rapr: Representative and Adequate Prioritisations in R

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A central aim in conservation is to maximise the long-term persistence of biodiversity. To fulfil this aim, reserve networks are used to safeguard biodiversity patterns (eg. species, populations) and processes (eg. evolutionary processes that underpin genetic variation). Reserve selection is often formulated as an optimisation problem to identify cost-effective prioritisations. However, most existing decision support tools are based on formulations that are well suited for preserving biodiversity patterns, but not biodiversity processes. To fill this gap in the conservation planning toolbox, we developed the rapr R package. This R package provides functions to solve reserve selection problems using two novel formulations. Here, we explore the functionality of this R package using simulated species and a conservation planning exercise in Queensland, Australia as a case-study. We demonstrate how explicitly considering biodiversity processes can alter a prioritisation. In most cases, we found that only a few additional plannning units are required to sufficiently preserve of biodiversity processes.

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## Introduction

The overarching aim of conservation is to maximise the long-term persistence of biodiversity (McNeely 1994; Margules and Pressey 2000). To achieve this, conservation actions must preserve biodiversity patterns (eg. species, populations) and the processes that sustain them. One of the major tangible achievements of modern conservation has been the act of setting aside areas for preservation (Sanderson *et al.* 2015). Reserve networks buffer species from threatening processes [Margules and Pressey (2000); eg. urbanisation] and set the stage for direct management interventions (eg. captive breeding and reintroduction programs; Kleiman 1989). However, the resources available for conservation action are limited, and so reserve networks must be sited in places that satisfy conservation objectives for minimum cost (Margules and Pressey 2000). To achieve this, reserve selection is often formulated as an optimisation problem and then solved to identify cost-effective candidate reserve systems (prioritisations; Margules and Pressey 2000).

To fulfil the overarching aims of conservation, reserve networks must preserve both ecological and evolutionary processes (Margules and Pressey 2000; Crandall *et al.* 2000). Ecological processes, such as predator-prey interactions, pollination, and decomposition, are required for biodiversity to persist over short time-scales. Typically, they operate over small geographic domains–with exceptions such as migration and refugial habitats–and can be preserved using suitably large planning units (Ciarleglio *et al.* 2009) that each contain a discrete unit of habitat (Klein *et al.* 2009). On the other hand, evolutionary processes are required for biodiversity to persist over long time-scales, and they typically operate over large geographic domains. Adaptive evolutionary processes can be preserved by securing populations with different adaptations and/or along selection pressure gradients (eg. environmental gradients; Moritz 2002; Crandall *et al.* 2000; Rouget *et al.* 2003; Cowling *et al.* 2003). Neutral evolutionary processes can be preserved by securing populations with different evolutionary histories and/or with limited gene flow (Moritz 2002; Carvalho *et al.* 2011; Ponce-Reyes *et al.* 2014). Due to advances in technology in recent decades, a wealth of data on biodiversity processes has become freely available to conservation planners. Yet this data is only rarely used to guide conservation planning exercises (Hendry *et al.* 2010). Existing decision support tools focus primarily on preserving biodiversity patterns or occasionally processes–but not both.

Many tools have been developed to assist conservation planners in preserving biodiversity patterns (eg. C-Plan, Pressey *et al.* 2009; ConsNet, Ciarleglio *et al.* 2009; Marxan, Ball *et al.* 2009; Zonation, Moilanen 2007). They use targets (eg. Marxan) or weights (eg. Zonation) to identify prioritisations that contain an adequate amount of individuals or habitat for a set of species (features). To accommodate information on biodiversity processes, conservation planners can split features into sub-features as a pre-processing step (eg. Carvalho *et al.* 2011). However, this approach is limited because data on biodiversity processes is often continuous and hyper-dimensional (eg. bioclimatic data; Hijmans *et al.* 2005), and therefore they often cannot be reduced to a few categories without significant information loss (Faith and Walker 1996). Additionally, these problem formulations cannot accommodate variation within sub-features, and nor can they account for relationships between sub-features (Faith and Walker 1996).

Very few tools have been developed with a specific focus on biodiversity processes. The DIVERSITY decision support tool (Faith 2003) uses continuous data to site reserves in places that secure a representative sample of variation across a study area (eg. environmental variation). Originally, this tool was developed to identify prioritizations that secure a comprehensive set of habitats without using any species-level data. As a consequence, the effectiveness of this tool has been highly contested (Araújo *et al.* 2001, 2003; Faith 2011). Additionally, this tool tended to deliver excessively fragmented prioritisations (cf. Marxan). However, unlike tools that primarily focus on biodiversity patterns, this tool can only accommodate data on the distribution of a single feature.

Today, one of the key issues preventing decision makers from explicitly considering both biodiversity patterns and processes in the reserve selection process is the lack of a decision support tool that can accommodate data on both in a multi-species context. To fill this void, we present the rapr R package. This R package provides decision makers with the tools to identify prioritisations that preserve biodiversity patterns and processes. These prioritisations are generated by solving novel formulations of the reserve selection problem that use adequacy- and representation-based targets. We also provide a tutorial showcasing the functionality of this R package using simulated species and a case-study conservation planning scenario in Queensland, Australia.

## Problem formulations

The rapr R package uses two novel formulations of the reserve selection problem to identify cost-effective prioritisations. These formulations share many constraints and variables. For brevity, the variables used by both formulations will be defined. Biodiversity features are defined as the entity(s) that the prioritisation is required to preserve (eg. species, populations). Spatial attributes are defined as the intra-feature variation that the prioritisation is required to sample. These attributes are related to the biodiversity processes that the prioritisation needs to represent (eg. environmental variation).

Each attribute is conceptualised as a space and planning units are thought to occupy points inside each space. This space is termed an attribute space. For example, a decision maker may require a prioritisation that preserves populations along climatic gradients. To achieve this, the decision maker might use an “climatic” attribute space with dimensions relating to mean annual temperature (C) and precipitation (mm). Any given combination of temperature and precipitation may be conceived as a point in this environmental space. By associating planning units with climatic data, they can be mapped from geographic space to this environmental attribute space.

Demand points are points that exist in an attribute space. They are designated by the decision maker to indicate regions of the attribute space that should be preserved in the prioritisation. The amount of variation in the attribute space that a prioritisation secures is a function of the distance between each demand point and each planning unit in the attribute space. The shorter the distances between the demand points and the planning units; the better the prioritisation is at representing the variation in the spatial attribute. To convert these amounts to a proportion–a meaningful unit for a decision maker–the distances between the selected planing units and the demand points are scaled by the distances between the demand points to the centroid of the demand points. In any attribute space there may exist points that are impossible (eg. mean annual rainfall -5 mm), do not occur in the study area (eg. mean annual temperature 30C in Antarctica), or are undesirable (eg. conditions known to be outside the physiological tolerance of a species). By placing demand points in desirable regions of an attribute space, the decision maker can ensure that prioritisations secure desirable values of a spatial attribute.

