PRIORITIZR WORKSHOP MANUAL

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Contents

Chapter 1

Welcome!

Here you will find the manual for the prioritizr module of the *Spatial Conservation Prioritization: Concepts, Methods and Application* workshop held at CIBIO-InBIO, Vairão, Portugal. **Before you arrive at the workshop, you should make sure that you have correctly set up your computer for the workshop and you have downloaded the data from here. We cannot guarantee a reliable Internet connection during the workshop, and so you may be unable to complete the workshop if you have not set up your computer beforehand.**

Chapter 2

Introduction

2.1 Overview

The aim of this workshop is to help you get started with using the prioritizr R package for systematic conservation planning. It is not designed to give you a comprehensive overview and you will not become an expert after completing this workshop. Instead, we want to help you understand the core principles of conservation planning and guide you through some of the common tasks involved with generating prioritizations. Phrased provocatively, we want to give you the knowledge base and confidence needed to start applying systematic conservation planning to your own work.

You are not alone in this workshop. If you are having trouble, please put your hand up and one of the instructors will help you as soon as they can. You can also ask the people sitting next to you for help too. If you are having trouble with using the prioritizr R package, please consult the package website: https://prioritizr.net. It has plenty of examples and tutorials. Finally, please note that the first thing an instructor will ask you will (probably) be "what have you tried so far?". We can't help you if you haven't tried anything.

2.2 Setting up your computer

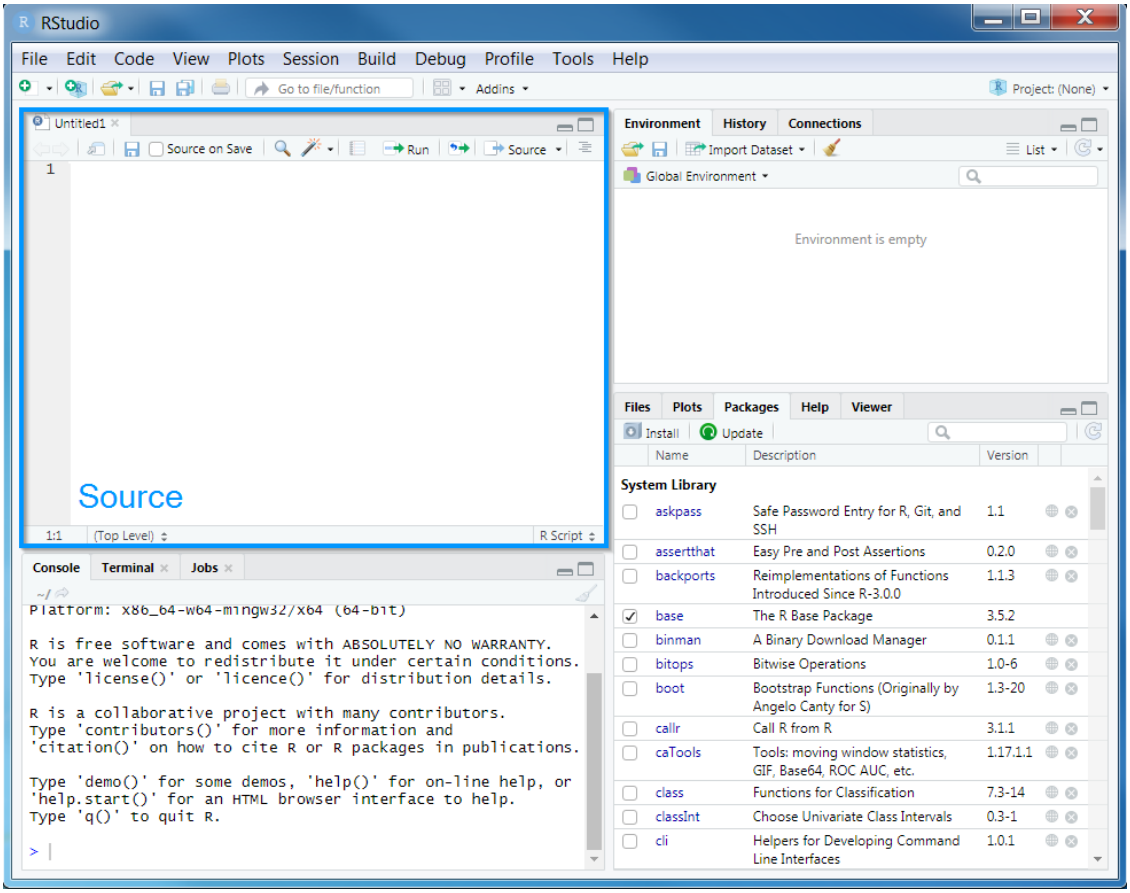
You will need to have both R and RStudio installed on your computer to complete this workshop. Although it is not imperative that you have the latest version of RStudio installed, **you will need the latest version of R installed (i.e. version 3.6.1)**. Please note that you meed need administrative permissions to complete install these programs. After installing them, you will also need to install various R packages too.

2.2.1 R

The R statistical computing environment can be downloaded from the Comprehensive R Archive Network (CRAN). You can download the latest version of R (version 3.6.1) from here: https://cloud.r-project.org. Please note that you will need to download the correct file for your operating system (i.e. Linux, Mac OSX, Windows).

2.2.2 RStudio

RStudio is an integrated development environment (IDE). In other words, it is a program that is designed to make your R programming experience more enjoyable. During this workshop, you will interact with R through RStudio—meaning that you will open RStudio when you want to code in R. You can download the latest version of RStudio here: http://www.rstudio.com/download. When you start RStudio, you will see two main parts of the interface:



You can type R code into the *Console* part of the interface and press the enter key to run the code.

2.2.3 R packages

An R package is a collection of R code and documentation that can be installed to enhance the standard R environment with additional functionality. Currently, there are over ten thousand R packages available on CRAN. Each of these R packages (mostly) aim to serve a specific need, such as reading Excel spreadsheets, downloading satellite imagery data, downloading and cleaning protected area data, or fitting environmental niche models. In fact, R has such a diverse ecosystem of R packages, that the question is (generally) not "can I use R to do …?" but "what R package can I use to …?". During this workshop, we will use various R packages. To install these R packages, please run enter the code below in the *Console* part of the RStudio interface and press enter. Please note that you will require an internet connection to install the packages and the installation process may take a while to complete.

```
install.packages(c("sf", "tidyverse", "sp", "rgeos", "rgdal", "raster", "units",
                   "prioritizr", "prioritizrdata" "Rsymphony", "mapview",
                   "assertthat", "velox", "remotes"))
remotes::install_bioc("lpsymphony")
```

