
Derived forest ecosystems: an evaluation of surrogacy value and internal biological variation

A report for the Department of the NSW Government, Sydney, NSW

DERIVED FOREST ECOSYSTEMS: AN EVALUATION OF SURROGACY VALUE AND INTERNAL BIOLOGICAL VARIATION

**NSW NATIONAL PARKS AND
WILDLIFE SERVICE**

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PROJECT SUMMARY

This working paper describes a project undertaken as part of the comprehensive regional assessments of forests in New South Wales. The comprehensive regional assessments (CRAs) provide the scientific basis on which the State and Commonwealth Governments will sign regional forest agreements (RFAs) for major forest areas of New South Wales. These agreements will determine the future of these forests, providing a balance between conservation and ecologically sustainable use of forest resources.

Project objective/s

The primary objectives of this project were to evaluate the effectiveness of forest ecosystem mapping derived for Upper North East and Lower North East CRA Regions as a surrogate for other elements of biodiversity, and to analyse the level and pattern of biological variation encompassed by each mapped ecosystem. The project also collated and prepared data on invertebrates for use in this and related CRA projects.

Methods

The evaluation used field survey data for a number of biological groups (canopy trees, understorey plants, birds, reptiles, bats, ground-dwelling arthropods) to evaluate how well the species in each group were represented in a 'reserved' set of survey sites selected on the basis of mapped forest ecosystems. The results obtained from the evaluation of forest ecosystem mapping were compared to those obtained for a number of other potential biodiversity surrogates. Biological variation within mapped forest ecosystems was investigated by analysing the biological dissimilarity between pairs of field survey sites located within the same ecosystem in relation to the environmental and geographical separation of those sites.

Key results and products

A database containing 11,347 invertebrate locality records was established for use in this and related CRA projects. The evaluation of forest ecosystem mapping produced the following key results and recommendations:

- ☑ In terms of performance as a biodiversity surrogate, forest ecosystem mapping represents an improvement over surrogates employed in earlier assessments in north-east NSW (forest type mapping and environmental unit mapping).
- ☑ The efficacy with which biodiversity is reserved through use of forest ecosystems can be improved further by considering information on floristic similarities between ecosystems when prioritising areas for reservation.
- ☑ However, even with this refinement, the performance of forest ecosystem mapping as a biodiversity surrogate is well below optimum. Shortcomings in the surrogate must therefore be addressed in the CRA/RFA negotiation process by giving due emphasis to other biodiversity criteria, including the representation of environmental and geographical gradients of biological variation within each ecosystem.
- ☑ Future conservation assessment and planning work in north-east NSW and other regions should consider seriously the potential role of biodiversity surrogates derived through alternative means such as species and assemblage modelling, which performed very favourably relative to forest ecosystem mapping in the current evaluation.

1. INTRODUCTION

1.1 BACKGROUND AND OBJECTIVES

The nationally agreed criteria for establishing a system of forest reserves in Australia (JANIS 1997) place considerable emphasis on using 'forest ecosystems' as a broad surrogate for biodiversity. The criteria also recognise, however, that there can never be perfect concordance between mapped forest ecosystems and the distributions of all individual elements of biodiversity. Two problems are likely to arise: 1) some biodiversity elements (e.g. particular species or groups of species) may be distributed independently of mapped forest ecosystems, and 2) these mapped ecosystems may contain substantial internal biological variation (heterogeneity) in relation to environmental, geographical and disturbance gradients. The first problem is addressed by JANIS Biodiversity Criterion 5 '*the reserve system should seek to maximise the area of high quality habitat for all known elements of biodiversity wherever practicable, but with particular reference to ... [areas of high diversity, refugia, centres of endemism] ... and those species whose distributions and habitat requirements are not well correlated with any particular forest ecosystem*', while the second problem is addressed by Criterion 7 '*to ensure representativeness, the reserve system should, as far as possible, sample the full range of biological variation within each forest ecosystem, by sampling the range of environmental variation typical of its geographic range*'.

Practical implementation of Biodiversity Criteria 5 and 7 presents a number of problems. For example, how much weight should be given to these criteria when selecting reserves, relative to the weight given to Biodiversity Criteria 1, 2 and 3 (specifying percentage reservation targets for forest ecosystems)? Furthermore, precisely which elements of biodiversity are not well correlated with forest ecosystems and therefore require special consideration under Criterion 5, and precisely which environmental or geographical gradients are most strongly correlated with biological variation within ecosystems and therefore require attention under Criterion 7? These questions can best be answered through a rigorous evaluation of the effectiveness of forest ecosystem mapping as a surrogate for other elements of biodiversity and the level and pattern of biological variation encompassed by each mapped ecosystem. The main objective of the current project was to perform such an evaluation using forest ecosystem mapping derived by the CRA process and all available biological survey data.

It was originally planned to perform the evaluation using forest ecosystem mapping for Upper North East, Lower North East and Southern CRA Regions. Unfortunately, due to differences in timing in the implementation of CRAs between regions, the forest ecosystem map for Southern Region was not completed early enough to be employed in this project. The evaluation reported on here therefore focused on forest ecosystem mapping for Upper North East and Lower North East Regions. However, a separate CRA project being performed by the Australian Museum is currently applying techniques developed in this project to an evaluation of forest ecosystem mapping in Southern Region using ground-dwelling arthropod survey data.

1.2 PROJECT STRUCTURE

The project was implemented as three sub-projects:

- ☑ Evaluation of the effectiveness of derived forest ecosystem mapping as a biodiversity surrogate;
- ☑ Analysis of biological variation within derived forest ecosystems; and
- ☑ Collation and preparation of invertebrate data.

The first two sub-projects were performed by NSW NPWS while the third was performed by the Australian Museum. The aim of the third sub-project was to collate, database and prepare data on selected invertebrate groups for use in the other two sub-projects and for use in the analysis and mapping of invertebrate 'centres of endemism' in Upper North East and Lower North East Regions (the latter analysis is documented in a separate CRA report).

The remainder of this report is structured around the three sub-projects, with a chapter devoted to each.

2. SUB-PROJECT 1: EVALUATION OF EFFECTIVENESS OF DERIVED FOREST ECOSYSTEM MAPPING AS A BIODIVERSITY SURROGATE

2.1 INTRODUCTION

The primary objective of this sub-project was to evaluate how well the forest ecosystem map derived for Upper North East and Lower North East CRA Regions functions as a surrogate for other elements of biodiversity. The evaluation builds on earlier research performed by Ferrier and Watson (1997) who developed a new analytical technique for evaluating the performance of biodiversity surrogates, and applied this technique to a number of surrogates and datasets in north-east NSW. The approach developed by Ferrier and Watson involves using field survey data for a given biological group (e.g. reptiles) to evaluate how well the species in this group are represented in a 'reserved' set of survey sites selected on the basis of a particular surrogate.

