparison of the modelled connectivity with and without dispersal costs from the gap crossing layer and landuse allows for the assessment of the importance of interpatch-dispersal distance thresholds for landscape-scale connectivity. The results can be interpreted in two ways:

- 1) Will uncertainty in the spatial data (especially the effect of not extracting difficult to derive fine-scaled connectivity elements) affect connectivity outputs?
- 2) Do corridors and scattered trees make a key contribution to connectivity?

All but one of the dispersal guilds, 'Arboreal' show very similar connectivity outputs regardless of the dispersal costs. In the case of large mammals the landscape is always connected and in the case of the two groups of small mammals, 'Not Woodland dependent and/or riparian' and 'Dense ground cover dependent', most patches and the majority of the large components are isolated due to the interpatch distances. However, the 'Arboreal' dispersal guild showed large differences with or without connectivity elements and landuse.



Further sensitivity analysis characterising the number of components versus interpatch-crossing distance for all combinations habitat input layers provides an overview of critical scales. Our analysis found that at around 1000 m there is a rapid drop off in connectivity within the landscape (Figure 22). This analysis did not include the impact of the gap-crossing threshold.

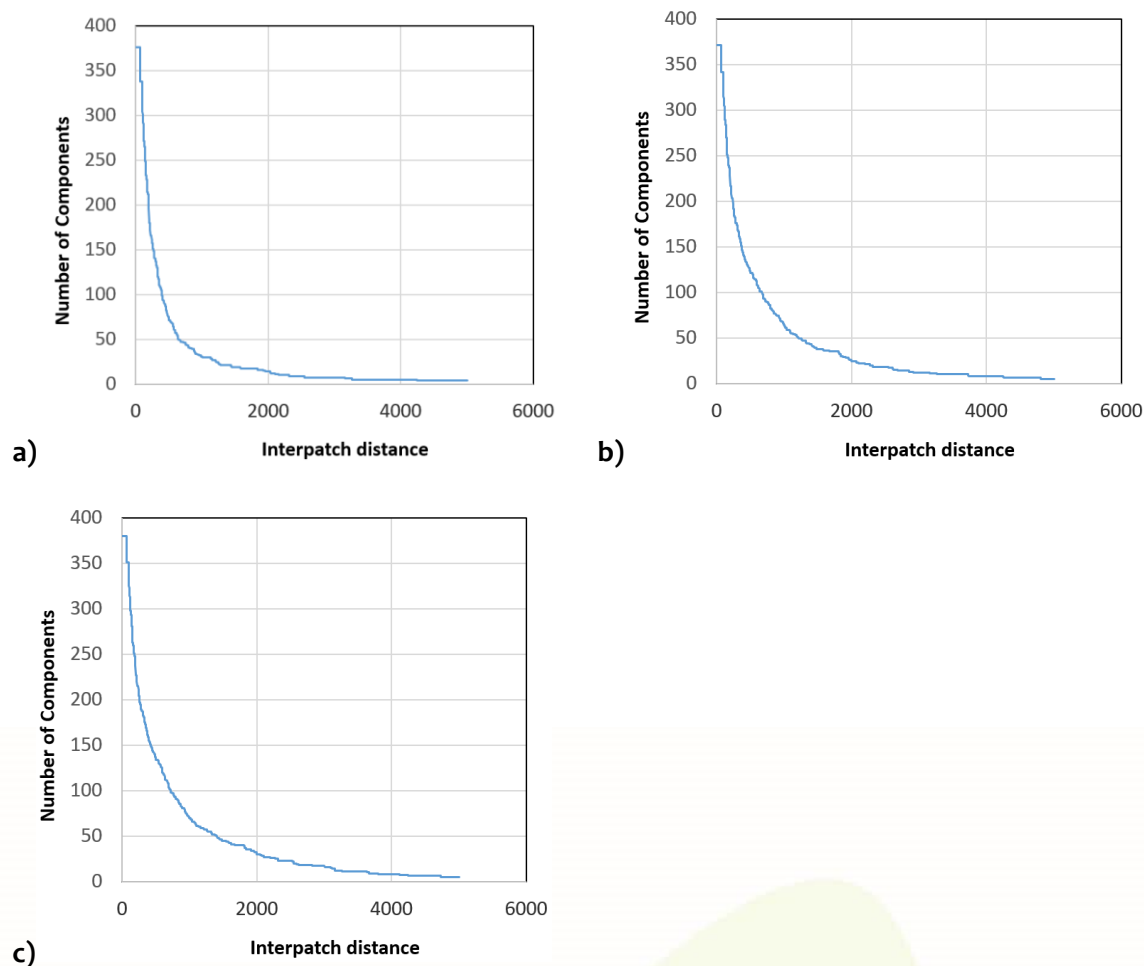


Figure 22: Sensitivity analysis for vegetation a) Over 1 m, b) Over 1 m and Under 1 m and c) Under 1m characterising the number of components versus the interpatch-crossing distance. For this analysis the gap-crossing distance was ignored.