To illustrate these concepts, we will briefly describe a conservation planning scenario example involving attribute spaces and demand points. A decision maker may wish to develop a prioritisation for a single species. This species has four populations in the study area. These populations are in the process of divergent evolution, with different populations inhabiting different environmental conditions and accruing different adaptations. However, the decision maker can only afford to preserve three of the populations. The decision maker needs to select a set of populations that will secure the most of intra-specific variation. To describe this intra-specific variation–given that no genetic data was available–the decision maker obtained data on the environmental conditions (rainfall (ml) and temperature (C)) where each population was found. The decision maker then used this environmental data to construct a two-dimensional environmental attribute space. Next, the decision maker generated demand points as equi-distant points between the range of values where the populations were found ( 20% to avoid edge effects; Faith and Walker 1996). By comparing the distribution of the demand points to the distribution of the populations in the attribute space, the decision maker can identify a suitable prioritisation (Figure 1). We can see that if the decision maker preserves both populations and , they will effectively “double-up” on the same environmental characteristics, and in turn their waste resources. Instead, a more representative sample of the intra-specific variation could be preserved by securing populations , , and . This example demonstrates how the inclusion of biodiversity processes can guide the reserve selection process.

![](data:application/pdf;base64,)

Example of an attribute space. This environmental attribute space has dimensions relating to annual temperature (C)and rainfall (ml) values. Letters denote the environmental conditions associated with the geographic locations where four hypothetical populations are found. Points represent demand points. In this space, populations closer to each other are considered more similar to each other.

The problem formulations used to guide reserve selection in the rapr R package are based on a combination of the Marxan reserve selection problem and uncapacitated facility location problems (all mathematical terms defined hereafter are described in Table S1 for convenience). For convenience, the cardinality of sets will be denoted using the same symbol used to denote the variable. Define to be the set of features (indexed by ). Let be a set of planning units (indexed by ). Also, let denote the area, and denote the cost of preserving planning unit . To assess the extent to which each feature is secured in a given prioritisation, let denote the probability of feature occupying planning unit . The level of fragmentation associated with a prioritisation is parametrised as the net exposed boundary length. Let the shared boundary length between each planning unit and be . In any real-world problem, some planning units will have edges that are not associated with any neighbouring planning units (eg. edges along coastlines), these cases will be denoted using for .

Let denote a set of attribute spaces (indexed by ). Each is associated with spatially explicit data that represent coordinates for each attribute space . Let denote a set of demand points (indexed by ) for each feature and each attribute space . Let denote the weighting for each demand point , and . Let denote the distance between each demand point and each planning unit for each feature and attribute space . Let denote the distance between each demand point and the centroid of the demand points. Demand points with greater weight are more important, and the optimal solution will be likely to select planning units close to highly weighted demand points. As a consequence, the decision maker will need to choose an appropriate weighting for each demand point. The decision maker will also need to choose an appropriate distance metric for each attribute space. For example, Euclidean, Mahalanobis (Mahalanobis 1936), Bray-Curtis, or other distance metrics may be appropriate given the nature of the attribute space (Faith *et al.* 1987).

Targets are used to ensure that prioritisations adequately preserve each species. Amount-based targets are used to ensure that the total amount of habitat preserved is sufficient. Let denote the expected amount of area that needs to be preserved for each feature . Space-based targets are ensure that a sufficient proportion of the intra-specific variation is secured. Let denote the space-based targets for feature and attribute space . For convenience, these both types of targets are expressed as proportions in the R package.

The R package provides two formulations for reserve selection. They are based on the unreliable (Fernández and Landete 2015) and reliable uncapacitated facility location (Cui *et al.* 2010) problems. The key difference between them is that the reliable formulation explicitly considers the probability that the planning units are occupied when calculating the proportion of variation that a given solution secures, whereas the unreliable formulation does not.

### Unreliable formulation

In the unreliable formulation, the control variables are the , , and variables, and the decision variables are the and variables.

$$\begin{aligned}
X\_j
&= \begin{cases}
1, & \text{if planning unit $j$ is selected for conservation action} \tag{1a} \\
0, & \text{otherwise} \\
\end{cases} \\
\hat{T}\_s &= \text{amount target for feature $f$} \tag{1b}\\
\bar{T}\_{sa} &= \text{representation target for feature $f$ in attribute space $a$} \tag{1c}\\
BLM &= \text{boundary length modifier: penalises overly fragmented solutions} \tag{1d}\\
Y\_{fsi} &= \begin{cases}
1, & \text{if planning unit $i$ is assigned to planning unit $j$ for feature $f$ in space $s$} \tag{1e} \\
0, & \text{otherwise} \\
\end{cases} \\\end{aligned}$$

The unreliable formulation (URAP) is a defined as a multi-objective optimisation problem.

$$\begin{aligned}
& \text{(URAP)} & \text{Min } & \sum\_{j=0}^{J-1} C\_j + BLM \times \sum\_{j=0}^{J-1} \sum\_{k=j}^{J-1} X\_j \left( 1-X\_k \right) b\_{jk} + & & \tag{2a} \\
& & & BLM \times \sum\_{j=0}^{J-1} x\_j b\_{jj} & & & \\
& & \text{s.t. } & \sum\_{j=0}^{J-1} A\_j q\_{jf} \geq \bar{T}\_{f} & \forall & 0 \leq f \leq F-1 \tag{2b}\\
& & & 1 - \frac{\sum\_{i=0}^{I-1} \sum\_{j=0}^{J-1} \left( \lambda\_{fsi} d\_{fsij} Y\_{fsij} \right)^2}{\sum\_{i=0}^{I-1} \left( \lambda\_{fsi} \hat{d}\_{fsi} \right)^2 } \geq \hat{T}\_{fs} & \forall & 0 \leq f \leq F-1, \tag{2c}\\
& & & & & 0 \leq s \leq S-1\\
& & & \sum\_{j=0}^{J-1} Y\_{fsij} = 1 & \forall & 0 \leq f \leq F-1, \tag{2d}\\
& & & & & 0 \leq s \leq S-1, \\
& & & & & 0 \leq i \leq I-1\\
& & & Y\_{fsij} \leq X\_j & \forall & 0 \leq f \leq F-1, \tag{2e}\\
& & & & & 0 \leq s \leq S-1, \\
& & & & & 0 \leq i \leq I-1,\\
& & & & & 0 \leq j \leq J-1\\
& & & X\_j, Y\_{fsij} \in {0,1} & \forall & 0 \leq f \leq F-1, \tag{2f}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1\\
$$

The objective function (2a) determines the utility of a given prioritisation: a combination of the total cost of a prioritisation and how fragmented it is. Constraints (2b–2c) ensure that all the amount-based and space-based targets are met. Constraints (2d) ensure that only one planning unit is assigned to each demand point. Constraints (2e) ensure that demand points are only assigned to selected planning units. Constraints (2f) ensure that the and variables are binary.

### Reliable formulation

The reliable formulation explicitly considers the probability that the planning units are inhabited. As a consequence, it may deliver prioritisations that will sufficiently represent an attribute space even if the features do not inhabit several of the planning units when the prioritisation is implemented. This behaviour is achieved by siting back-up planning units near selected planning units with low occupancy probabilities in the attribute space(s). To ensure that prioritisations are robust against multiple planning units being uninhabited, the problem assigns planning units at multiple backup levels.