2.3 Further reading

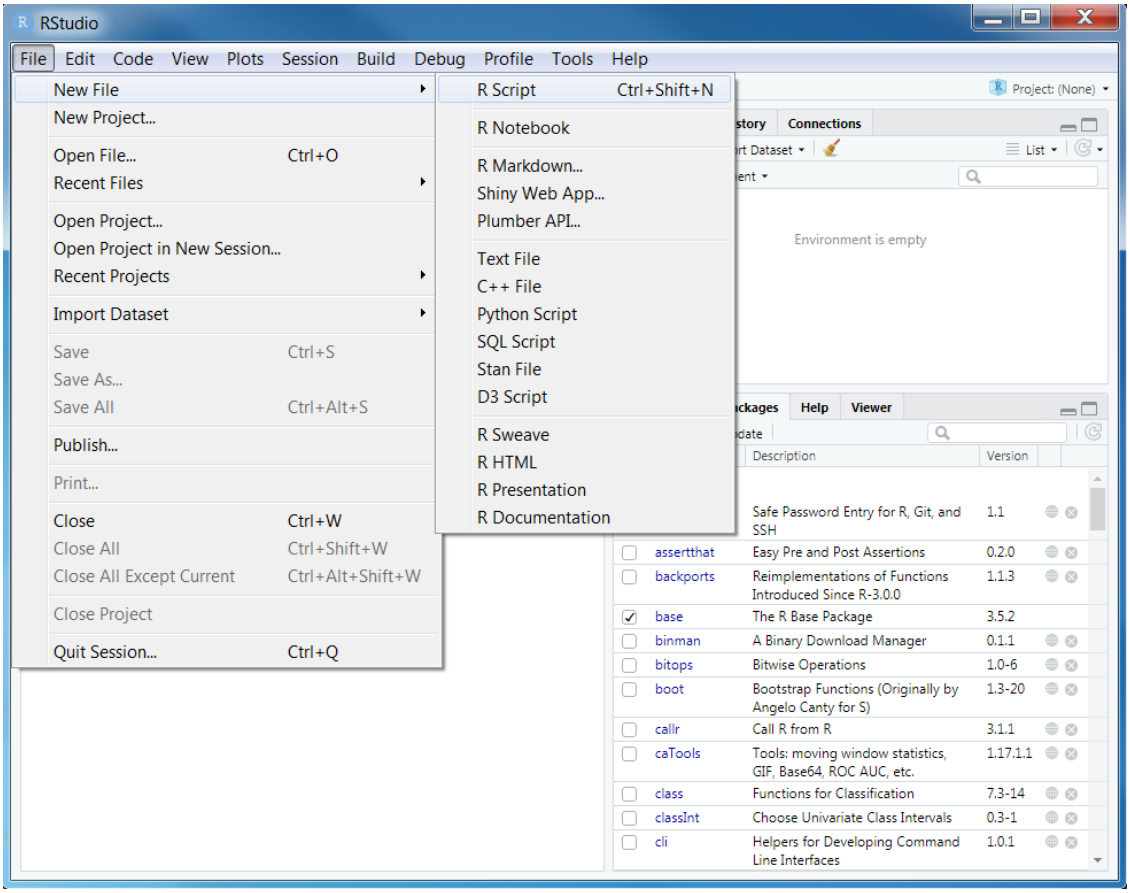
There is a wealth of resources available for learning how to use R. Although not required for this workshop, I would highly recommend that you read *R for Data Science* by Garrett Grolemund and Hadley Wickham. **This veritable trove of R goodness is freely available online.** If you spend a week going through this book then you will save months debugging and rerunning incorrect code. I would urge any and all ecologists – especially those working on Masters or PhD degrees – to read this book. I even bought this book as a Christmas present for my sister—and, yes, she was happy to receive it! For intermediate users looking to skill-up, I would recommend the *The Art of R Programming: A Tour of Statistical Software Design* by Norman Matloff and *Advanced R* by Hadley Wickham. Finally, if you wish to learn more about using R as a geospatial information system (GIS), I would recommend *Geocomputation with R* by Robin Lovelace, Jakub Nowosad, and Jannes Muenchow which is also freely available online. I also recommend *Applied Spatial Data Analysis* by Roger S. Bivand, Edzer Pebesma, and Virgilio Gómez-Rubio too.

Chapter 3

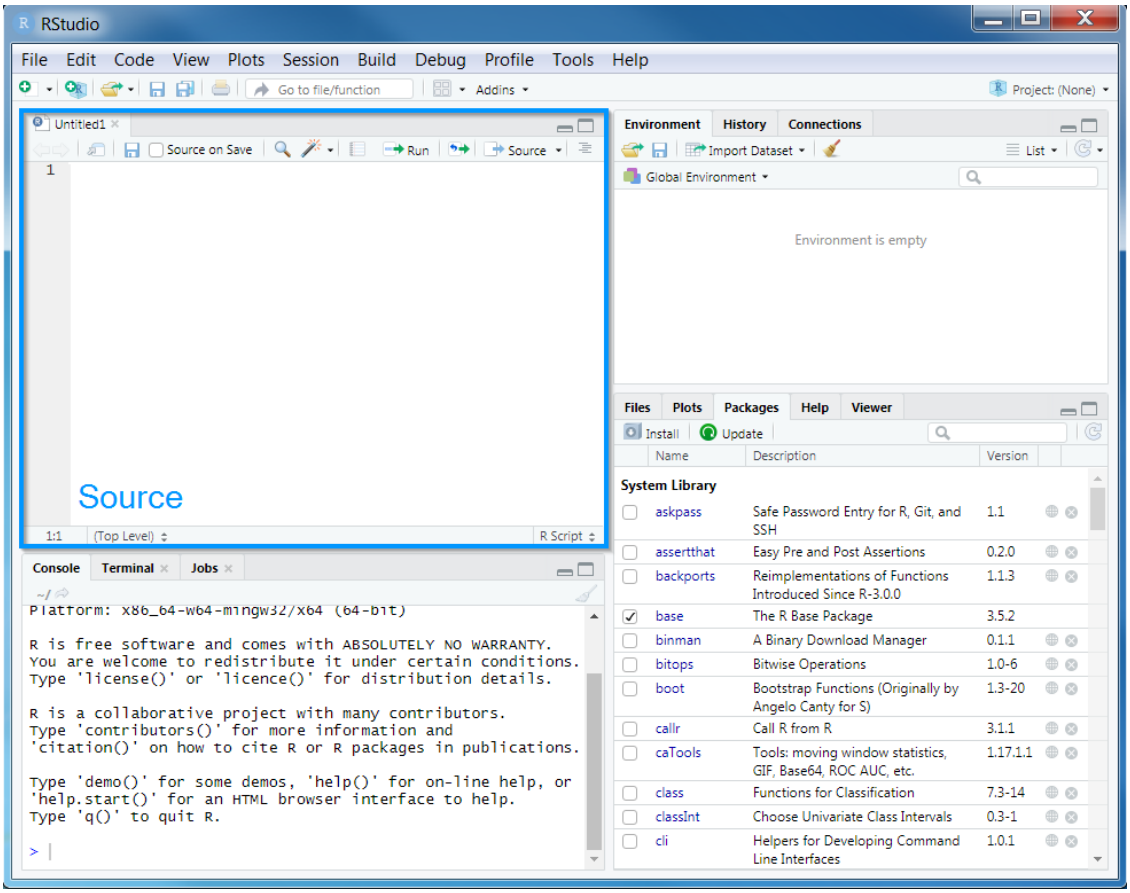
Data

3.1 Starting out

We will start by opening RStudio. Ideally, you will have already installed both R and Rstudio before the workshop. If you have not done this already, then please see the Setting up your computer section. **During this workshop, please do not copy and paste code from the workshop manual into RStudio. Instead, please write it out yourself in an R script.** When programming, you will spend a lot of time fixing coding mistakes – that is, debugging your code – so it is best to get used to making mistakes now when you have people here to help you. You can create a new R script by clicking on *File* in the RStudio menu bar and then *R Script*.