4.0 Discussion

4.1. Overview

The methods outlined in this report shows great potential for application to conservation planning by providing a focal conservation target that is an intermediate between a single species connectivity model and a general habitat-based approach. In conjunction with the multiple methods for testing the sensitivity of the parameterisations and dispersal distances, a broad picture of connectivity for all species in a region can be characterised. More complex analytical methods can be applied as outlined in the previous report (Lechner & Lefroy 2014; Lechner et al 2015b) using this new kind of connectivity conservation target. These other forms of analysis include scenario analysis and local scale analysis using the Circuitscape connectivity software.

4.2. Applying this approach to conservation planning.

The dispersal guild approach provides a way of allocating conservation effort and/or research based on the general patterns of connectivity for multiple dispersal guilds. Certain dispersal guilds do not need including in conservation targets for connectivity due to their dispersal and habitat characteristics (that is, large carnivorous mammals) as almost no patches in the landscape are isolated meaning connectivity can only be increased with large investment in restoring habitat. For other dispersal guilds ('Not Woodland dependent and/or riparian' and 'Dense ground cover dependent'), patches within the landscape are separated by distances greater than their interpatch-crossing distance threshold even without the presence or absence of connectivity elements. Furthermore, these assessments represent the best case scenario where the presence or absence of connectivity elements is not included, indicating that the true state of connectivity for these species is most likely to be worse.

Connectivity for all species can be examined by plotting the number of components against the interpatch-crossing distance. This shows that at around 1000 m the landscape becomes very fragmented. All but four species tested have interpatch-crossing distances less than or equal to 1000 m (Table 9). For those species, the landscape is highly fragmented and reconnecting the landscape is likely to have positive impacts on these species persistence.

The analysis also shows that there will be large differences in conclusions reached based on the general approach using TASVEG 3.0 subsets compared to the dispersal guild approach. Landscapes based on TASVEG 3.0 appeared connected while small mammal species' habitat using the dispersal guild approach is highly fragmented. This is likely to be a product of the greater amount of vegetation included in the TASVEG scenarios from 5719 km² to 6325 km² compared to 4681 km² to 4810 km² for 'Not Woodland dependent and/or riparian' and 'Dense ground cover dependent'. Thus, it appears that both the dispersal characteristics and habitat area and configuration are likely to have a large impact on connectivity when approaching critical scales.

4.3. Next steps for the connectivity modelling in the Tasmanian Midlands

The results of the analysis presented here only represent a regional overview of connectivity and provide generalisations on connectivity patterns between species across the landscape. It is likely that local scale restoration efforts of known high valued patches could have great impact on population viability. Thus, the outputs need to be interpreted in light of local knowledge and should be used to provide guidance as to where future research need to be focused on critical conservation challenges. Furthermore, patch scale and scenario analysis may provide a more precise assessment of connectivity and the value of restoration for a specific location.

It is important to recognise that the outputs presented using this modelling approach represent general patterns. As such, they are easier to interpret than multiple single species models, but they do not actually represent habitat for a single species, even for the large carnivores. A second stage of analysis could focus on specific subsets of species such as those with interpatch-crossing distance thresholds of around 1000 m. Further analysis could also involve more complex modelling methods such as species distribution modelling to provide a more precise definition of habitat.

4.1. Applying the dispersal guild approach using expert opinion

The process of identifying dispersal guilds used in this study provides a template for future analysis in other areas. The method can be applied rapidly (~three months) following the process used in this report, as long as experts with sufficient knowledge are available. It is important though to ensure that experts have sufficient knowledge for parameterising the model. The identification of these parameters was time consuming and the resulting estimates were highly uncertain. However, addressing these uncertainties for all 12 species with empirical field based research would be a substantial undertaking. Furthermore, the literature review found very few empirical studies that could be applied outside of their study area due to differences specific to each study area. Thus in most cases an expert approach would be the only option.

While the processing of the spatial data using the GAP CLoSR framework is fully automated and can be used simply and quickly, the cluster analysis method is perhaps the most complex aspect of the process and may be beyond the experience of some users. It is probably not necessary to apply the full approach described in this report. The cluster analysis is only exploratory and serves as a guide for experts to identify the dispersal guilds.