The current evaluation was designed to address five specific questions:

- How well does the forest ecosystem map perform as a surrogate for a range of biological groups and which groups, if any, are addressed particularly poorly by the surrogate?
- How does the performance of the forest ecosystem map compare with that of other surrogates previously evaluated in north-east NSW?
- How would generalising the forest ecosystem classification (i.e. amalgamating similar ecosystems) affect the classification's performance as a biodiversity surrogate?

- ☑ How would consideration of the floristic distinctiveness of pairs of forest ecosystems when selecting reserves affect surrogate performance?
- ☑ How does geographical bias in the location of reservation within each forest ecosystem (i.e. clumped rather than evenly spread reservation) affect surrogate performance?

2.2 ANALYTICAL METHODOLOGY

The performance of forest ecosystem mapping and other surrogates was evaluated using a refined version of the Species Accumulation Index (SAI) technique developed by Ferrier and Watson (1997). With this technique a surrogate is used to build a hypothetical reserve system by selecting survey sites (for a particular biological group) in a sequence that maximises representation of variation within the surrogate. The performance of the surrogate is then assessed using the real biological data from the survey sites to calculate the cumulative number of species reserved after selecting each site. The results of this assessment are plotted as a species accumulation curve. A number of improvements have been made to the technique since its original application. These changes have been made partly by the current project and partly by the separate consultancy performed by NSW NPWS for Environment Australia (Ferrier et al. 1999). Two of the changes are of particular significance (the others are relatively minor):

1. In the original technique the y-axis of the species accumulation curves simply represented the number of species present within the hypothetical reserve system (i.e. occurring at one or more reserved sites). This simple measure has now been replaced by a more complex y-axis measure of accumulation:

$$y = \frac{\sum_{i=1}^{species} \left(1 - e^{-\left(\frac{R_i}{tN_i}\right)} \right)}{species}$$

where *species* is the total number of species in the evaluation dataset
N_i is the total number of sites at which species *i* occurs in the dataset
t is the 'targeted' proportion of sites to be reserved (0.15 in the current analysis)
R_i is the number of reserved sites at which species *i* occurs

This new measure reflects not just the occurrence (presence/absence) of species in a hypothetical reserve system but the proportion of each species' distribution that has been reserved. The employed transformation imposes an asymptotic relationship between this proportion and the contribution each species makes to the y-axis measure. A species' contribution increases rapidly between zero and the targeted proportion and then levels out gradually once the targeted proportion has been achieved. Extensive trialling of this and alternative measures has suggested that the adopted measure is a very informative and robust measure of reservation achievement for use in surrogate evaluation. A major advantage of the new measure is that it places greater emphasis on rarer species.

2. In the original technique, if two or more sites were considered equally worthy of reservation in terms of the surrogate under evaluation (e.g. sites occurring within the same vegetation type) then these sites were selected in random order. A 'spatial constraint' option is now provided which, in situations where 'all else is equal', selects sites in order of proximity to sites already reserved.

All other components of the Ferrier and Watson (1997) methodology remain essentially unchanged. The species accumulation curve yielded by a surrogate is used to derive a Species Accumulation Index of surrogate performance by relating this curve to two other 'reference' curves: 1) an 'optimum' species accumulation curve derived by using the real biological data to select sites in a sequence that maximises the height of the curve at each step, and 2) a 'mean random' species accumulation curve representing the mean of a sample of species accumulation curves derived by selecting sites in random order, without reference to either the surrogate or the biological data. Values for the index range from zero (or less than zero) for a surrogate that performs no better than a random selection of sites, up to one for a surrogate exhibiting 'perfect' performance. Confidence limits for observed values of the index are estimated by bootstrapping (see Ferrier and Watson 1997 for details).

2.3 DATA

2.3.1 Biological datasets

The biological datasets used to evaluate the performance of forest ecosystem mapping as a biodiversity surrogate were almost identical to those described by Ferrier and Watson (1997):

- ☑ Open-forest canopy trees surveyed at 1467 sites;
- ☑ Open-forest understorey plants surveyed at 1103 sites;
- ☑ Diurnal birds surveyed at 445 sites;
- ☑ Small reptiles surveyed at 647 sites;
- ☑ Microchiropteran bats surveyed at 344 sites;
- ☑ Ants (ground-dwelling) surveyed at 198 sites;
- ☑ Beetles (ground-dwelling) surveyed at 187 sites; and
- ☑ Spiders (ground-dwelling) surveyed at 200 sites.

The rainforest plant datasets employed by Ferrier and Watson were not used in the current study because forest ecosystem mapping is primarily a classification of open forest and aggregates all rainforest into a single class. The invertebrate datasets used by Ferrier and Watson were augmented in this study with data on additional taxa generated by Sub-project 3. The main benefit conferred by employing virtually the same datasets as Ferrier and Watson was that the performance of surrogates could be compared across the two studies. All surrogates were evaluated using data from half of the sites available for each biological group. This allowed an unbiased comparison of performance to be made between forest ecosystem mapping and surrogates derived using the biological data itself (e.g. species modelling). To avoid bias, such surrogates were derived using one half of the sites (randomly selected) and evaluated using the other half of the sites (for details see Ferrier and Watson 1997).

2.3.2 Surrogates evaluated

The primary surrogate evaluated in this sub-project was the map of forest ecosystems derived for Upper North East and Lower North East CRA regions, and used as a basis for applying JANIS Biodiversity Criteria 1, 2 and 3. The techniques used to derive the forest ecosystem map are documented in a separate CRA project report. The performance of the forest ecosystem

map as a biodiversity surrogate was also compared to that of a number of other surrogates evaluated in two separate studies (Ferrier and Watson 1997, and Ferrier et al. 1999).

The total list of surrogates for which results are presented in this report is as follows (the names in italics are used throughout the remainder of the report:

- ☑ *Forest ecosystems (raw)* which simply consists of the original mapped forest ecosystems (as used in CRA/RFA negotiations). The forest ecosystem classification for north-east NSW includes 166 classes, of which 149 classes contain one or more biological survey sites.
- ☑ *Forest ecosystems (100)* which is a generalised version of the original forest ecosystem map derived by amalgamating the original ecosystems into 100 classes, based on a hierarchical numerical classification of ecosystems performed during the forest ecosystem mapping project (this numerical classification was performed using full floristic plot data).
- ☑ *Forest ecosystems (50)* which is a generalised version of the original forest ecosystem map derived by amalgamating the original ecosystems into 50 classes.
- ☑ *Forest ecosystems (spatial constraint)* which employs the original forest ecosystem classification but applies a different strategy for selecting reserved sites in the surrogate evaluation. Instead of selecting sites within each ecosystem in a random order, they are selected in order of proximity to previously selected sites. This simulates the formation of a reserve system consisting of spatial clumps of sites within each ecosystem rather than a random scattering.
- ☑ *Forest ecosystems (PD)* which also employs the original forest ecosystems classification but applies another alternative strategy for selecting sites in the surrogate evaluation. Normally, at each step in the selection process, the next site is selected from that forest ecosystem with the lowest representation in the hypothetical reserve system (this is essentially the strategy employed in real CRA/RFA negotiations). However, a number of authors have suggested that, to maximise the representation of biodiversity, prioritisation of vegetation types (or other land classes) for reserve selection needs to account for varying levels of distinctiveness between these types (e.g. Faith and Walker 1996, Woinarski et al. 1996). This approach was tested by using the hierarchical classification (see above) as an indicator of floristic relationships between ecosystems, and then selecting sites in an order which maximises coverage of this diversity using the 'phylogenetic diversity' (PD) algorithm described by Faith (1992).
- ☑ *Forest types* as mapped by State Forests of NSW using the Research Note 17 classification (see Ferrier and Watson 1997).
- ☑ *Environmental units* which is a land classification of north-east NSW derived purely from abiotic environmental variables (rainfall, temperature, soil fertility, slope) with 81 classes (see Ferrier and Watson 1997). This classification has been employed in earlier conservation assessment work in the region.
- ☑ *Modelled species (within group)* in which reserved sites are selected on the basis of predicted probabilities of occurrence for species in the biological group of interest (see Ferrier and Watson 1997). These predictions are derived from distributional models fitted to data from half of the available survey sites. The other half of the sites is then used to evaluate the performance of the predictions as a surrogate.
- ☑ *Modelled species assemblages* in which modelled species distributions for the biological group of interest have been subjected to numerical pattern analysis to group species into 'assemblages' according to similarities in predicted distribution. In this evaluation 20 assemblages were derived for each biological group (see Ferrier et al. 1999).

- ☑ *Modelled trees* in which predicted probabilities of occurrence for canopy tree species is used as a basis for selecting reserved sites, and then evaluated using survey data for each of the other biological groups.

2.4 RESULTS

Table 1 summarises the evaluation results obtained for each of the surrogates described in Section 2.3.2 using survey data for each of the biological groups described in Section 2.3.1. Each value in this table is an estimate of surrogate performance, measured in terms of the Species Accumulation Index (SAI, see Section 2.2). Recall that values for the index range from zero (or less than zero) for a surrogate that performs no better than a random selection of sites, up to one for a surrogate exhibiting ‘perfect’ performance.

TABLE 1: SPECIES ACCUMULATION INDEX RESULTS OBTAINED FROM THE EVALUATION OF FOREST ECOSYSTEM MAPPING AND RELATED SURROGATES

	Canopy trees	Under-storey plants	Birds	Reptiles	Bats	Ants	Beetles	Spiders
Forest ecosystems (raw)	0.252	0.060	0.058	0.124	0.065	0.093	-0.178	0.175
Forest ecosystems (100)	0.277	0.067	0.087	0.218	0.071	0.064	-0.259	0.206
Forest ecosystems (50)	0.123	0.020	0.099	0.272	-0.110	0.157	-0.222	0.243
Forest ecosystems (constrained)	0.206	0.007	0.023	0.089	0.019	0.076	-0.173	0.090
Forest ecosystems (PD)	0.355	0.107	0.087	0.173	-0.065	0.128	-0.249	0.265
Forest types	0.097	-0.007	0.029	-0.059	0.149	-0.070	0.081	0.079
Environmental units	0.116	0.073	0.041	0.025	-0.052	-0.006	-0.032	-0.016
Modelled species (within group)	0.484	0.487	0.308	0.619	0.208	0.058	0.092	0.164
Modelled species assemblages	0.406	0.387	0.221	0.356	Not available	0.076	0.151	-0.074
Modelled trees	0.484	0.433	0.267	0.144	Not available	0.099	-0.129	-0.101

The results are further illustrated in the graphs (a to h) in Figure 1. Each graph depicts the results obtained using survey data for a particular biological group. Confidence limits (95%) are also depicted for each estimated SAI value. The solid horizontal line indicates an SAI value of zero which is the (average) performance achieved by reserving sites in a totally random sequence (i.e. without using any surrogate or biological data). The broken horizontal line indicates the performance achieved by the *Forest ecosystems (raw)* surrogate, thereby providing a benchmark for comparison with the other surrogates.

As with previous evaluations of this type (e.g. Ferrier and Watson 1997, Ferrier et al. 1999) the patterns exhibited by the results presented here are rather ‘noisy’, and often lack consistency

across biological groups and across surrogates. Nevertheless, a number of general trends are worth noting:

- ☑ Forest ecosystem mapping in the form used in CRA/RFA negotiations – *Forest ecosystems (raw)* – did not appear to be a particularly effective surrogate for biodiversity in north-east NSW. Although performing reasonably well as a surrogate for canopy trees, it performed relatively poorly for understorey plants and for most of the vertebrate and invertebrate faunal groups.
- ☑ The performance of forest ecosystem mapping as a biodiversity surrogate was nevertheless better, on average, than that of other surrogates previously used in forest assessments in north-east NSW, i.e. forest types and environmental units. Forest ecosystem mapping performed better than forest types for all biological groups except bats and beetles, and better than environmental units for all groups except understorey plants and beetles.
- ☑ Amalgamation of forest ecosystems into fewer classes (100 or 50) does not have a clear and consistent effect on surrogate performance. When evaluated using canopy trees, understorey plants and bats, *Forest ecosystems (raw)* performed better than *Forest ecosystems (50)* but marginally worse than *Forest ecosystems (100)*. For birds, reptiles and spiders, performance dropped progressively as the number of classes is increased from 50 to 100 to the full classification. These results may seem surprising – surely refining a forest ecosystem classification by increasing the number of classes must result in a better surrogate for biodiversity! The problem would appear to lie not with the forest ecosystem surrogate itself but with the way in which this is employed in selecting reserves, both in the evaluation process and in the real CRA/RFA negotiation process. As mentioned above, the standard approach used to select the next site for reservation is to choose a site containing that forest ecosystem which is most poorly represented in the hypothetical reserve system. This approach does not normally consider information on the biological similarities between the ecosystems involved. For example, at a given stage in the selection process, two forest ecosystems may be equally under-represented in the reserve system and therefore equally likely to be selected at the next step. Yet one of these ecosystems could be reasonably similar to other ecosystems already well represented in reserves while the other is quite different from anything currently reserved. Failure to consider such information may reduce the effectiveness of a biodiversity surrogate. The severity of this problem is likely to increase as the number of classes (e.g. forest ecosystems) is increased. A further problem with the evaluation procedure employed here is that sites within a given forest ecosystem are selected in random order. Therefore, even if an amalgamated forest ecosystem encompasses considerable heterogeneity, sites will be selected randomly across this variation. However, in a real negotiation process the areas reserved within a forest ecosystem are likely to be distributed in a non-random (i.e. biased) fashion, both environmentally and geographically. The next two dot points shed some further light on these problems. At this stage, however, the results relating to the effect of amalgamation of ecosystems on surrogate performance should be regarded as inconclusive. This whole issue warrants further research.
- ☑ *Forest ecosystems (PD)* performed better than *Forest ecosystems (raw)* for all groups except bats and beetles. This result supports the proposition made above that the performance of forest ecosystem mapping as a biodiversity surrogate can be improved by considering information on similarities between ecosystems when selecting reserves.
- ☑ *Forest ecosystems (raw)* performed better than *Forest ecosystems (spatial constraint)* for all groups except beetles. This result suggests that biological variation within mapped forest ecosystems is at least partly correlated with geographical location.