Backup levels levels are defined as -levels (similar to failure levels in Snyder and Daskin 2005). The first backup -level is used to calculate the level of representation when all of the selected planning units are occupied by all . For this scenario, the closest selected planning unit to each demand point for attribute space is assigned at -level. This scenario essentially represents in the unreliable formulation. The second backup -level is used to assess the level of representation when the closest planning unit to each demand point is unoccupied. For this scenario, the second closest planning units are assigned at -level. The third backup -level is used to assess representation when the first two closest planning units are unoccupied. The third closest planning units are assigned at -level. Continuing on, in this manner, the selected planning units in a prioritisation are assigned to each demand point , attribute space , and each feature at an -level.

A final backup -level when is used to assess the level of representation when the features do not occupy any selected planning units in a prioritisation. Each demand point for each and is assigned to an “imaginary” planning unit at . The distance variables associated with this imaginary planning unit denote the loss of biological value associated with failing to secure a representative sample of feature in attribute space . However, the variables are in distance units which are meaningless units in this context. Thus these variables are calculated using a failure multiplier () and the maximum distance between the planning units and the demand points for , (3).

$$\begin{aligned}
& d\_{fsiJ} = M \times \max\limits\_{0 \leq i \leq I-1, 0 \leq j \leq J-1} d\_{fsij} & \forall & 0 \leq f \leq F-1, \tag{3} \\
& & & 0 \leq s \leq S-1\\\end{aligned}$$

Moderately-sized conservation planning problems often include several thousand planning units. It is currently not be feasible to solve this problem when considering all possible failure scenarios. As a consequence, the variable can be any . For instance, when only 2 backup levels are considered in addition to the final backup level. Cui et al. (2010) found that yields similar solutions to when . However, depending on the number of features, demand points, attribute spaces, and planning units, decision makers will likely be limited to to obtain prioritisations in a feasible amount of time.

In the reliable formulation, the control variables are the , , , , and variables. The decision variables are the , , variables.

$$\begin{aligned}
& \text{(1a--1d)} \\
R &= \text{number of failure levels} \tag{4a} \\
M &= \text{failure multiplier} \tag{4b}\\
P\_{fsijr} &= \parbox{25em}{probability that demand point $i$ is assigned to planning unit $j$ at back-up level $r$ for feature $f$ and space $s$} \tag{4c}\\\end{aligned}$$

The reliable formulation (RRAP) is a multi-objective optimisation problem.

$$\begin{aligned}
& \text{(RRAP)} & \text{Min } & \text{(2a)}\\
& & \text{s.t. } & \text{(2b)}\\
& & & 1 - \frac{\sum\_{i=0}^{I-1} \sum\_{j=0}^{J-1} \left( \lambda\_{fsi} d\_{fsij} P\_{fsijr} Y\_{fsij} \right)^2}{\sum\_{i=0}^{I-1} \left( \lambda\_{fsi} \hat{d}\_{fsi} \right)^2 } \geq \hat{T}\_{fs} & \forall & 0 \leq f \leq F-1, \tag{5a}\\
& & & & & 0 \leq s \leq S-1\\
& & & \sum\_{j=0}^{J-1} Y\_{fsijr} = 1 & \forall & 0 \leq f \leq F-1, \tag{5b}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1,\\
& & & & & 0 \leq r \leq R\\
& & & \sum\_{r=0}^{R} Y\_{fsijr} = 1 & \forall & 0 \leq f \leq F-1, \tag{5c}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1,\\
& & & & & 0 \leq j \leq J\\
& & & \sum\_{r=0}^{R-1} Y\_{fsijr} \leq X\_j & \forall & 0 \leq f \leq F-1, \tag{5d}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1,\\
& & & & & 0 \leq j \leq J-1\\
& & & Y\_{fsiJR} = 1 & \forall & 0 \leq f \leq F-1, \tag{5e}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1\\
& & & P\_{fsij0} = q\_{fj} & \forall & 0 \leq f \leq F-1, \tag{5f}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1,\\
& & & & & 0 \leq j \leq J\\
& & & P\_{fsijr} = \left(1 - \right) \sum\_{k=0}^{J-1} \frac{1 - q\_k}{q\_k} P\_{f,s,i,k,r-1} Y\_{f,s,i,k,r-1} & \forall & 0 \leq f \leq F-1, \tag{5g}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1,\\
& & & & & 0 \leq j \leq J,\\
& & & & & 1 \leq r \leq R\\
& & & X\_j, Y\_{fsijr} \in {0,1} & \forall & 0 \leq f \leq F-1, \tag{5h}\\
& & & & & 0 \leq s \leq S-1,\\
& & & & & 0 \leq i \leq I-1,\\
& & & & & 0 \leq j \leq J,\\
& & & & & 0 \leq r \leq R\\\end{aligned}$$

The objective function for the reliable formulation is the same as for the unreliable formation (2a). Similar to the unreliable formulation, constraints (2b) and (5a) ensure that the amount-based and space-based targets are met. Constraint (5b–5c) ensure that each planning unit is only assigned to one backup -level for . Constraints (5d) ensure that only selected planning units are assigned to demand points . Constraints (5e) ensure that the imaginary planning unit is always assigned to the highest backup -level. Constraints (5f–5g) determine the probability that planning unit will be used to sample demand point for and (Cui *et al.* 2010). Constraints (5h) ensure that the and variables are binary.

### Optimisation

The unreliable and reliable formulations are non-linear. However, the non-linear components can be linearised using existing techniques. First, the expression in (2a) can be linearised using methods described by Beyer et al. (2015). Second, the expression in (5a) can be linearised using techniques described by Sherali and Alameddine (1992) as implemented in Cui et al. (2010). Linearised versions of the problems can be solved using commercial exact algorithm solvers.

The rapr R package provides functions to express conservation planning data as an optimisation problems using linearised versions of the unreliable and reliable formulations. These optimisation problems can then be solved to generate prioritisations using the commercial Gurobi software suite (<http://www.gurobi.com>). Note that academics can obtain a [license at no cost from the Gurobi website](http://user.gurobi.com/download/licenses/free-academic). After installing the Gurobi software suite, users will need to install the Gurobi R package. This R package can be installed on [Windows](http://www.gurobi.com/documentation/6.5/quickstart_windows/r_installing_the_r_package.html), [Mac OSX](http://www.gurobi.com/documentation/6.5/quickstart_mac/r_installing_the_r_package.html), and [Linux](http://www.gurobi.com/documentation/6.5/quickstart_linux/r_installing_the_r_package.html) operating systems.

## Package overview

To load the rapr R package and learn more about the package, type the following code into R.

[] (rapr)

?rapr

The rapr R package uses a range of S4 classes to store conservation planning data, parameters, and prioritisations (Table 1).

Table 1: Main classes in the rapr R package

[c]@cll@ Class Name & Description & Slots  
ManualOpts & &  
GurobiOpts & &  
RapUnreliableOpts & &  
RapReliableOpts & &  
SimplePoints & &  
DemandPoints & &  
AttributeSpace & &  
RapData & &  
RapUnsolved & &  
RapResults & &  
RapSolved & &

## Package tutorial

This tutorial is designed to provide users with an understanding of how to use the rapr R package to generate and compare solutions. This tutorial uses several additional packages, so first we will run the following code to load them.