After creating a new script, you will notice that a new *Source* panel has appeared. In this new *Source* panel, you can type and edit code. You can run code in the *Source* panel by placing the cursor (i.e. the blinking line) on the desired line of code and pressing `Control + Enter` on your keyboard (or `CMD + Enter` if you are using an Apple computer). You can save the code in the *Source* panel by pressing `Control + s` on your keyboard (or `CMD + s` if you are using an Apple computer).



You can also make notes and write your answers to the workshop questions inside the *Source* panel. When writing notes and answers, add a `#` symbol so that the text following the `#` symbol is treated as a comment and not code. This means that you don't have to worry about highlighting specific parts of the script to avoid errors.

```
# this is a comment and R will ignore this text if you run it
# R will run the code below because it does not start with a # symbol
print("this is not a comment")
```

```
## [1] "this is not a comment"
```

```
# you can also add comments to the same line of R code too
print("this is also not a comment") # but this is a comment
```

```
## [1] "this is also not a comment"
```

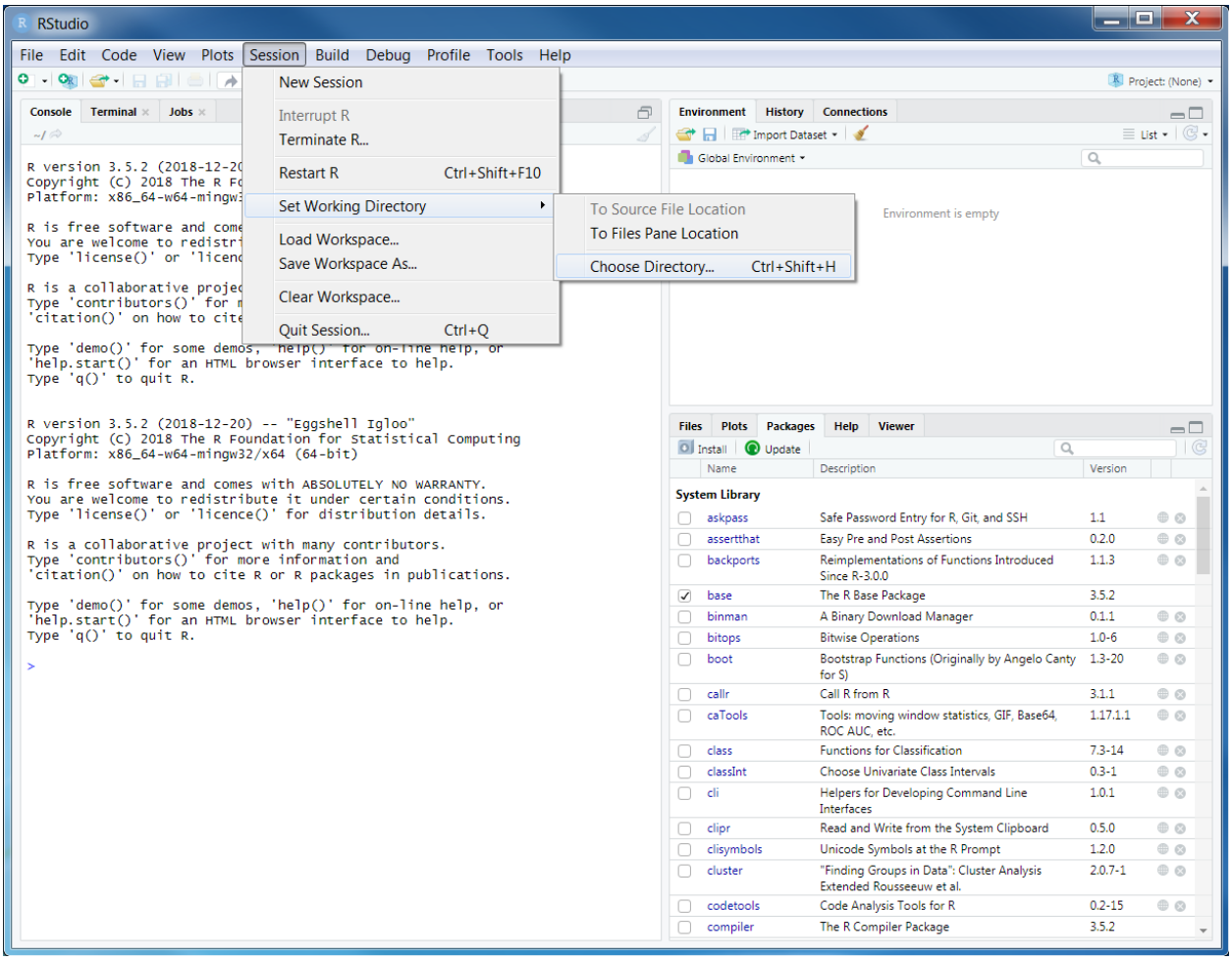
Remember to save your script regularly to ensure that you don't lose anything in the event that RStudio crashes (e.g. using `Control + s` or `CMD + s`)!

3.2 Attaching packages

Now we will setup our R session for the workshop. Specifically, enter the following R code to attach the R packages used in this workshop.

```
# load packages
library(tidyverse)
library(prioritizr)
library(rgdal)
library(raster)
library(rgeos)
library(mapview)
library(units)
library(assertthat)
```

You should have already downloaded the data for the prioritizr module of this workshop. If you have not already done so, you can download it from here: https://github.com/prioritizr/cibio-workshop/raw/master/data.zip. After downloading the data, you can unzip the data into a new folder. Next, you will need to set the working directory to this new folder. To achieve this, click on the *Session* button on the RStudio menu bar, then click *Set working directory*, and then *Choose Directory*.