The emphasis of the approach outlined is on a transferable approach lead by local experts that have the knowledge to identify the important habitat and dispersal parameters to model. We recognised through our experience in the Hunter Valley and the Tasmanian Midlands that in order for users to apply the model and have confidence in the outputs they need to have ownership of the parameterisation. Furthermore, it was clear that for some taxa, even using expert opinion, it may be difficult to parameterise connectivity models due to the lack of scientific knowledge (such as plant species).

4.2. Limitations

The application of GAP CLoSR in the Tasmanian Midlands provided a greater opportunity for stakeholder and expert engagement than was possible in the previous analysis developed in the Lower Hunter Region, allowing for an assessment of a greater number of species. Further analysis assessing spatial data accuracy, connectivity model type, target species and community and ecological parameterisation could be carried out using a combination of real data and simulation models to address potential sources of uncertainty (Lechner et al 2009; Lechner et al 2012a; Lechner et al 2012b). Uncertainty has the potential to confound spatially explicit modelling methods and needs to be assessed to ensure the robustness of the output. However, this report addressed one of the main forms of uncertainty identified by stakeholders in the Hunter associated with using only the general model.

In the Tasmanian Midlands a key source of uncertainty was from the lack of spatial resolution of the vegetation data, which does not adequately capture fine-scale connectivity elements. Actual connectivity for the Tasmanian Midlands is likely to be something between the connectivity with and without the dispersal costs as described by the two panels in Figure 17 to Figure 21. Qualitatively it appeared as though landuse will not have a great impact on the outputs as high resistant landcover is predominantly found in areas with very little vegetation in the surrounding area, and usually beyond the interpatch-crossing distance. In the case of the method used in this study it is likely that implicit assessment through a review of the model outputs by experts may suffice and that model outputs should be used only as a first step in an interpretation for conservation planning.

4.3. Conclusions

Decision makers need tools that are sufficiently flexible and dynamic to assess connectivity without being too complex, difficult to use or time-consuming. The approach described in this report of characterising dispersal guilds provides greater ecological resolution than single species connectivity modelling, and is therefore likely to be better suited to a whole of landscape, multi-species approach to conservation planning.

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Appendix

R code for cluster analysis

```
library(cluster)
require(plotrix)

setwd("Z:/Data")
SDataOrig<- read.csv("../Midlands file.csv", header = TRUE)
SData <- subset(SDataOrig)
Names <- SData$Common_name

#Subset data - remove categorical variables
SDataCat <- subset(SData, select = c(Hab_Over:Hab_Under,Struct_Over:Struct_Under))
SDataCont <- subset(SData, select = c(Min_Patch_size:Interpatch_dis,Gap_crossing))

#Scale continuous data
SDataCont<-scale(SDataCont, center = TRUE, scale = TRUE)

##### Addressing the categorical data
MatrixCat <- cbind(model.matrix(~o+Hab_Over, SDataCat ), model.matrix(~o+Hab_Under, SDataCat ),
                   model.matrix(~o+Struct_Over, SDataCat ),model.matrix(~o+Struct_Under, SDataCat ))

#Use Singular value decomposition to convert into continuous variables
singularMatrixCat <- svd(MatrixCat)

singularMatrixCatOut = scale(singularMatrixCatOut)

#Attached SVD to original non-categorical variables
finalData <- cbind(SDataCont , singularMatrixCatOut)

row.names(finalData ) <-as.matrix(Names)

#####Hierachial cluster analysis
distance <- dist(finalData , method="euclidean")
cluster <- hclust(distance, method="average")
plot(cluster)

#####PAM cluster analysis
maxclus <- length(finalData [,1])
silWidth <- data.frame(1:(maxclus-2))
#Plotting silohette
for(clus.no in 1:(maxclus-2)){
  PamOut <- pam(finalData,clus.no+1)
  #plot(silhouette(PamOut))
  #According to Kaufmann and Rousseuw (1990), a value below 0.25 means that the data are not structured.
  #Between 0.25 and 0.5, the data might be structured, but it might also be an artifice
  silWidth[clus.no,<- as.numeric(summary(silhouette(PamOut))[4])
}
plot(c(2:(maxclus-1)),silWidth[,], type ="b", xlab="# of Clusters", ylab = "Average silhouette width", col ="red")
abline(h =0.25, col="blue", lty=2)
abline(h =0.5, col="green", lty=2)

clusplot(finalData, pam(finalData,6)$clustering, lines=0, labels=2, cex = 1, xlim = c(-6,3),ylim = c(-3,2), span=FALSE)
```