[] (plyr) (dplyr) (ggplot2) (RandomFields)

()

### Simple simulated species

#### Data

To investigate the behaviour of the problem, we will generate prioritisations for three simulated species. We will use the unreliable formulation of the problem to understand the basics, and later move onto the reliable formulation. The first species (termed ‘uniform’) will represent a hyper-generalist. This species will inhabit all areas with equal probability. The second species (termed ‘normal’) will represent a species with a single range core. The third species (termed ‘bimodal’) will represent a species with two distinct ecotypes, each with their own range core. To reduce computational time for this example, we will use a 10 10 grid of square planning units.

[] simpus <-(100L)

simspp <-( (, , ), sim.species, , simpus, )

Let’s see what these species’ distributions look like.

[] ( (simspp), (,,), function(){(simpus)}, )

![](data:application/pdf;base64,)

Distribution of three simulated species. Each square represents a planning unit. The colour of each square denotes the probability that individuals from each species occupy it.

Next, we will generate a set of demand points. To understand the effects of probabilities and weights on the demand points, we will generate the demand points in geographic space. These demand points will be the centroids of the planning units. Additionally, we will use the same set of demand points for each species and only vary the weights of the demand points between species. **Note that we are only using the same distribution of demand points for different species for teaching purposes. It is strongly recommended to use different demand points for different species in real-world conservation planning exercises.** See the case-study section of this tutorial for examples on how to generate suitable demand points.

[] pucoords <-rgeos::(simpus, )

simdps <-( simspp, function(x) { ((x, pucoords)) } )

simdps <-( simdps, function(x) { ( ( (pucoords@coords), (x) ) ) } )

Now, we will construct a RapUnsolved object to store our input data and parameters. This contains all the information to generate prioritisations.

[] ## create RapUnreliableOpts object simro <-()

## create RapData object species <-( (, , ) )

## create data.frame with species and space targets targets <-( :, :, )

puprobabilities <-(simpus, (simspp))

## create AttributeSpace object attrspace <-( (pucoords@coords), simdps )

boundary <-(simpus)

## create RapData object simrd <-( simpus@data, species, targets, puprobabilities, (attrspace), boundary, (simpus) )

## create RapUnsolved object simru <-(simro, simrd)

#### Single-species prioritisations

##### Amount-based targets

To investigate the effects of space-based targets, we will generate a prioritisation for each species using only amount-based targets and compare them to prioritisations generated using amount- and space-based targets. To start off, we will generate a prioritisation for the uniform species using amount-based targets. To do this we will generate a new sim\_ru object by subsetting out the data for the uniform species from the sim\_ru object containing data for all the species. Then, we will update the targets in the new object. Finally, we will solve the object to generate a prioritisation that fulfills the targets for minimal cost.

[] simrus1 <-(simru, )

simrus1 <-(simrus1, , , )

[] simrss1amount <-(simrus1)

[] ## show summary (simrss1amount)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 20 20 20 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 42 168 10  
## Connectivity\_In\_Fraction  
## 1 0.1909091

[] (simrss1amount)

## uniform  
## 1 0.2

[] (simrss1amount)

## uniform (Space 1)  
## 1 -0.2363636

Now that we have generated a prioritisation, we will see what it looks like. We can use the spp.plot method to see how the prioritisation overlaps with the uniform species’ distribution. Note that since all planning units have equal probabilities for this species, all planning units have the same fill.

[] (simrss1amount, , )

A prioritisation for the uniformly distributed species generated using amount-based targets (20%). Sqaures represent planning units. Planning units with a green border are selected for prioritisation, and their colour denotes the probability they are inhabited by the species.

A prioritisation for the uniformly distributed species generated using amount-based targets (20%). Sqaures represent planning units. Planning units with a green border are selected for prioritisation, and their colour denotes the probability they are inhabited by the species.

[fig:unnamed-chunk-12]

The prioritisation for the uniform species appears to be just a random selection of planning units. This behavior is due to the fact that any prioritisation with 20 planning units is optimal. By relying on just amount targets, this solution may preserve a section of the species’ range core, or just focus on the range margin, or some random part of its range–no emphasis is directed towards preserving different parts of the species’ range. This behavior highlights a fundamental limitation of just using amount-based targets. In the absence of additional criteria, conventional reserve selection problems do not contain any additional information to identify the most effective prioritisation.

Now, we will generate a prioritisation for the normally distributed species using amount-targets. We will use a similar process to what we used for the uniformly distributed species, but for brevity, we will use code to generate solutions immediately after updating the object.

[] simrus2 <-(simru, )

[] simrss2amount <-(simrus2, , , )

[] (simrss2amount)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 10 10 10 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 12 192 16  
## Connectivity\_In\_Fraction  
## 1 0.05454545

[] (simrss2amount)

## normal  
## 1 0.2026153

[] (simrss2amount)

## normal (Space 1)  
## 1 0.6519926

Now let’s visualise the prioritisation we made for the normal species.

[] (simrss2amount, , )

A prioritisation for the normally distributed species generated using amount-based targets (20%). See Figure 3 caption for conventions.

A prioritisation for the normally distributed species generated using amount-based targets (20%). See Figure 3 caption for conventions.

[fig:unnamed-chunk-17]

The amount-based prioritisation for the normal species focuses only on the species’ range core. This prioritisation fails to secure any peripheral parts of the species’ distribution. As a consequence, it may miss out on populations with novel adaptations to environmental conditions along the species’ range margin.

Now, let’s generate an amount-based target for the bimodally distributed species view it.

[] simrus3 <-(simru, )

[] simrss3amount <-(simrus3, , )

[] (simrss3amount, , )

A prioritisation for the bimodally distributed species generated using amount-based targets (20%). See Figure 3 caption for conventions.

A prioritisation for the bimodally distributed species generated using amount-based targets (20%). See Figure 3 caption for conventions.

[fig:unnamed-chunk-21]

[] (simrss3amount)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 8 8 8 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 9 197 14  
## Connectivity\_In\_Fraction  
## 1 0.04090909

[] (simrss3amount)

## bimodal  
## 1 0.2018391

[] (simrss3amount)

## bimodal (Space 1)  
## 1 0.2829105

The amount-based prioritisation for the bimodally distributed species only selects planning units in the bottom left corner of the study area. This prioritisation only preserves individuals belonging to one of the two ecotypes. As a consequence, this prioritisation may fail to preserve a representative sample of the genetic variation found inside this species.

##### Amount-based and space-based targets

Now that we have generated a prioritisation for each species using only amount-based targets, we will generate a prioritisations using both amount-based and space-targets. To do this we will update the space targets in our amount-based prioritisations to 50%, and store the new prioritisations in new objects.

First, let’s do this for the uniform species.

[] simrss1space <-(simrss1amount, , )

[] (simrss1space)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 20 20 20 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 18 147 55  
## Connectivity\_In\_Fraction  
## 1 0.08181818

[] (simrss1space)

## uniform  
## 1 0.2

[] (simrss1space)

## uniform (Space 1)  
## 1 0.8793939

Let’s take a look at the prioritisation for the uniform species with amount-based and space-based targets. Then, let’s compare the solutions for the amount-based prioritisation with the new prioritisation using both amount and space targets.