- ☑ The clearest, and probably most important, pattern exhibited by the results is that surrogates based on predictive modelling of species distributions performed much better overall than did forest ecosystem mapping. *Modelled species (within group)* and *Modelled species assemblages* performed better than all versions of forest ecosystem mapping for all biological groups except ants and spiders (in some cases markedly better, e.g. trees, understorey plants, birds and reptiles). Even *Modelled trees* performed better than forest ecosystem mapping as a surrogate for all other biological groups except spiders.

2.5 IMPLICATIONS FOR THE CRA PROCESS

The results of this sub-project have the following implications for the CRA process:

- ☑ Forest ecosystem mapping provides an improved basis for conservation of biodiversity in north-east NSW relative to previously employed surrogates (forest type mapping and environmental unit mapping).
- ☑ The efficacy with which biodiversity is reserved through use of forest ecosystems can be improved further by considering information on floristic similarities between ecosystems when prioritising areas for reservation. The C-Plan decision support software needs to be extended to address this issue.
- ☑ However, even with this refinement, the performance of forest ecosystem mapping as a biodiversity surrogate is well below optimum. Shortcomings in the surrogate must therefore be addressed in the CRA/RFA negotiation process by giving due emphasis to JANIS Biodiversity Criteria 5 and 7.
- ☑ Future conservation assessment and planning work in north-east NSW and other regions should consider seriously the potential role of biodiversity surrogates derived through alternative means such as species and assemblage modelling. Such surrogates, used in addition to, or in place of, traditional vegetation mapping can greatly improve the efficacy of reserve selection in terms of biodiversity conservation. An example from this evaluation is the superior performance of modelled species assemblages relative to forest ecosystem mapping. This performance is particularly impressive given that the former consisted of only 20 entities whereas the latter consisted of over 160 entities.

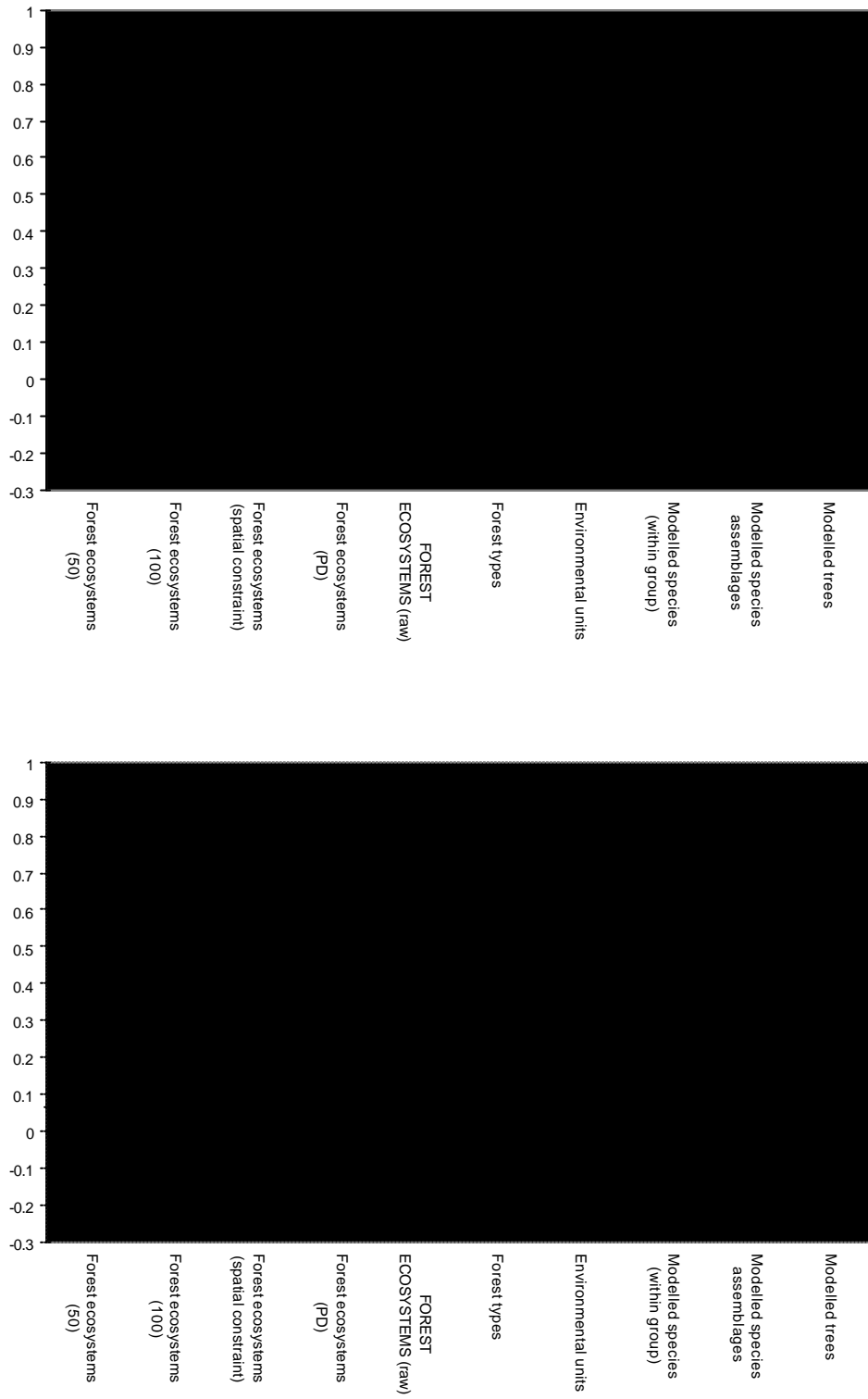


Figure 1. Species Accumulation Index results obtained from the evaluation of forest ecosystem mapping and related surrogates.