CSV Table format

Common_name	Species_name	Weight	Hab_Ove rs	Hab_Unde r	Min_Patc h_size	Interpatch_ dis	Struct_O ver	Struct_Un der	Gap_crossi ng
Tasmanian Devil	<i>Sarcophilus harrisii</i>	12	Yes	No	800	10000	Yes	Yes	2000
Spotted-tail Quoll	<i>Dasyurus maculatus</i>	4	Yes	No	150	10000	Yes	Yes	750
Eastern-Barred Bandicoot	<i>Perameles gunnii</i>	0.64	No	Yes	30	1000	No	Yes	100

Classification of Landuse classes into dispersal classes

Lu_code	Lu_descrip	Feature
6.1.0	Lake	Hydrology
6.1.1	Lake-conservation	Hydrology
6.2.0	Reservoir or dam	Hydrology
6.2.2	Water storage-intensive use/farm dams	Hydrology
6.3.0	River	Hydrology
6.3.1	River-conservation	Hydrology
6.4.0	Channel/aqueduct	Hydrology
4.2.0	Grazing irrigated modified pastures	Intensive agriculture
4.2.2	Irrigated pasture legumes	Intensive agriculture
4.3.0	Irrigated cropping	Intensive agriculture
4.3.1	Irrigated cereals	Intensive agriculture
4.3.3	Irrigated hay and silage	Intensive agriculture
4.3.4	Irrigated oil seeds	Intensive agriculture
4.3.7	Irrigated alkaloid poppies	Intensive agriculture
4.4.0	Irrigated perennial horticulture	Intensive agriculture
4.4.5	Irrigated shrub nut, fruits and berries	Intensive agriculture
4.4.9	Irrigated grapes	Intensive agriculture
5.2.1	Dairy sheds and yards	Intensive agriculture
5.2.2	Cattle feedlots	Intensive agriculture
5.2.7	Horse studs	Intensive agriculture
5.2.8	Stockyards/saleyards	Intensive agriculture
5.4.5	Farm buildings/infrastructure	Intensive agriculture
5.1.2	Glasshouses	Intensive landuse
5.2.6	Aquaculture	Intensive landuse



Lu_code	Lu_descrip	Feature
5.3.0	Manufacturing and industrial	Intensive landuse
5.3.5	Abattoirs	Intensive landuse
5.3.7	Sawmill	Intensive landuse
5.5.5	Research facilities	Intensive landuse
5.6.0	Utilities	Intensive landuse
5.7.0	Transport and communication	Intensive landuse
5.7.1	Airports/aerodromes	Intensive landuse
5.8.0	Mining	Intensive landuse
5.8.2	Quarries	Intensive landuse
5.9.0	Waste treatment and disposal	Intensive landuse
5.9.3	Solid garbage	Intensive landuse
5.9.5	Sewage/sewerage	Intensive landuse
1.1.1	Strict nature reserves	no resistance
1.1.3	National park	no resistance
1.1.4	Natural feature protection	no resistance
1.1.5	Habitat/species management area	no resistance
1.1.6	Protected landscape	no resistance
1.1.7	Other conserved area	no resistance
1.2.0	Managed resource protection	no resistance
1.3.0	Other minimal use	no resistance
1.3.1	Defence land-natural areas	no resistance
1.3.3	Residual native cover	no resistance
2.1.0	Grazing native vegetation	no resistance
2.2.0	Production forestry	no resistance
3.1.1	Hardwood plantation	no resistance
3.1.2	Softwood plantation	no resistance
3.2.0	Grazing modified pastures	no resistance
3.2.1	Native/exotic pasture mosaic	no resistance
3.2.3	Pasture legumes	no resistance
3.2.4	Pasture legume/grass mixtures	no resistance
3.2.5	Sown grasses	no resistance
3.3.0	Cropping	no resistance
3.3.3	Hay and silage	no resistance
3.6.0	Land in transition	no resistance



Lu_code	Lu_descrip	Feature
3.6.1	Degraded land	no resistance
6.5.0	Marsh/wetland	no resistance
6.5.1	Marsh/wetland-conservation	no resistance
6.5.4	Marsh/wetland-saline	no resistance
5.7.3	Railways	Railways
5.7.2	Roads	Roads
5.4.1	Urban residential	Urban - CBD
5.4.2	Rural residential with agriculture	Urban - Suburban
5.4.3	Rural residential without agriculture	Urban - Suburban
5.4.4	Remote communities	Urban - Suburban
5.5.1	Commercial services	Urban - Suburban
5.5.2	Public services	Urban - Suburban
5.5.3	Recreation and culture	Urban - Suburban
5.6.4	Electricity substations and transmission	Urban - Suburban

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