[] (simrss1space, , )

A prioritisation for the uniformly distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 3 caption for conventions.

A prioritisation for the uniformly distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 3 caption for conventions.

[fig:unnamed-chunk-26]

[] (simrss1amount, simrss1space, , , )

Difference between two prioritisations for the uniformly distributed species. Prioritisation was generated using just amount-based targets (20%), and prioritisation was generated using an additional space-based target (85%).

Difference between two prioritisations for the uniformly distributed species. Prioritisation was generated using just amount-based targets (20%), and prioritisation was generated using an additional space-based target (85%).

[fig:unnamed-chunk-27]

Here we can see that by including a space-target, the prioritisation is spread out evenly across the species’ distribution. Unlike the amount-based prioritisation, this prioritisation samples all the different parts of the species’ distribution.

Now, let’s generate a prioritisation for the normally distributed species that considers amount-based and space-based targets. Then, let’s visualise the new prioritisation and compare it to the old amount-based prioritisation.

[] simrss2space <-(simrss2amount, , )

[] (simrss2space)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 13 13 13 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 7 175 38  
## Connectivity\_In\_Fraction  
## 1 0.03181818

[] (simrss2space)

## normal  
## 1 0.2122983

[] (simrss2space)

## normal (Space 1)  
## 1 0.8523318

[] (simrss2space, , )

A prioritisation for the normally distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 3 caption for conventions.

A prioritisation for the normally distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 3 caption for conventions.

[fig:unnamed-chunk-31]

[] (simrss2amount, simrss2space, , , )

Difference between two prioritisations for the normally distributed species. See Figure 7 caption for conventions.

Difference between two prioritisations for the normally distributed species. See Figure 7 caption for conventions.

[fig:unnamed-chunk-32]

We can see by using both amount-based and space-based targets we can obtain a prioritisation that secures both the species’ range core and parts of its range margin. As a consequence, it may capture any novel adaptations found along the species’ range margin–unlike the amount-based prioritisation.

Finally, let’s generate a prioritisation for the bimodal species using amount-based and space-based targets.

[] simrss3space <-(simrss3amount, , )

[] (simrss3space)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 9 9 9 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 9 193 18  
## Connectivity\_In\_Fraction  
## 1 0.04090909

[] (simrss3space)

## bimodal  
## 1 0.219729

[] (simrss3space)

## bimodal (Space 1)  
## 1 0.8813757

[] (simrss3space, , )

A prioritisation for the normally distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 3 caption for conventions.

A prioritisation for the normally distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 3 caption for conventions.

[fig:unnamed-chunk-36]

[] (simrss3amount, simrss3space, , , )

Difference between two prioritisations for the bimodally distributed species. See Figure 7 caption for conventions.

Difference between two prioritisations for the bimodally distributed species. See Figure 7 caption for conventions.

[fig:unnamed-chunk-37]

Earlier we found that the amount-based prioritisation only preserved individuals from a single ecotype, and would have failed to adequately preserve the intra-specific variation for this species. However, here we can see that by including space-based targets, we can develop prioritisations that secure individuals belonging to both ecotypes. This new prioritisation is much more effective at sampling the intra-specific variation for this species.

Overall, these results demonstrate that under the simplest of conditions, the use of space-based targets can improve prioritisations. However, these prioritisations were each generated for a single species. It is possible that prioritisations generated using multiple species may do a better job at preserving the intra-specific variation for individuals species by preserving them in different parts of their range. We will investigate this in the next section.

#### Multi-species prioritisations

##### Effects of including space-based targets

So far we have generated prioritisations using only a single species at a time. However, real world prioritisations are often generated using multiple species to ensure that they preserve a comprehensive set of biodiversity. Here, we will generate multi-species prioritisations that preserve all three of the simulated species. First, we will generate a prioritisation using amount-based targets that only aims to preserve 20% of the area they occupy. Then, we will generate a prioritisation that also incoperate space-based targets to also preserve 85% of their geographic distribution. We will then compare the two prioritisations.

[] simmrsamount <-( simru, (,,), (,,) )

simmrsspace <-( simru, (,,), (, , ) )

[] (simmrsamount)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 20 20 20 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 17 147 56  
## Connectivity\_In\_Fraction  
## 1 0.07727273

[] (simmrsspace)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 20 20 20 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 7 142 71  
## Connectivity\_In\_Fraction  
## 1 0.03181818

[] (simmrsamount)

## uniform normal bimodal  
## 1 0.2 0.201559 0.2012952

[] (simmrsspace)

## uniform normal bimodal  
## 1 0.2 0.2185579 0.2232897

[] (simmrsamount)

## uniform (Space 1) normal (Space 1) bimodal (Space 1)  
## 1 0.8593939 0.8205165 0.8866593

[] (simmrsspace)

## uniform (Space 1) normal (Space 1) bimodal (Space 1)  
## 1 0.9321212 0.8805152 0.9261063

[] (simmrsamount, , )

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using just amount-based targets (20%). Squares represent planning units. Dark green planning units are selected for preservation.

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using just amount-based targets (20%). Squares represent planning units. Dark green planning units are selected for preservation.

[fig:unnamed-chunk-41]

[] (simmrsspace, , )

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 12 caption for conventions.

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using amount-based targets (20%) and space-based targets (85%). See Figure 12 caption for conventions.

[fig:unnamed-chunk-42]

[] (simmrsamount, simmrsspace, , , )

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

[fig:unnamed-chunk-43]

Here we can see that the inclusion of space-based targets changes which planning units are selected for prioritisation, but also the number of planning units that are selected. The amount-based prioritisation is comprised of 20 units, and the space-based prioritisation is comprised of 20 units. This result suggests that an adequate and representative prioritisation can be achieved for only a minor increase in cost.

##### Uncertainty in species’ distributions

The unreliable formulation does not consider the probability that the planning units are occupied by features when calculating how well a given solution secures a representative sample of an attribute space. Thus solutions identified using the unreliable formulation may select regions of an attribute space for a species using planning units that only have a small chance of being inhabited. As a consequence, if the prioritisation is implemented, it may fail to secure regions of an attribute space if individuals do not inhabit these planning units, and ultimately fail to fulfil the space-based targets.

A simple solution to this issue would be to ensure that planning units cannot be assigned to demand points if they have a low probability of occupancy. This can be achieved by setting a probability threshold for planning units, such that planning units with a probability of occupancy below the threshold are effectively set to zero.

[] simmrsspace2 <-( ( simmrsspace, :, (,,) ) )

[] (simmrsspace2)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 20 20 20 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 7 143 70  
## Connectivity\_In\_Fraction  
## 1 0.03181818

[] (simmrsspace2, )

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using amount-based targets (20%) and space-based targets (85%). This priorititisation was generated to be robust against low occupancy probabilities, by preventing planning units with low probabilities from being used to represent demand points. See Figure 12 caption for conventions.

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using amount-based targets (20%) and space-based targets (85%). This priorititisation was generated to be robust against low occupancy probabilities, by preventing planning units with low probabilities from being used to represent demand points. See Figure 12 caption for conventions.