Now navigate to the folder where you unzipped the data and select *Open*. You can verify that you have correctly set the working directory using the following R code. You should see the output `TRUE` in the *Console* panel.

```
file.exists("data/pu.shp")
```

```
## [1] TRUE
```

3.3 Data import

Now that we have downloaded the dataset, we will need to import it into our R session. Specifically, this data was obtained from the "Introduction to Marxan" course and was originally a subset of a larger spatial prioritization project performed under contract to Australia's Department of Environment and Water Resources. It contains vector-based planning

unit data (`pu.shp`)and the raster-based data describing the spatial distributions of 62 vegetation classes (`vegetation.tif`) in Tasmania, Australia. We can import the data into our R session using the following code.

```
# import planning unit data
pu_data <- readOGR("data/pu.shp")
```

```
## OGR data source with driver: ESRI Shapefile
## Source: "/home/travis/build/prioritizr/cibio-workshop/data/pu.shp", layer: "pu"
## with 1130 features
## It has 5 fields
```

```
# format planning unit data
pu_data$locked_in <- as.logical(pu_data$locked_in)
pu_data$locked_out <- as.logical(pu_data$locked_out)

# import vegetation data
veg_data <- stack("data/vegetation.tif")
```

3.4 Planning unit data

The planning unit data contains spatial data describing the geometry for each planning unit and attribute data with information about each planning unit (e.g. cost values). Let's investigate the `pu_data` object. The attribute data contains 5 columns with contain the following information:

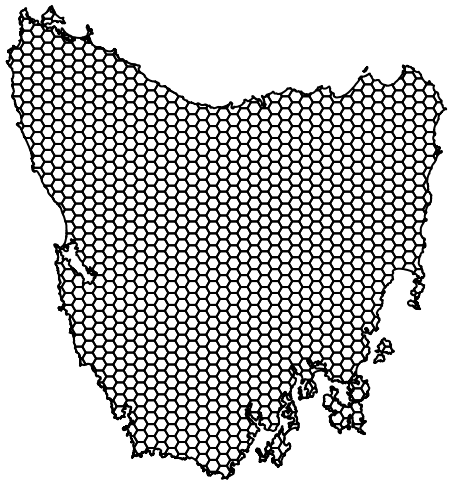
- `id`: unique identifiers for each planning unit
- `cost`: acquisition cost values for each planning unit
- `status`: status information for each planning unit (only relevant with Marxan)
- `locked_in`: logical values (i.e. `TRUE`/`FALSE`) indicating if planning units are covered by protected areas or not.
- `locked_out`: logical values (i.e. `TRUE`/`FALSE`) indicating if planning units cannot be managed as a protected area because they contain too much anthropologically altered land.

```
# print a short summary of the data
print(pu_data)
```

```
## class       : SpatialPolygonsDataFrame
## features    : 1130
## extent      : 1080623, 1399989, -4840595, -4497092  (xmin, xmax, ymin, ymax)
## crs         : +proj=aea +lat_1=-18 +lat_2=-36 +lat_0=0 +lon_0=132 +x_0=0 +y_0=0 +ellp
```

```
## variables   : 5
## names       :   id,              cost, status, locked_in, locked_out
## min values  :    1, 0.192488262910798,      0,         0,          0
## max values  : 1130,  61.9272727272727,      2,         1,          1
```

```
# plot the planning unit data
plot(pu_data)
```



```
# plot an interactive map of the planning unit data
mapview(pu_data)
```

```
# print the structure of object
str(pu_data, max.level = 2)
```

```
## Formal class 'SpatialPolygonsDataFrame' [package "sp"] with 5 slots
##   ..@ data       :'data.frame':  1130 obs. of  5 variables:
##   ..@ polygons   :List of 1130
##   ..@ plotOrder  : int [1:1130] 217 973 506 645 705 975 253 271 704 889 ...
##   ..@ bbox       : num [1:2, 1:2] 1080623 -4840595 1399989 -4497092
```

```
##   .. ..- attr(*, "dimnames")=List of 2
##   ..@ proj4string:Formal class 'CRS' [package "sp"] with 1 slot
```

```
# print the class of the object
class(pu_data)
```

```
## [1] "SpatialPolygonsDataFrame"
## attr(,"package")
## [1] "sp"
```

```
# print the slots of the object
slotNames(pu_data)
```

```
## [1] "data"        "polygons"    "plotOrder"   "bbox"        "proj4string"
```

```
# print the geometry for the 80th planning unit
pu_data@polygons[[80]]
```

```
## An object of class "Polygons"
## Slot "Polygons":
## [[1]]
## An object of class "Polygon"
## Slot "labpt":
## [1]  1289177 -4558185
##
## Slot "area":
## [1] 1060361
##
## Slot "hole":
## [1] FALSE
##
## Slot "ringDir":
## [1] 1
##
## Slot "coords":
##          [,1]     [,2]
##  [1,] 1288123 -4558431
##  [2,] 1287877 -4558005
##  [3,] 1288177 -4558019
##  [4,] 1288278 -4558054
##  [5,] 1288834 -4558038
##  [6,] 1289026 -4557929
##  [7,] 1289168 -4557928
```

```
##  [8,] 1289350 -4557790
##  [9,] 1289517 -4557744
## [10,] 1289618 -4557773
## [11,] 1289836 -4557965
## [12,] 1290000 -4557984
## [13,] 1290025 -4557987
## [14,] 1290144 -4558168
## [15,] 1290460 -4558431
## [16,] 1288123 -4558431
##
##
##
## Slot "plotOrder":
## [1] 1
##
## Slot "labpt":
## [1]  1289177 -4558185
##
## Slot "ID":
## [1] "79"
##
## Slot "area":
## [1] 1060361
```

```
# print the coordinate reference system
print(pu_data@proj4string)
```

```
## CRS arguments:
##  +proj=aea +lat_1=-18 +lat_2=-36 +lat_0=0 +lon_0=132 +x_0=0 +y_0=0
## +ellps=GRS80 +units=m +no_defs
```

```
# print number of planning units (geometries) in the data
nrow(pu_data)
```

```
## [1] 1130
```

```
# print the first six rows in the attribute data
head(pu_data@data)
```

```
##   id     cost status locked_in locked_out
## 0  1 60.24638      0     FALSE       TRUE
## 1  2 19.86301      0     FALSE      FALSE
## 2  3 59.68051      0     FALSE       TRUE
```

```
## 3  4 32.41614      0     FALSE      FALSE
## 4  5 26.17706      0     FALSE      FALSE
## 5  6 51.26218      0     FALSE       TRUE
```

```
# print the first six values in the cost column of the attribute data
head(pu_data$cost)
```

```
## [1] 60.24638 19.86301 59.68051 32.41614 26.17706 51.26218
```

```
# print the highest cost value
max(pu_data$cost)
```

```
## [1] 61.92727
```

