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Classification of aquatic bioregions through the use of distributional modelling of freshwater fish

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ABSTRACT

Bioregional classifications are used to manage natural resources including the conservation of biota. There are a variety of ways to define bioregions and mostly a combination of data analysis and subjective expert judgement is used, mainly because data on the distributions of biota are sparse or uneven. We trialled a method of using distributional modelling of individual freshwater fish species to produce a classification of rivers in New South Wales, Australia. Distributional modelling was done for 44 fish taxa using the genetic algorithm for rule set production (GARP) and a classification was done using non-hierarchical clustering. The data used was a combination of museum records (presence only records) and data from designed surveys. The natural distributions of seven fish species could not be modelled due to insufficient records. The models for the majority of remaining species displayed substantial to almost perfect model accuracy. The classification produced similar bioregions as had been previously defined for freshwater fish in New South Wales. Our study demonstrates that distributional modelling of individual species is a feasible and practical approach to defining regions using data derived from a variety of sources. The potential benefits of the method would be that a description of the potential "natural" fish assemblage could be described for any given site, separation between zones can be clearly delineated and it is independent of the actual fish sampling locations.

1. Introduction

Australia has a large range of natural conditions resulting in a very diverse range of ecosystems with complex interactions and conditions (Wells and Newall, 1997). The range of biodiversity and ecological conditions creates difficulties in managing the natural resources because water quality and biological management guidelines for aquatic systems in one part of the continent may not be applicable to other parts. Classification of biodiversity into bioregions assists with management of natural resources, for example the interim biogeographic regionalisation of Australia (IBRA) was developed to assess and plan for the protection of terrestrial biodiversity by developing a national reserve system throughout Australia (Cummings and Hardy, 2000). However, many authors have demonstrated that there is little similarity between terrestrially derived regionalisation and those developed just considering aquatic fauna (Wells and Newall, 1997; Hawkins et al., 2000; Hawkins and Vinson, 2000; Pan et al., 2000; Abell et al., 2002). Classification of rivers into aquatic bioregions is therefore necessary for successful management of water resources (Gallant et al., 1991). For example, the United States, Environmental

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Protection Agency is currently using an aquatic ecoregional classification for the purposes of water management across the USA (Omernik, 1987).

There are several possible approaches to define bioregions at a variety of spatial scales (e.g. Higgings et al., 2005). The main premise of all approaches is to define units of land or water of relative homogeneity that are distinct from other regions. The approaches range from the purely 'objective' methods, mainly using data analysis, through to the 'Delphic' (collaborative expert judgement) approaches (Gallant et al., 1991). Delphic approaches are generally used when data are sparse or uneven, but where there are experts with intimate knowledge for the system based on their long experience (DEH, 2003). Scientific-analytic approaches have been employed where there are detailed data with adequate spatial coverage. In practice a combination of methods are used, for example, the one of latest classification of ecoregions in North America was based on Maxwell et al. (1995), who defined ecological units for fish assemblages, but was modified by biodiversity experts to better represent the distributions of molluscs and crayfish (Abell et al., 2000). Another example of a range of approaches being used is the IBRA which was developed using a combination of expert opinion and/or base datasets of geological or biotic data. The outcome also depended upon the different Australian states which had developed their own individual bioregional classifications.

Scientific-analytic approaches often use data describing the distributions of various taxa based on survey data but require adequate spatial coverage. Species distribution models (SDMs) are useful tools for converting individual point data into the hypothetical natural range of a species (Corsi et al., 2000; Loiselle et al., 2003). SDMs have great potential utility for management because conservation biologists are often pressed to make recommendations about conserving biodiversity based on limited species-distribution data (Peterson et al., 2002; Loiselle et al., 2003). Deficiencies in knowledge of the ecology of Australian rivers mean that ecological regions have not yet been well defined for riverine fauna (Gehrke and Harris, 2000). The aim of this paper was to trial a method of developing an aquatic bioregional classification of rivers and streams in New South Wales based on the predicted natural distributions of freshwater fish species. The potential benefits of the method would be that a description of the potential "natural" fish assemblage could be described for any given site, separation between zones can be clearly delineated and it is independent of the actual fish sampling locations. The applicability of the method to other aquatic biota is also considered.

2. Methods

2.1. *Environmental data layers and fish site data*

Ten environmental data layers were used for modelling the distribution of fish. Climatic data, including average rainfall, rainfall variability, maximum and minimum temperature, were obtained from the Australian Bureau of Meteorology. Slope and elevation were obtained from a digital elevation model supplied by the Department of Natural Resources. Major catchment boundaries for rivers in the state were provided by the Department of Environment and Conservation. Layers for latitude and longitude were derived from the other GIS data. Catchment area for each grid cell was obtained from the Australian National University. All environmental layers were resampled to 0.01° or approximately 1-km grid squares.

Records of native freshwater fish species throughout New South Wales (NSW) were obtained from the collections of the Australian Museum and two freshwater fish databases of the Department of Primary Industries (DPI). The museum data consisted of single records for more than 4000 fish collected between 1880 and 2004. The DPI data consisted of records of over 220,000 individual native fish sampled between 1974 and 2004. A total of 2483 sampling locations were recorded. Due to the long record of data there have been some taxonomic changes to the names of species. To maximise the number of taxa to be modelled, species in the genera *Craterocephalus* and *Hypseleotris* from the Murray-Darling Basin (MDB) were pooled. Records of fish known to be stocked or translocated populations were excluded from analysis.

2.2. *Species distributional mapping and bioregional classification*

We used the genetic algorithm for rule-set production (GARP) (Stockwell and Noble, 1991; Stockwell, 1999; Stockwell and Peters, 1999) to produce distributional maps for native freshwater fish species in New South Wales. Details on how GARP functions can be obtained from those authors but in summary GARP relates the ecological characteristics of known occurrence points to those of points sampled randomly from the rest of the study region. The algorithm then develops a series of decision rules that best summarise those factors associated with the species presence (Feria and Peterson, 2002). GARP was used in preference to other modelling techniques (e.g. logistic regression) because it can cater for presence only data, such as museum records.

GARP works using an iterative process of rule selection, evaluation, testing and incorporation or rejection. A method is chosen from a set of possibilities (e.g. bioclimatic rules), applied to a dataset and the rule is developed or evolved (Peterson et al., 2002). Predictive accuracy was evaluated based on 1250 points resampled from the data and 1250 points sampled randomly from the study region as a whole. The predictive accuracy was calculated as the sum of points actually present predicted as present plus absent predicted as absent, divided by the total number of points on the map (Stockwell and Noble, 1991). The change in predictive accuracy from one iteration to the next is used to evaluate whether a particular rule should be incorporated in the model. The algorithm runs a large number of iterations (e.g. 1000) or until addition of extra rules has no appreciable effect on the accuracy measure. All modelling was carried out on a desktop implementation of GARP (Scachetti-Pereira, 2001).

Previous applications of GARP have used single models to predict species' distribution (Peterson, 2001; Peterson et al., 2002), combined multiple models to incorporated model-to-model variation (Peterson and Vieglais, 2001) or combined multiple models meeting various accuracy criteria using the 'Best Models Option' within Desktop-GARP (Anderson et al.,