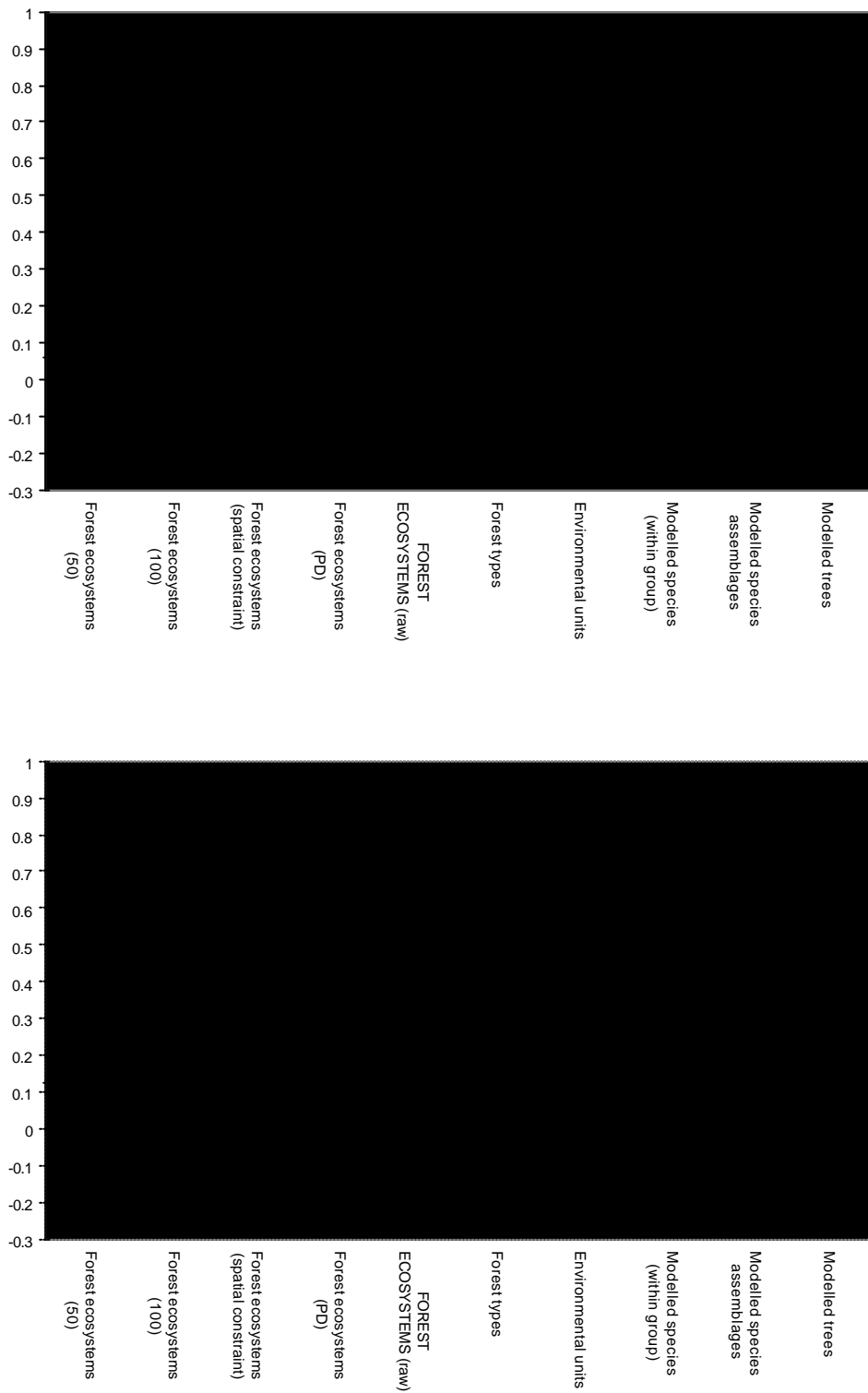


Figure 1 (continued). Species Accumulation Index results obtained from the evaluation of forest ecosystem mapping and related surrogates.

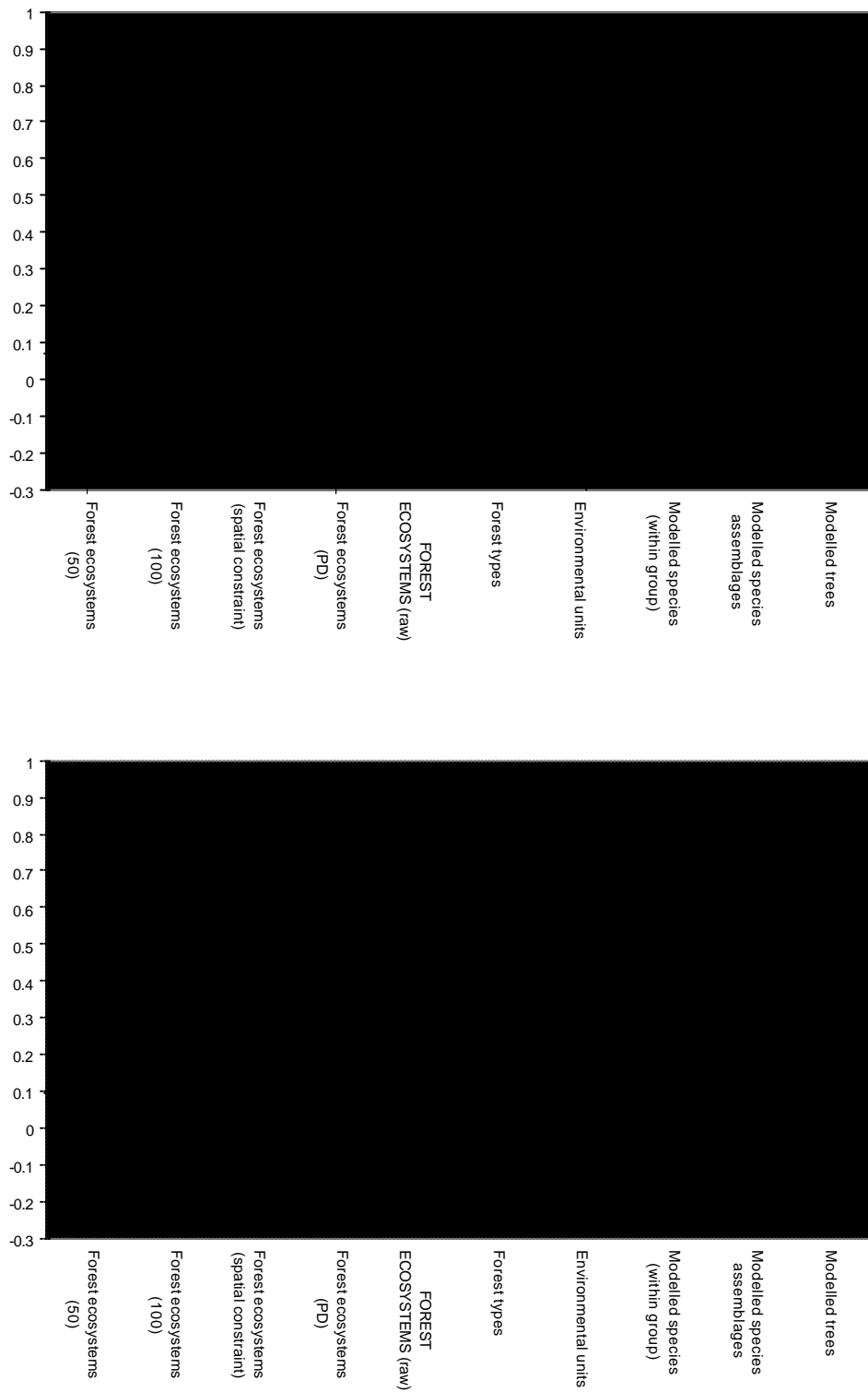


Figure 1 (continued). Species Accumulation Index results obtained from the evaluation of forest ecosystem mapping and related surrogates.