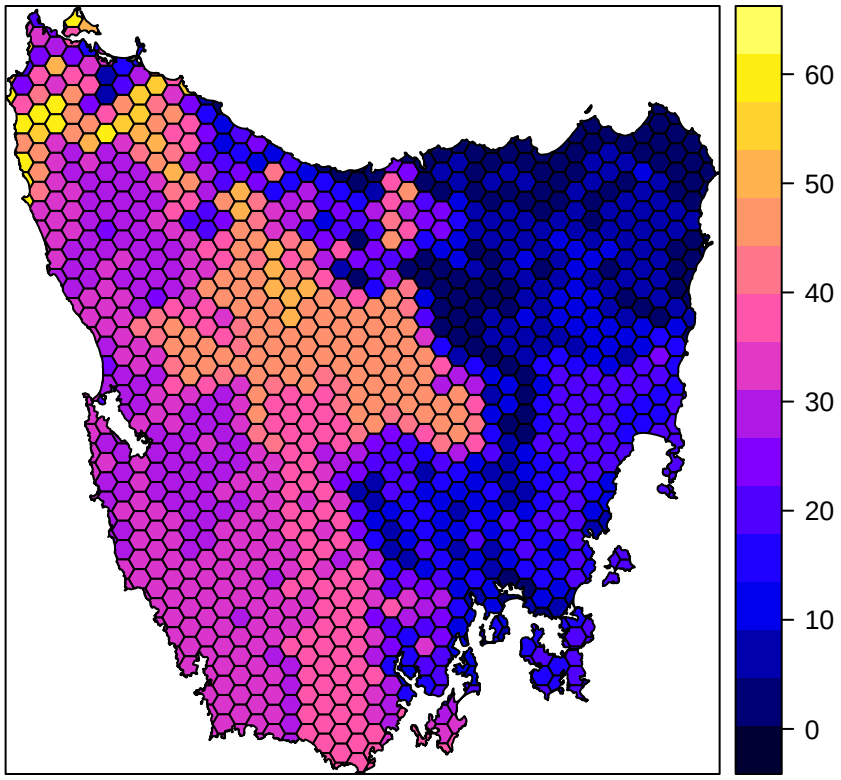
```
# print the smallest cost value
min(pu_data$cost)
```

```
## [1] 0.1924883
```

```
# print average cost value
mean(pu_data$cost)
```

```
## [1] 25.13536
```

```
# plot a map of the planning unit cost data
spplot(pu_data, "cost")
```




```
# plot an interactive map of the planning unit cost data
mapview(pu_data, zcol = "cost")
```

Now, you can try and answer some questions about the planning unit data.

1. How many planning units are in the planning unit data?
2. What is the highest cost value?
3. How many planning units are covered by the protected areas (hint: `sum(x)`)?
4. What is the proportion of the planning units that are covered by the protected areas (hint: `mean(x)`)?
5. How many planning units are dominated by anthropologically altered land (hint: `sum(x)`)?
6. What is the proportion of planning units dominated by anthropologically altered land (hint: `mean(x)`)?
7. Can you verify that all values in the `locked_in` and `locked_out` columns are zero or one (hint: `min(x)` and `max(x)`)?.
8. Can you verify that none of the planning units are missing cost values (hint: `all(is.finite(x))`)?.
9. Can you very that none of the planning units have duplicated identifiers? (hint: `sum(duplicated(x))`)?
10. Is there a spatial pattern in the planning unit cost values (hint: make a map).
11. Is there a spatial pattern in where most planning units are covered by protected areas (hint: make a map of `locked_in`).

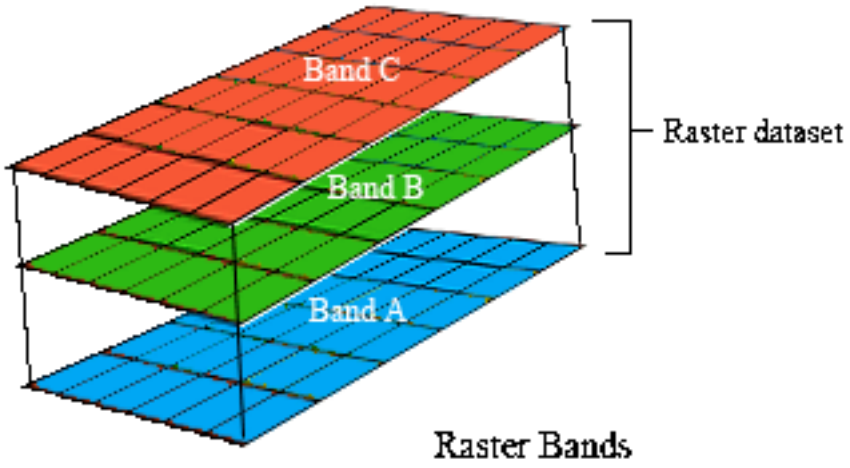
1. `nrow(pu_data)`
2. `max(pu_data$cost)`
3. `sum(pu_data$locked_in)`
4. `mean(pu_data$locked_in)`
5. `sum(pu_data$locked_out)`
6. `mean(pu_data$locked_out)`
7.
```
assert_that(min(c(pu_data$locked_in, pu_data$locked_out)) == 0)

assert_that(max(c(pu_data$locked_in, pu_data$locked_out)) == 1)
```
8. `all(is.finite(pu_data$cost))`
9. `assert_that(sum(duplicated(pu_data$id)) == 0)`
10. Yes, the eastern side of Tasmania is generally much cheaper than the western side.
11. Yes, most planning units covered by protected areas are located in the south-western side of Tasmania.

3.5 Vegetation data

The vegetation data describes the spatial distribution of 62 vegetation classes in the study area. This data is in a raster format and so the data are organized using a regular spatial

grid with square grid cells. In our case, our raster data contains multiple layers (also called "bands") and each layer has corresponds to a spatial grid with exactly the same area and has exactly the same dimensionality (i.e. number of rows, columns, and cells). In this dataset, there are 62 different regular spatial grids layered on top of each other – with each layer corresponding to a different vegetation class – and each of these layers contains a grid with 343 columns, 320 rows, and 109760 cells. Within each layer, each cell corresponds to a 1 by 1 km square. The values associated with each grid cell contain values (i.e. one or zero) indicating the presence or absence of a given vegetation class in the cell.