[fig:unnamed-chunk-47]

[] (simmrsspace2, simmrsspace, , , )

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

[fig:unnamed-chunk-48]

But this method requires setting somewhat arbitrary thresholds. A more robust solution to this issue is to actually use the probability that species occupy planning units to generate the prioritisations. This is what the reliable formulation does. First we will try and generate a solution using existing targets and the reliable formulation. To reduce computational time, we will set the maximum backup -level to 1.

[] simmrsspace3 <-((simmrsspace, , 1L))

## Warning for adding variables: zero or small (< 1e-13) coefficients, ignored  
## Optimize a model with 364206 rows, 181900 columns and 3847200 nonzeros  
## Coefficient statistics:  
## Matrix range [6e-05, 1e+02]  
## Objective range [1e+00, 1e+00]  
## Bounds range [1e+00, 1e+00]  
## RHS range [7e-03, 6e+01]  
## Presolve removed 349813 rows and 90706 columns  
## Presolve time: 3.98s  
##   
## Explored 0 nodes (0 simplex iterations) in 6.76 seconds  
## Thread count was 1 (of 2 available processors)  
##   
## Model is infeasible  
## Best objective -, best bound -, gap -  
## Try setting lower space-based targets.  
## Below are the maximum targets for each species and space.  
## Proportion Target  
## 1 -1.97000 uniform (Space 1)  
## 2 -12.67570 normal (Space 1)  
## 3 -21.69092 bimodal (Space 1)

However, this fails. The reason why we cannot generate a prioritisation is because we require more planning units to generate a solution that fulfills the targets when we consider probabilities. This is confirmed by the negative maximum targets shown in the error message. Now, we will set lower targets and generate solution.

[] simmrsspace3 <-( simmrsspace, , 1L, - )

[] (simmrsspace3)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 20 20 20 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 28 161 31  
## Connectivity\_In\_Fraction  
## 1 0.1272727

[] (simmrsspace3, )

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using amount-based targets (20%) and space-based targets (85%). This priorititisation was generated to be robust against low occupancy probabilities, by explicitly using the probability of occupancy data when deriving a solution. See Figure 12 caption for conventions.

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using amount-based targets (20%) and space-based targets (85%). This priorititisation was generated to be robust against low occupancy probabilities, by explicitly using the probability of occupancy data when deriving a solution. See Figure 12 caption for conventions.

[fig:unnamed-chunk-53]

[] (simmrsspace3, simmrsspace, , , )

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

[fig:unnamed-chunk-54]

An additional planning unit was selected using the reliable formulation. The prioritisation based on the unreliable formulation had 20 planning units, but the prioritisation based on the reliable formlation has 20 planning units. This differnce occurs because the reliable formulation needs to ensure that all selected planning units with a low chance of being occupied have a suitable backup planning unit. While the reliable formulation can deliver more robust prioritisations, it takes much longer to solve conservation planning problems expressed using this formulation than the unreliable formulation. As a consequence, the reliable formulation is only feasible for particularly small problems, such as those involving few features and less than several hundred planning units.

##### Fragmentation

Fragmentation is an important consideration in real-world planning situations. Up until now, we haven’t considered the effects of fragmentation on the viability of the prioritisation. As a consequence, our prioritisations have tended to contain planning units without any neighbours. We can use the BLM parameter to penalise fragmented solutions.

Let’s generate a new prioritisation that heavily penalises fragmentation. Here, we will update the sim\_mrs\_amount object with BLM of 100.

[] simmrsamountblm <-(simmrsamount, )

[] (simmrsamountblm)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 1420 20 20 220  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 35 171 14  
## Connectivity\_In\_Fraction  
## 1 0.1590909

[] (simmrsamountblm)

## uniform normal bimodal  
## 1 0.2 0.2645832 0.3911267

[] (simmrsamountblm)

## uniform (Space 1) normal (Space 1) bimodal (Space 1)  
## 1 0.4545455 0.4517326 0.6539667

[] (simmrsamountblm, )

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using only amount-based targets (20%). Additionally, this priorititisation was specified to have high connectivity, by using a high parameter. See Figure 12 caption for conventions.

A multi-species prioritisation for the uniformly, normally, and bimodally distributed species generated using only amount-based targets (20%). Additionally, this priorititisation was specified to have high connectivity, by using a high parameter. See Figure 12 caption for conventions.

[fig:unnamed-chunk-58]

[] (simmrsamountblm, simmrsamount, , , )

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

Difference between two multi-species prioritisations. See Figure 7 caption for conventions.

[fig:unnamed-chunk-59]

Here we can see that the prioritisation generated using a BLM parameter of 100 is much more clustered than the prioritisation generated using a BLM of 0. In practice, conservation planners will need to try a variety of BLM parameters to find a suitable prioritisation.

### Complex simulated species

#### Data

In the previous examples, we have only used Euclidean distances to determine how much of an attribute space is sampled by a prioritisation. However, Euclidean distances can be poor measures of distance for multivariate, binary, or correlated variables (Faith *et al.* 1987). As a consequence this may lead to over- or under-estimates of the quality of a given solution.

The rapr R package provides a suite of distance metrics that can be used to calculate spatial representation (see ?AttributeSpace for available metrics and their equations). To illustrate how using different distance metrics can affect the optimal solution, we will generate a new suite of prioritisations using different distance metrics.

First, we will simulate a new species and a three-dimensional attribute space. Note that unlike the previous examples, the attribute space will not be geographic space. Rather, each dimension in the attribute space will have values that map onto geographic space (eg. like climatic variables across the landscape). To add further complexity, we simulate their distributions using Gaussian processes.

[] ()

## simulate planning units simpus <-(25L)

simgspp <-(simpus, (), , )

simgspace <-(simpus, (), , )

## ...

[] simgspace <-simgspace +

[] simrugp <-( simpus, simgspp, simgspace, , , 50L, , , , )

## Choosing repsperpoint=1500 (use a larger value for more accuracy.)  
## Evaluating probability density...  
## Building tree... done.  
## Querying tree... 2.33918e-06 0.0233942 0.046786 0.0701778 0.0935696 0.116961 0.140353 0.163745 0.187137 0.210529 0.23392 0.257312 0.280704 0.304096 0.327488 0.35088 0.374271 0.397663 0.421055 0.444447 0.467839 0.49123 0.514622 0.538014 0.561406 0.584798 0.608189 0.631581 0.654973 0.678365 0.701757 0.725149 0.74854 0.771932 0.795324 0.818716 0.842108 0.865499 0.888891 0.912283 0.935675 0.959067 0.982458 done.  
## Finished evaluating probability density.  
## Beginning volume calculation... done.   
## Quantile requested: 0.20 obtained: 0.20

Let’s visualise the species’ distribution and the distribution of the attribute space across geographic space.

[] ( simgspp, , ((, , , , , , , , ))() ) (simpus)

Distribution map of a species simulated using Gaussian prorceses. See Figure 2 caption for conventions.

Distribution map of a species simulated using Gaussian prorceses. See Figure 2 caption for conventions.

[fig:unnamed-chunk-62]

[] ( simgspace, (, , ), function(){(simpus)}, )

Distribution of spatial variables across the species’ geographic range. These variables each represent a dimension of a three-dimensional attribute space.

Distribution of spatial variables across the species’ geographic range. These variables each represent a dimension of a three-dimensional attribute space.