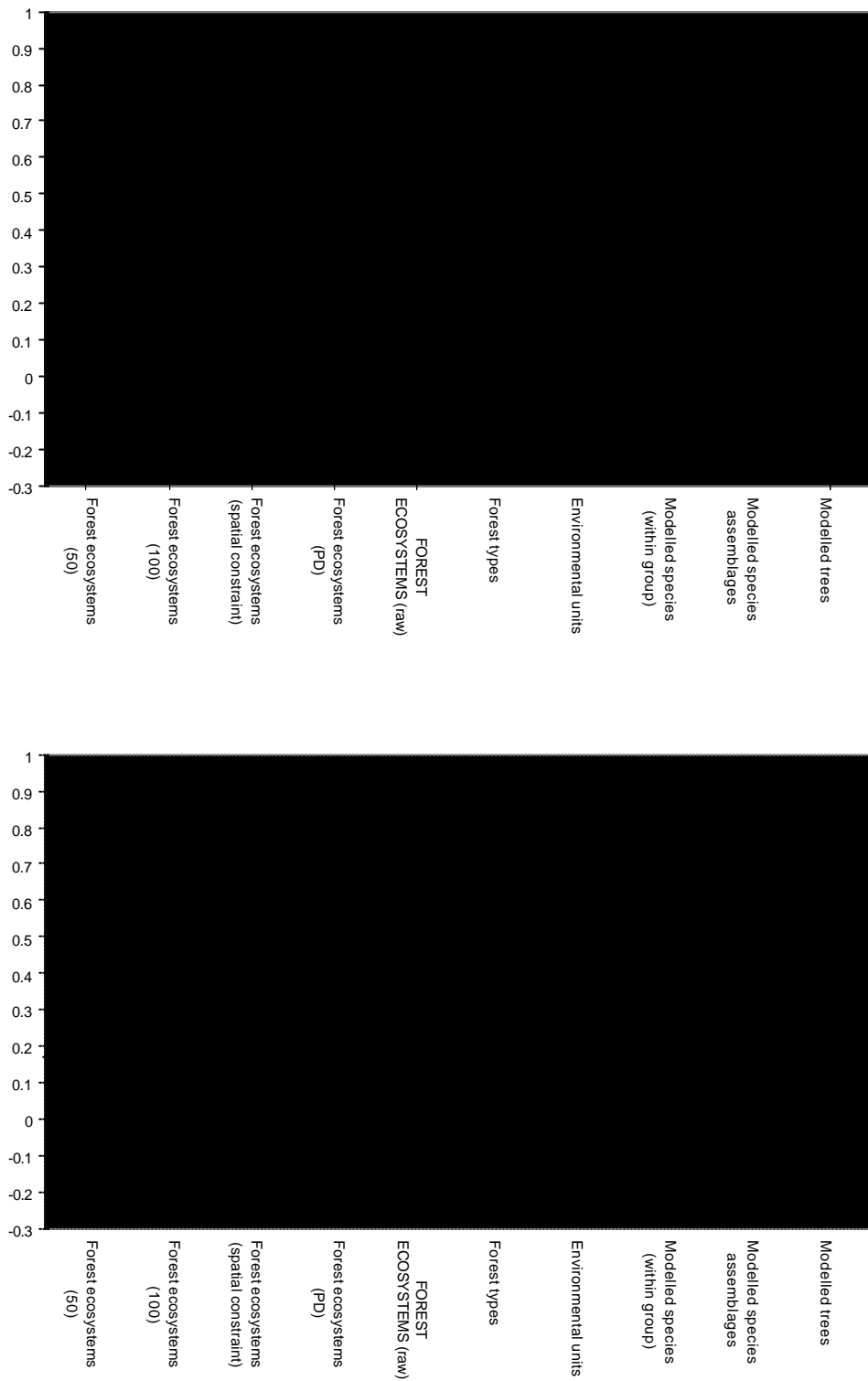


Figure 1 (continued). Species Accumulation Index results obtained from the evaluation of forest ecosystem mapping and related surrogates.

3. SUB-PROJECT 2: ANALYSIS OF BIOLOGICAL VARIATION WITHIN DERIVED FOREST ECOSYSTEMS

3.1 INTRODUCTION

The results of Sub-project 1 (see Section 2) suggest that the forest ecosystems derived for Upper North East and Lower North East CRA Regions are not particularly homogeneous. It appears that each mapped ecosystem can exhibit a considerable level of biological variation (heterogeneity). The purpose of Sub-project 2 was to investigate the extent to which this internal variation is correlated with measurable environmental and geographical gradients. This investigation was aimed at providing an improved basis for applying JANIS Biodiversity Criterion 7 *'to ensure representativeness, the reserve system should, as far as possible, sample the full range of biological variation within each forest ecosystem, by sampling the range of environmental variation typical of its geographic range'*.

The approach employed resembled that described by Ferrier et al. (in press). The observed biological dissimilarity between pairs of field survey sites located within the same forest ecosystem was analysed in relation to the environmental and geographical separation of these sites.

3.2 DATA

3.2.1 Biological datasets

The biological datasets used in this analysis were almost identical to those described by Ferrier and Watson (1997), and used in Sub-project 1:

- ☑ Open-forest canopy trees surveyed at 1467 sites;
- ☑ Open-forest understorey plants surveyed at 1103 sites;

- ☑ Diurnal birds surveyed at 445 sites;
- ☑ Small reptiles surveyed at 647 sites;
- ☑ Microchiropteran bats surveyed at 344 sites;
- ☑ Ants (ground-dwelling) surveyed at 198 sites;
- ☑ Beetles (ground-dwelling) surveyed at 237 sites; and
- ☑ Spiders (ground-dwelling) surveyed at 241 sites.

The rainforest plant datasets employed by Ferrier and Watson were not used in the current study because forest ecosystem mapping is primarily a classification of open forest and aggregates all rainforest into a single class. The invertebrate datasets used by Ferrier and Watson were augmented in this study with data on additional taxa generated by Sub-project 3.

3.2.2 Environmental and geographical variables

The abiotic environmental variables employed in the analysis were standard layers included in the GIS databases for the CRA process:

- ☑ Rainfall (mean annual)
- ☑ Temperature (mean annual)
- ☑ Solar radiation (mean annual, terrain adjusted)
- ☑ Moisture index
- ☑ Compound topographic index (wetness index)
- ☑ Soil depth
- ☑ Soil fertility rating
- ☑ Prescott index
- ☑ Site productivity index (derived from modelling of canopy height data).