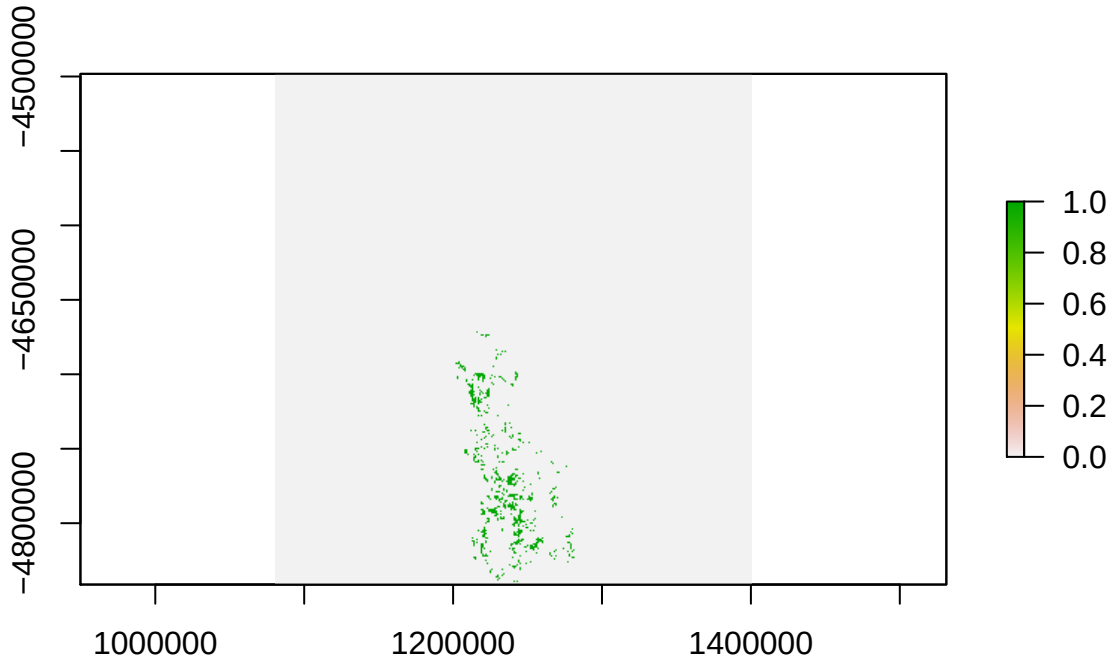


Let's explore the vegetation data.

```
# print a short summary of the data
print(veg_data)
```

```
## class      : RasterStack
## dimensions : 343, 320, 109760, 62  (nrow, ncol, ncell, nlayers)
## resolution : 1000, 1000  (x, y)
## extent     : 1080496, 1400496, -4841217, -4498217  (xmin, xmax, ymin, ymax)
## crs        : +proj=aea +lat_1=-18 +lat_2=-36 +lat_0=0 +lon_0=132 +x_0=0 +y_0=0 +ellps
## names      : vegetation.1, vegetation.2, vegetation.3, vegetation.4, vegetation.5, ve
## min values :            0,            0,            0,            0,            0,
## max values :            1,            1,            1,            1,            1,
```

```
# plot a map of the 36th vegetation class
plot(veg_data[[36]])
```




```
# plot an interactive map of the 36th vegetation class
mapview(veg_data[[36]])
```

```
# print number of rows in the data
nrow(veg_data)
```

```
## [1] 343
```

```
# print number of columns  in the data
ncol(veg_data)
```

```
## [1] 320
```

```
# print number of cells in the data
ncell(veg_data)
```

```
## [1] 109760
```

```
# print number of layers in the data
nlayers(veg_data)
```

```
## [1] 62
```

```
# print  resolution on the x-axis
xres(veg_data)
```

```
## [1] 1000
```

```
# print resolution on the y-axis
yres(veg_data)
```

```
## [1] 1000
```

```
# print spatial extent of the grid, i.e. coordinates for corners
extent(veg_data)
```

```
## class      : Extent
## xmin       : 1080496
## xmax       : 1400496
## ymin       : -4841217
## ymax       : -4498217
```

```
# print the coordinate reference system
print(veg_data@crs)
```

```
## CRS arguments:
##  +proj=aea +lat_1=-18 +lat_2=-36 +lat_0=0 +lon_0=132 +x_0=0 +y_0=0
## +ellps=GRS80 +units=m +no_defs
```

```
# print a summary of the first layer in the stack
print(veg_data[[1]])
```

```
## class      : RasterLayer
## band       : 1  (of  62  bands)
```

```
## dimensions : 343, 320, 109760  (nrow, ncol, ncell)
## resolution : 1000, 1000  (x, y)
## extent     : 1080496, 1400496, -4841217, -4498217  (xmin, xmax, ymin, ymax)
## crs        : +proj=aea +lat_1=-18 +lat_2=-36 +lat_0=0 +lon_0=132 +x_0=0 +y_0=0 +ellps
## source     : /home/travis/build/prioritizr/cibio-workshop/data/vegetation.tif
## names      : vegetation.1
## values     : 0, 1  (min, max)
```

```
# print the value in the 800th cell in the first layer of the stack
print(veg_data[[1]][800])
```

```
##
## 0
```

```
# print the value of the cell located in the 30th row and the 60th column of
# the first layer
print(veg_data[[1]][30, 60])
```

```
##
## 0
```

```
# calculate the sum of all the cell values in the first layer
cellStats(veg_data[[1]], "sum")
```

```
## [1] 36
```

```
# calculate the maximum value of all the cell values in the first layer
cellStats(veg_data[[1]], "max")
```

```
## [1] 1
```

```
# calculate the minimum value of all the cell values in the first layer
cellStats(veg_data[[1]], "min")
```

```
## [1] 0
```

```
# calculate the mean value of all the cell values in the first layer
cellStats(veg_data[[1]], "mean")
```

```
## [1] 0.0003279883
```

```
# calculate the maximum value in each layer
as_tibble(data.frame(max = cellStats(veg_data, "max")))
```

```
## # A tibble: 62 x 1
##      max
##    <dbl>
##  1     1
##  2     1
##  3     1
##  4     1
##  5     1
##  6     1
##  7     1
##  8     1
##  9     1
## 10     1
## # ... with 52 more rows
```

Now, you can try and answer some questions about the vegetation data.

1. What part of the study area is the 51st vegetation class found in (hint: make a map)?
2. How many rows does the 23rd layer contain?
3. Is the third vegetation class present at the 400th cell?
4. How many cells contain the 56th vegetation class?
5. What proportion of cells contain the 12th vegetation class?
6. Which vegetation class is present in the greatest number of cells?
7. Make an new object by summing together all the layer values into a single grid (i.e. `sum_veg_data <- sum(veg_data)`) and make a map showing this data (i.e. `plot(sum_veg_data)`). What does it mean if cells contain zeros in this new object? What reasons could there be to explain why some cells in this new object contain zeros?

1. Central-north Tasmania
2. `nrow(veg_data[[23]])`
3. `veg_data[[3]][400]`
4. `ncell(veg_data[[56]])`
5. `cellStats(veg_data[[12]], "mean")`
6. `names(veg_data)[which.max(cellStats(veg_data, "sum"))]`
7. Cells which do not contain habitat in any of the layers are denoted with a zero in `sum_veg_data`. These zero cells occur in places which do not contain any remnant vegetation (e.g. due to habitat destruction) or they occur in the ocean

(i.e. because terrestrial vegetation does not occur in the ocean).

Chapter 4

Gap analysis

4.1 Introduction

Before we begin to prioritize areas for protected area establishment, we should first understand how well existing protected areas are conserving our biodiversity features (i.e. native vegetation classes in Tasmania, Australia). This step is critical: we cannot develop plans to improve conservation of biodiversity if we don't understand how well existing policies are currently conserving biodiversity! To achieve this, we can perform a "gap analysis". A gap analysis involves calculating how well each of our biodiversity features (i.e. vegetation classes in this exercise) are represented (covered) by protected areas. Next, we compare current representation by protected areas of each feature (e.g. 5% of their spatial distribution covered by protected areas) to a target threshold (e.g. 20% of their spatial distribution covered by protected areas). This target threshold denotes the minimum amount (e.g. minimum proportion of spatial distribution) that we need of each feature to be represented in the protected area system. Ideally, targets should be based on an estimate of how much area or habitat is needed for ecosystem function or species persistence. In practice, targets are generally set using simple rules of thumb (e.g. 10% or 20%), policy (17%; https://www.cbd.int/sp/targets/rationale/target-11) or standard practices [e.g. setting targets for species based on range-size; Butchart et al., 2015, Rodrigues et al., 2004].