[fig:unnamed-chunk-63]

#### Distance metrics

For each different distance metric, we will update the sim\_gru object with the new distance metric, solve it, and store the solution in a list.

[] dist.metrics <-( , , ,, , , , )

solutions <-() for (i in dist.metrics) { solutions[[i]] <-(simrugp, i) }

Now, let’s plot the solutions to see how they differ.

[] ((,), (, , , ))

## create plots showing the selected planning units (dark green) for (i in (solutions)) { ( simpus, dist.metrics[i], ( (,(simpus@data)), ((solutions[[i]])==), ), ) }

((,), (, , , ))

![](data:application/pdf;base64,)

Prioritisations generated using different distance metrics. See Figure 12 for conventions.

It appears that main difference between the solutions is which planning units get selected in the bottom section of the study area. Some solutions tend to select a lot of planning units in this region (eg. Euclidean, Gower, and Manhattan), whereas others select fewer planning units (eg. Bray-Curtis, Jaccard, and Kulczynski). Conservation planners should think carefully which distance metric is most appropriate for their attribute spaces. See the discussion section below for guidelines on selecting an appropriate distance metric.

### Case-study examples

#### Overview

Here we will investigate how space-based targets can affect prioritisations using a more realistic dataset. We will generate prioritisations for the four bird species– [blue-winged kookaburra](http://www.birdlife.org/datazone/speciesfactsheet.php?id=1092&gclid=CjwKEAiApYGyBRC-g_jIstuduV8SJABCEzhZoONUy8VlwRZqeFB1Z5M03CjyneIvX8KdVKIPZvckrRoCgJDw_wcB), [brown-backed honeyeater](http://www.birdlife.org/datazone/species/factsheet/22704394?gclid=CjwKEAiApYGyBRC-g_jIstuduV8SJABCEzhZHxCTcR38YnFlhePYt19gD31lqxxwrMmtIuWFhUwLmRoCGJjw_wcB), [brown falcon](http://www.birdlife.org/datazone/speciesfactsheet.php?id=3588), [pale-headed rosella](http://www.birdlife.org/datazone/speciesfactsheet.php?id=1466)–in Queensland, Australia. This region contains a broad range of different habitats–such as rainforests, woodlands, and deserts–making it ideal for this tutorial. First, we will generate a typical amount-based prioritisation that aims to capture 20% of the species’ distributions. Then we will generate a prioritisation that also aims to secure populations in representative parts of the species’ distributions in terms of their geographic location and their environmental heterogeneity. To do this we will generate a prioritisation using 20% amount-based targets and 85% space-based targets. Finally, we will compare these prioritisations to Australia’s existing protected network.

#### Data

Survey data for the species were obtained from [BirdLife Australia](http://birdlife.org.au/projects/atlas-and-birdata). The survey data was rarefied using a 100km grid, wherein the survey with the greatest number of repeat visits in each grid cell was chosen. To model the distribution of each species, environmental data were obtained at survey location (site). Specifically, [climatic data](http://www.worldclim.org/bioclim) (bio1, bio4, bio15, bio16, bio17) and [classifications of the vegetation at the site](http://www.environment.gov.au/fed/catalog/search/resource/details.page?uuid=%7BEBBCC6FA-8C13-422A-BCD7-24A9F8B52A9A%7D) were used. Occupancy-detection models (MacKenzie *et al.* 2002) were fit using Stan (Stan Development Team 2015) using manually tuned parameters (adapt deta=0.9, maximum treedepth=20, chains=4 , warmup iterations=1000, total iterations=1500) with five-fold cross-validation. In each replicate, data were partitioned into training and test sites. A full model was fit using quadratic terms for environmental variables in the site-component, and an intercept in the detection-component of the model. The full model was then subject to a step-wise backwards term deletion routine. Terms were retained when their inclusion resulted in a model with a greater area under the curve (AUC) value as calculated using the test data. Maps were generated for each species as an average of the predictions from the best model in each best replicate. To further improve the accuracy of these maps, areas well outside of the species’ known distributions were set to 0. For each species, this was achieved by masking out [biogeographic regions](https://www.environment.gov.au/land/nrs/science/ibra) where the species was not observed, and regions that did not have a neighbouring planning unit where the species was observed. The maps were then resampled (10km resolution) and cropped to the study area. The resulting maps are stored in the cs\_spp object.

[] (csspp)

(csspp, ( , , , ))

![](data:application/pdf;base64,)

Distribution map for four Australian bird species. Pixel colours denote probability of occupancy.

Planning units (50km resolution) were generated across Australia, and then clipped to the [Queensland state borders and coastline](http://www.abs.gov.au/ausstats/abs@.nsf/mf/1259.0.30.001?OpenDocument). **Note that we are using excessively coarse planning units so that our examples will complete relatively quickly. In a real-world planning exercise, we would use much finer planning units.** To compare our prioritisations to [Queensland’s existing protected area network](http://www.protectedplanet.net/country/AU), this network was intersected with the planning units. Planning units with more than 50% of their area inside a protected area had their status set to 2 ([following conventions in Marxan](http://www.uq.edu.au/marxan/tutorial/module4.html)). Since we do not have cost data, the prioritisations will aim to select the minimum number of planning units required to meet the targets. The planning units are stored in the cs\_pu object.

[] (cspus)

## plot planning units cspus2 <-(cspus)

cspuscols <-(, (cspus@data)) cspuscols[)] <-

((, , , ))

PBSmapping::( cspus2, cspuscols, , , , , )

Planning units for the case-study examples. Yellow polygons represent planning units with more then 50% of their area already in existing reserves.

Planning units for the case-study examples. Yellow polygons represent planning units with more then 50% of their area already in existing reserves.

[fig:unnamed-chunk-68]

[] ((, , , ))

To map the distribution of environmental conditions across the species’ range, 21 [bioclimatic layers](http://www.worldclim.org/bioclim) were obtained. These layers were cropped to Australia and subject to [detrended correspondence analysis](http://cc.oulu.fi/~jarioksa/softhelp/vegan/html/decorana.html) to produce two new variables. These layers are stored in the cs\_space object.

[] (csspace)

(csspace, (, ))

![](data:application/pdf;base64,)

Broad-scale environmental variation across Australia. The variable DC1 describes the transition from wet and cool to dry and hot conditions. The variable DC2 describes the transition from wet and hot to dry and cool conditions.

#### Effectiveness of Australia’s reserve network compared to optimal prioritisations

To simplify the process of formatting data and generating prioritisations, we can use the rap function. First, we will generate an amount-based prioritisation that aims to capture 20% of the rosella’s range. We will use 50 demand points to map the geographic and environmental spaces. **Be warned, the examples hereafter can take 5-10 minutes to run.**

[] csrsamount <-( cspus[,-], csspp, csspace, , , 50L, , , )

## Warning in (function (pus, species, spaces = NULL, amount.target = 0.2, :  
## argument to pus does not have a 'status' column, creating default with all  
## status=0L

[] csrsamount <-(csrsamount, :, (,))

[] csrsamount <-(csrsamount)

[] (csrsamount)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 136 136 136 98882414  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 9636021 81120163 8126230  
## Connectivity\_In\_Fraction  
## 1 0.09744929

[] (csrsamount, )

Multi-species prioritisation generated for four bird species using amount-based targets (20%). See Figure 12 captions for conventions.