The geographical distance between pairs of sites was calculated from the map coordinates of the sites.

3.3 ANALYTICAL METHODOLOGY

The analytical methodology employed closely resembled that described by Ferrier et al. (in press). Each biological group (e.g. beetles) was analysed separately. The level of biological dissimilarity between all possible pairwise combinations of sites (surveyed for the group) was estimated using the Bray-Curtis dissimilarity measure. This yielded a sites-by-sites dissimilarity matrix in which each cell of the matrix contained the Bray-Curtis dissimilarity between a given pair of sites.

A second sites-by-sites matrix was prepared in which each cell contained the geographical distance between a pair of sites. Additional sites-by-sites matrices were also prepared to record the distance between sites in terms of each of the abiotic environmental variables. This distance was calculated as the absolute difference between values of a given variable at two sites (for example, if the first site had a rainfall of 1200mm and the second site had a rainfall of 1500mm then the difference is 300mm).

The biological dissimilarity between sites was analysed in relation to geographical separation and environmental differences using the multiple matrix regression technique described by Manly (1986) and Smouse et al. (1986). Legendre (1993) and Burgman (1987) provide good examples of the application of this general approach to ecological analysis. Linear regression modelling was used to regress biological dissimilarity, between all possible pairs of sites, against specified sets of geographical and environmental distance variables (matrices). The statistical significance of differences in explanatory power (measured in terms of R^2) between regression models fitted to different sets of predictors was tested using Monte Carlo randomization.

An important difference between the analyses presented here and those described by Ferrier et al. (in press) is that here we are analysing geographical and environmental patterns of biological variation within mapped forest ecosystems whereas the original study analysed patterns across the entire region, regardless of forest ecosystem. The specific aim of the current analysis was addressed by making a slight modification to the original analytical approach. The regression models were fitted using only pairs of sites that occurred within the same mapped ecosystem. For example, if we were considering four sites – 1 and 2 occurring in forest ecosystem A and 3 and 4 occurring in ecosystem B – then the site pairs analysed would be 1-2 and 3-4 (site pairs 1-3, 1-4, 2-3, 2-4 would be excluded). This meant that biological variation between forest ecosystems was effectively controlled for, and that the analysis therefore focused exclusively on variation within ecosystems.

3.4 RESULTS

The results of the analysis are summarised in Table B.

TABLE 2: RESULTS OF ANALYSIS OF BIOLOGICAL VARIATION WITHIN FOREST ECOSYSTEMS IN RELATION TO ENVIRONMENTAL AND GEOGRAPHICAL GRADIENTS

	Env + Geo	Env only	Geo only	1	2	3	4	5	6	7	8	9
Trees	19.8	19.0	7.6	•	•		•	•		•		•
Understorey	22.6	21.5	8.9		•	•	•			•	•	•
Birds	8.7	7.6	2.2		•		•	•				
Reptiles	15.7	8.8	12.0		•		•	•		•		•
Bats	19.0	15.2	11.1		•			•				•
Ants	20.5	19.7	3.0	•	•	•						•
Beetles	18.0	2.1	16.8	•	•	•						
Spiders	27.7	13.2	20.5	•	•				•	•	•	

Env + Geo: R^2 (%) for matrix regression model containing both environmental variables and geographical separation

Env only: R^2 (%) for matrix regression model containing only environmental variables

Geo only: R^2 (%) for matrix regression model containing only geographical separation

1 to 9: Environmental variables included in each regression model (1=rainfall, 2=temperature, 3=solar radiation, 4=moisture index, 5=compound topographic index, 6=soil depth, 7=soil fertility, 8=Prescott index, 9=site productivity index).

The column labelled 'Env + Geo' lists the R^2 values (%) obtained from matrix regression models fitted to the data for each biological group, using both environmental variables and geographical separation as predictors of biological dissimilarity. Monte Carlo testing indicated that all of these

R^2 values were significantly greater than zero ($p < 0.001$), suggesting that biological variation within the mapped forest ecosystems is at least partly correlated with measurable environmental and geographical gradients. The columns labelled 1 to 9 indicate which environmental variables were included in each model (these variables were selected using a forward selection procedure, as described by Ferrier et al. in press).

The column labelled 'Env only' lists R^2 values obtained from models fitted using only environmental variables, i.e. excluding geographical separation. The column labelled 'Geo only' lists R^2 values for models fitted using geographical separation alone, i.e. excluding the environmental variables. These results suggest that the relative importance of environmental and geographical factors (as correlates of biological variation within forest ecosystems) varies between biological groups. For example, in the case of canopy and understorey plants, birds and ants most of the variation explained by a full model (with both environmental and geographical variables) can also be explained by a model containing only environmental variables. Geographical separation on its own is a poor predictor of biological variation in these groups. On the other hand, geographical separation is a reasonably good predictor of variation in beetles and spiders (and to a lesser extent reptiles), whereas a model containing only environmental variables performs relatively poorly for these groups.

3.5 IMPLICATIONS FOR THE CRA PROCESS

The results of this sub-project have the following implications for the CRA process:

- ☑ Biological variation within mapped forest ecosystems in Upper North East and Lower North East CRA Regions is significantly correlated with broad-scale (GIS-based) environmental variables and geographical location. This internal variation needs to be addressed by applying JANIS Biodiversity Criterion 7 *'to ensure representativeness, the reserve system should, as far as possible, sample the full range of biological variation within each forest ecosystem, by sampling the range of environmental variation typical of its geographic range'*.
- ☑ In applying Biodiversity Criterion 7, due consideration needs to be given to sampling both the geographical range and the environmental range covered by each forest ecosystem. Sampling only one of these may not achieve effective representation of variation for particular biological groups (variation in some groups appears to be most strongly correlated with geographical separation while others are more strongly correlated with environmental variation).
- ☑ Practical application of Biodiversity Criterion 7 has now been facilitated by the development of new 'spatial configuration' functionality within C-Plan (see separate CRA report). This functionality uses information on the distance between pairs of planning units to derive various measures of 'geographical and environmental spread' of reservation within forest ecosystems. Matrix regression models such as those developed here could provide an effective basis for using both environmental and geographical information to estimate 'distance' in terms of predicted biological dissimilarity.

4. SUB-PROJECT 3: COLLATION AND PREPARATION OF INVERTEBRATE DATA

4.1 INTRODUCTION

The purpose of this sub-project was to collate, database and prepare data on selected invertebrate groups in the Upper North East and Lower North East Regions, for use in Sub-projects 1 and 2 (see Sections 2 and 3 of this report) and for use in the analysis and mapping of invertebrate 'centres of endemism' (the methodology and results of this analysis are documented in a separate CRA project report). The sub-project was performed by the Australian Museum.