4.2 Feature abundance

Now we will perform some preliminary calculations for the gap analysis. First, we will calculate how much of each vegetation feature occurs inside each planning unit (i.e. the abundance of the features). To achieve this, we will use the `problem` function to create an empty conservation planning problem that only contains the planning unit and biodiversity data. We will then use the `feature_abundances` function to calculate the total amount of each feature in each planning unit.

```
# create prioritizr problem with only the data
p0 <- problem(pu_data, veg_data, cost_column = "cost")

# print empty problem,
# we can see that only the cost and feature data are defined
print(p0)
```

```
## Conservation Problem
##   planning units: SpatialPolygonsDataFrame (1130 units)
##   cost:           min: 0.19249, max: 61.92727
##   features:       vegetation.1, vegetation.2, vegetation.3, ... (62 features)
##   objective:      none
##   targets:        none
##   decisions:      default
##   constraints:    <none>
##   penalties:      <none>
##   portfolio:      default
##   solver:         default
```

```
# calculate amount of each feature in each planning unit
abundance_data <- feature_abundances(p0)

# print abundance data
print(abundance_data)
```

```
## # A tibble: 62 x 3
##    feature       absolute_abundance relative_abundance
##    <chr>                      <dbl>              <dbl>
##  1 vegetation.1                  33                  1
##  2 vegetation.2                 173                  1
##  3 vegetation.3                  24                  1
##  4 vegetation.4                  31                  1
##  5 vegetation.5                  23                  1
##  6 vegetation.6                  22                  1
##  7 vegetation.7                  15                  1
##  8 vegetation.8                  45                  1
##  9 vegetation.9                 384                  1
## 10 vegetation.10                 14                  1
## # ... with 52 more rows
```

```
# note that only the first ten rows are printed,
# this is because the abundance_data object is a tibble (i.e. tbl_df) object
```

```
# and not a standard data.frame object
print(class(abundance_data))
```

```
## [1] "tbl_df"     "tbl"        "data.frame"
```

```
# we can print all of the rows in abundance_data like this
print(abundance_data, n = Inf)
```

```
## # A tibble: 62 x 3
##    feature       absolute_abundance relative_abundance
##    <chr>                      <dbl>              <dbl>
##  1 vegetation.1                  33                  1
##  2 vegetation.2                 173                  1
##  3 vegetation.3                  24                  1
##  4 vegetation.4                  31                  1
##  5 vegetation.5                  23                  1
##  6 vegetation.6                  22                  1
##  7 vegetation.7                  15                  1
##  8 vegetation.8                  45                  1
##  9 vegetation.9                 384                  1
## 10 vegetation.10                 14                  1
## 11 vegetation.11                 39                  1
## 12 vegetation.12                 26                  1
## 13 vegetation.13                 20                  1
## 14 vegetation.14                123                  1
## 15 vegetation.15                 18                  1
## 16 vegetation.16                 11                  1
## 17 vegetation.17                 24                  1
## 18 vegetation.18                 19                  1
## 19 vegetation.19                 24                  1
## 20 vegetation.20                895                  1
## 21 vegetation.21                258                  1
## 22 vegetation.22                  8                  1
## 23 vegetation.23                 10                  1
## 24 vegetation.24                 21                  1
## 25 vegetation.25                 13                  1
## 26 vegetation.26                  9                  1
## 27 vegetation.27                 15                  1
## 28 vegetation.28                660                  1
## 29 vegetation.29                 30                  1
## 30 vegetation.30                 26                  1
## 31 vegetation.31                 52                  1
## 32 vegetation.32                 30                  1
```

```
## 33 vegetation.33              312                   1
## 34 vegetation.34               36                   1
## 35 vegetation.35              173                   1
## 36 vegetation.36              714                   1
## 37 vegetation.37               26                   1
## 38 vegetation.38               17                   1
## 39 vegetation.39               18                   1
## 40 vegetation.40               28                   1
## 41 vegetation.41               59                   1
## 42 vegetation.42                9                   1
## 43 vegetation.43               80                   1
## 44 vegetation.44              139                   1
## 45 vegetation.45               40                   1
## 46 vegetation.46               25                   1
## 47 vegetation.47               24                   1
## 48 vegetation.48              224                   1
## 49 vegetation.49                4                   1
## 50 vegetation.50               41                   1
## 51 vegetation.51              223                   1
## 52 vegetation.52                2                   1
## 53 vegetation.53                4                   1
## 54 vegetation.54                5                   1
## 55 vegetation.55                7                   1
## 56 vegetation.56                8                   1
## 57 vegetation.57               18                   1
## 58 vegetation.58                4                   1
## 59 vegetation.59               36                   1
## 60 vegetation.60                2                   1
## 61 vegetation.61                0                 NaN
## 62 vegetation.62                1                   1
```

The `abundance_data` object contains three columns. The `feature` column contains the name of each feature (derived from `names(veg_data)`), the `absolute_abundance` column contains the total amount of each feature in all the planning units, and the `relative_abundance` column contains the total amount of each feature in the planning units expressed as a proportion of the total amount in the underlying raster data. Since all the raster cells containing vegetation overlap with the planning units, all of the values in the `relative_abundance` column are equal to one (meaning 100%)—except for the 61st feature which has a value on `NaN` because it does not occur in the study area at all (i.e. all of its raster values are zeros). Now let's add a new column with the feature abundances expressed in aerial units (i.e. km^2).

```
# add new column with feature abundances in km^2
abundance_data$absolute_abundance_km2 <-
  (abundance_data$absolute_abundance * prod(res(veg_data))) %>%
```

```
  set_units(m^2) %>%
  set_units(km^2)

# print abundance data
print(abundance_data)
```