Multi-species prioritisation generated for four bird species using amount-based targets (20%). See Figure 12 captions for conventions.

[fig:unnamed-chunk-73]

We can also see how well the prioritisation secures the species’ distributions in the geographic and environmental attribute spaces.

[] p1 <-(csrsamount, , , ) p2 <-(csrsamount, , , ) p3 <-(csrsamount, , , ) p4 <-(csrsamount, , , ) gridExtra::(p1, p2, p3, p4, )

![](data:application/pdf;base64,)

Distribution of amount-based prioritisation in the geographic attribute space. Points denote combinations of environmental conditions. Green and grey points represent planning unit selected for and not selected for prioritisation (respectively). Blue points denote demand points, and their size indicates their weighting.

[] p1 <-(csrsamount, , , ) p2 <-(csrsamount, , , ) p3 <-(csrsamount, , , ) p4 <-(csrsamount, , , ) gridExtra::(p1, p2, p3, p4, )

![](data:application/pdf;base64,)

Distribution of amount-based prioritisation in the environmental attribute space. See Figure 28 caption for conventions.

Next, let’s generate a prioritisation using amount- and space-based targets. This prioritisation will secure 50% of the species distribution in geographic and environmental space.

[] csrsspace <-(csrsamount, )

[] (csrsspace)

## Run\_Number Status Score Cost Planning\_Units Connectivity\_Total  
## 1 1 MANUAL 137 137 137 98882414  
## Connectivity\_In Connectivity\_Edge Connectivity\_Out  
## 1 9738090 80918598 8225726  
## Connectivity\_In\_Fraction  
## 1 0.09848151

[] (csrsspace,)

image

[] p1 <-(csrsspace, , , ) p2 <-(csrsspace, , , ) p3 <-(csrsspace, , , ) p4 <-(csrsspace, , , ) gridExtra::(p1, p2, p3, p4, )

![](data:application/pdf;base64,)

Distribution of the amount- and space-based prioritisation in the geographic attribute space. See Figure 28 caption for conventions.

[] p1 <-(csrsspace, , , ) p2 <-(csrsspace, , , ) p3 <-(csrsspace, , , ) p4 <-(csrsspace, , , ) gridExtra::(p1, p2, p3, p4, )

![](data:application/pdf;base64,)

Distribution of the amount- and space-based prioritisation in the environmental attribute space. See Figure 28 caption for conventions.

Let’s compare these prioritisations with Queensland’s existing protected areas system. To do this, we can create update the cs\_rs\_space with manually specified solutions to create a RapSolved object to represent the Queensland’s reserve network.

[] ausselections <-)

csrsaus <-(csrsamount, ausselections)

Now, let’s plot the performance metrics for these prioritisations.

[] se=function(x){(x,)/((!(x)))}

csresults <-( (((, , ), ),), ((, , ), ), ((csrsamount)), ( (csrsamount)[,], (csrsspace)[,], (csrsaus)[,], (csrsamount, )[,], (csrsspace, )[,], (csrsaus, )[,], (csrsamount, )[,], (csrsspace, )[,], (csrsaus, )[,] ) ( name, variable ( (value), (value) )

((variable, mean, name), csresults) + ((), ) + ( (mean-se, mean+se), (), ) + () + () + ( ) + () + (,)

![](data:application/pdf;base64,) We can see that a greater number of planning units is needed to satisfy the space-based targets. The prioritisation generated using just amount-based targets has 136 planning units, and the prioritisations using amount-based and space-based targets has 137 targets. These results suggest that prioritisations based only on amount-based targets can obtain a moderately representative sample of the species’ geographic distribution and climatic niche.

## Implications and future directions

The rapr R package provides a unified approach to reserve selection. This R package provides a decision maker with the tools to generate prioritisations that secure an adequate amount of a representative sample of biodiversity patterns and processes. Additionally, the decision maker can accommodate uncertainty in the distribution of features, and also identify suitably connected reserves. Both the simulated and case-study species suggest that conservation planning exercises need to explicitly consider biodiversity processes during the reserve selection process.

One of the key advantages of the rapr R package is that it is general enough that any spatial variation could be considered an attribute space, regardless of whether this variation is intrinsic or extrinsic to the feature(s). As a consequence, in addition to biodiversity processes, this R package could be used to secure intra-specific (within feature) biodiversity patterns. For example, advances in genomic fields produced high resolution data on genetic information (eg. amplified fragment length polymorphisms (AFLPs), single nucleotide polymorphisms (SNPs)). By using geostatistical analysis (eg. generalised dissimilarity modelling GDMs (Ferrier et al. (2007)); gradients forests (GFs)), this data has been used to generate maps describing the spatial distribution of genomic variation within a species (Thomassen *et al.* 2010; Fitzpatrick and Keller 2015). These maps in turn could be used to construct a genomic attribute space, and in turn, could be used to generate prioritisations that secure a representative sample of genomic variation within a species. However, because the problem formulations used in this package are so general, the tools in this package could be misused, and generate poor quality prioritisations.

The degree to which a prioritisation truly secures a representative sample of a feature depends on the attribute spaces and distribution of demand points chosen by the decision maker. The space-based targets are set as a proportion based on the level of representation if all the planning units are selected, and the worst prioritisation containing only one planning unit. As a consequence, if the decision maker uses an inappropriate set of spatial variables to construct an attribute space, or an inappropriate set of demand points, then the optimal solution based on this data will not be a cost-effective prioritisation. We therefore stress that decision makers must carefully consider which biodiversity processes need to preserved in the prioritisation, and what spatial data can be used to map these processes. To assist in the selection of appropriate demand points, the R package provides several routines for generating demand points (see the make.DemandPoints function). These routines essentially use the distribution of a feature in the attribute space to define a polygon. Demand points are then generated as random points within the polygon. A kernel is then fit to the distribution of the feature in the space (using Blonder *et al.* 2014; Duong 2015), and the demand points are weighted based on the estimated density of the feature at the demand points’ coordinates.

The rapr R package could be further extended to identify more effective prioritisations. First, the formulation of fragmentation used in this package may be too simplistic in some cases (eg. exercises involving multiple species with different dispersal capabilities), and more realistic measures of fragmentation (eg. those used in Zonation) could be used to identify more effective prioritisations. Second, the problem does not consider temporal dynamics. Here, conservation actions are assumed to be implemented simultaneously in all selected planning units and assumed to remain implemented for all time. As a consequence, this R package is not useful for scenarios where actions are implemented during multiple discrete periods in time (eg. actions are made adue to annual funding cycles), or scenarios involving threatening processes that vary across space and time (reviewed in Pressey *et al.* 2007). Future research may look into incorporating such elements into this R package.

To maximise the long-term persistence of biodiversity–the stated goal of conservation–decision makers need to identify prioritisations that preserve existing patterns of biodiversity and the processes that support them. To achieve this, conservation planners need a decision support tool that can explicitly accommodate biodiversity patterns and processes. Here, we developed the rapr R package to fill this void. By exploring the functiontality of this package using several simulated species, we found that including space-based targets can radically change a prioritisation for the simplest of species.

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