4.2 COLLATION AND DATABASING OF INVERTEBRATE RECORDS

Data were collated for the following invertebrate groups, yielding a total of 11,347 records (see Map 1):

- Worms (Family Megascolecidae);
- Snails (Families Rhytididae, Camaenidae, Helicaronidae, Charopidae, Caryodidae);
- Insects (Families Scarabaeidae, Lucanidae, Hybosoridae, Staphylinidae, Carabidae, Tenebrionidae, Curculinidae);
- Crustacea (Families Parastacidae, Phreatocidae); and
- Spiders (Families Hexathelidae, Idiopidae).

Work on each of the groups was carried out separately up until the data preparation stage when all the data were amalgamated for analysing and mapping centres of endemism, and a subset of the amalgamated data was sent to NSW NPWS for the evaluation of surrogacy and analysis of biological variation within forest ecosystems. All collated records had a spatial accuracy of better than 10km.

Snails (Molluscs)

The mollusc data were obtained largely from the Australian Museum collections. Any relevant material from recent field work was incorporated and this, together with much of the existing

material in the research collection, had to be databased for the project. All of the material used was reidentified by contracted experts in the groups involved. Every specimen in the collection was reexamined to ensure accurate and consistent identification of snail species. In addition, data from the Queensland Museum were purchased and specimens were identified by the same experts to ensure consistency. During the course of the project up to 6 individuals were involved in processing the mollusc data on any one day to ensure that the results were obtained within the required 6 week time frame.

Insects

The insect data were obtained from a combination of:

- existing Australian Museum collections which had already been sorted, labelled and databased including data from the North East Forest Biodiversity Study (Gray and Cassis 1994);
- existing Australian Museum collections not yet databased but sorted and labelled;
- existing Australian Museum collections not yet sorted, labelled or databased including specimens from the North East Forests Biodiversity Study;
- databased records purchased from the Queensland Museum – who sorted, labelled and databased the records; and
- specimens from the private collection of Geoff Williams which were checked (for identification) and databased by the Australian Museum.

In the case of unsorted specimens from the North East Biodiversity Study, six technical staff spent six weeks extracting specimens of the groups of interest from the pitfall trap 'soup'. Each of these specimens was then mounted, labelled and all their site details were databased. A taxonomic expert (Dr Chris Reid) was used to identify each specimen to species level.

Spiders

The spider data were collated from several available sources, including survey reports; published literature; and Australian Museum & Queensland Museum collection databases. New data were made available from the existing collections by sorting and identifying relevant unworked spider material.

Three Australian Museum staff (Mike Gray, Graham Milledge, Rebecca Harris) spent two weeks gathering, verifying and collating the spider data for this project.

Worms and Crustacea

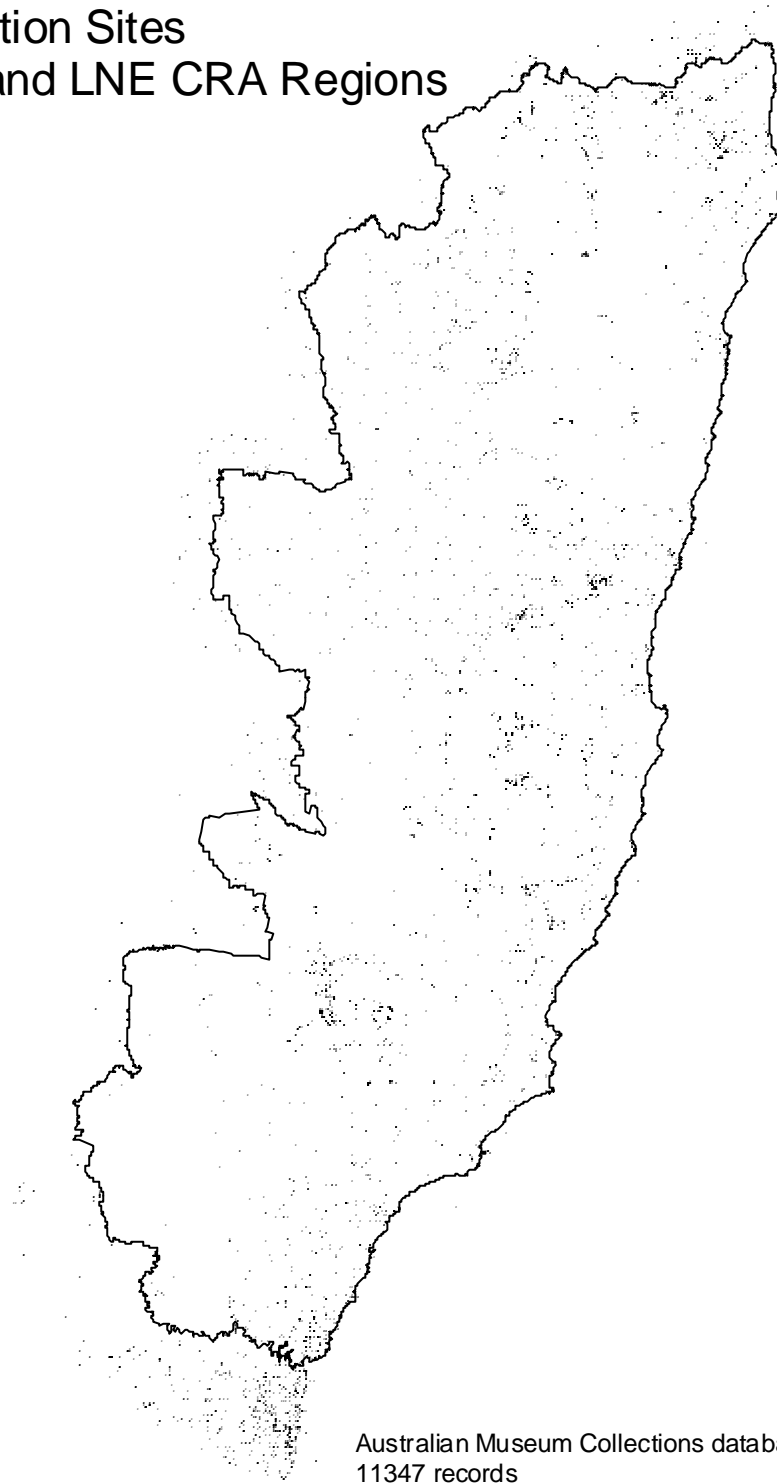
Worms and Crustacea data were obtained through identification of existing Australian Museum specimens by relevant taxonomic experts from both within and external to the museum.

4.3 PREPARATION OF DATA FOR ANALYSIS

Two different amalgamated datasets were prepared for analysis:

- The evaluation of surrogacy and analysis of biological variation within derived forest ecosystems utilised only those records collected by systematic pitfall trapping surveys. All of these records had a locational accuracy of better than one kilometre.
- The analysis of centres of endemism utilised all records made available by the above collation process (all of these records had a spatial accuracy of better than 10km).

Collection Sites
UNE and LNE CRA Regions



Map 1. Locations of invertebrate records collated and databased by Sub-project 3.

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