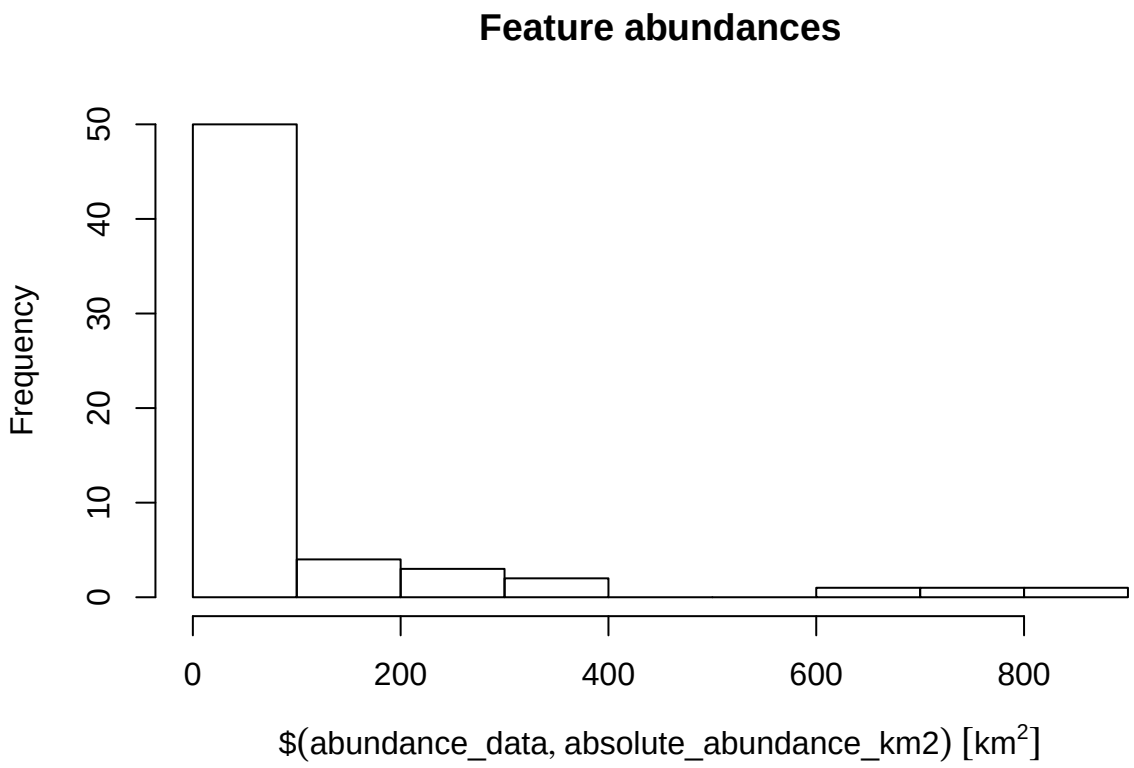
```
## # A tibble: 62 x 4
##    feature       absolute_abundance relative_abundan~ absolute_abundance_k~
##    <chr>                      <dbl>             <dbl>                 [km^2]
##  1 vegetation.1                  33                 1                     33
##  2 vegetation.2                 173                 1                    173
##  3 vegetation.3                  24                 1                     24
##  4 vegetation.4                  31                 1                     31
##  5 vegetation.5                  23                 1                     23
##  6 vegetation.6                  22                 1                     22
##  7 vegetation.7                  15                 1                     15
##  8 vegetation.8                  45                 1                     45
##  9 vegetation.9                 384                 1                    384
## 10 vegetation.10                 14                 1                     14
## # ... with 52 more rows
```

Now let's explore the abundance data.

```
# calculate the average abundance of the features
mean(abundance_data$absolute_abundance_km2)
```

```
## 86.67742 [km^2]
```

```
# plot histogram of the features' abundances
hist(abundance_data$absolute_abundance_km2, main = "Feature abundances")
```




```
# find the abundance of the feature with the largest abundance
max(abundance_data$absolute_abundance_km2)
```

```
## 895 [km^2]
```

```
# find the name of the feature with the largest abundance
abundance_data$feature[which.max(abundance_data$absolute_abundance_km2)]
```

```
## [1] "vegetation.20"
```

Now, try to answer the following questions.

1. What is the median abundance of the features (hint: `median`)?
2. What the abundance of the feature with smallest abundance?
3. What the name of the feature with smallest abundance?
4. What is the total abundance of all features in the planning units summed together?
5. How many features have a total abundance greater than 100 km^2 (hint: `sum(abundance_values > set_units(threshold_value, km^2))`)?

1. `median(abundance_data$absolute_abundance_km2)`
2. `min(abundance_data$absolute_abundance_km2)`
3. `abundance_data$feature[which.min(abundance_data$absolute_abundance_km2)]`
4. `sum(abundance_data$absolute_abundance_km2)`
5. `sum(abundance_data$absolute_abundance_km2 > set_units(100, km^2))`

4.3 Feature representation by protected areas

After calculating the total amount of each feature in the planning units (i.e. the features' abundances), we will now calculate the amount of each feature in the planning units that are covered by protected areas (i.e. feature representation by protected areas). We can complete this task using the `feature_representation` function. This function requires (i) a conservation problem object with the planning unit and biodiversity data and also (ii) an object representing a solution to the problem (i.e an object in the same format as the planning unit data with zeros and ones indicating if the planning units are contained in the prioritization problem or not).

```
# create column in planning unit data with binary values (zeros and ones)
# indicating if a planning unit is covered by protected areas or not
pu_data$pa_status <- as.numeric(pu_data$locked_in)

# calculate feature representation by protected areas
repr_data <- feature_representation(p0, pu_data[, "pa_status"])

# print feature representation data
print(repr_data)
```

```
## # A tibble: 62 x 3
##    feature       absolute_held relative_held
##    <chr>                 <dbl>         <dbl>
##  1 vegetation.1              1        0.0303
##  2 vegetation.2             14        0.0809
##  3 vegetation.3              2        0.0833
##  4 vegetation.4              1        0.0323
##  5 vegetation.5              0        0
##  6 vegetation.6              0        0
##  7 vegetation.7              0        0
##  8 vegetation.8              6        0.133
##  9 vegetation.9             20        0.0521
## 10 vegetation.10             0        0
## # ... with 52 more rows
```

Similar to the abundance data before, the `repr_data` object contains three columns. The `feature` column contains the name of each feature, the `absolute_held` column shows the total amount of each feature held in the solution (i.e. the planning units covered by protected areas), and the `relative_held` column shows the proportion of each feature held in the solution (i.e. the proportion of each feature's spatial distribution held in protected areas). Since the `absolute_held` values correspond to the number of grid cells in the `veg_data` object with overlap with protected areas, let's convert them to aerial-based units (i.e. km^2) so we can report them.

```
# add new column with the areas represented in km^2
repr_data$absolute_held_km2 <-
  (repr_data$absolute_held * prod(res(veg_data))) %>%
  set_units(m^2) %>%
  set_units(km^2)

# print representation data
print(repr_data)
```

```
## # A tibble: 62 x 4
##    feature       absolute_held relative_held absolute_held_km2
##    <chr>                 <dbl>         <dbl>             [km^2]
##  1 vegetation.1              1        0.0303                 1
##  2 vegetation.2             14        0.0809                14
##  3 vegetation.3              2        0.0833                 2
##  4 vegetation.4              1        0.0323                 1
##  5 vegetation.5              0        0                      0
##  6 vegetation.6              0        0                      0
##  7 vegetation.7              0        0                      0
##  8 vegetation.8              6        0.133                  6
##  9 vegetation.9             20        0.0521                20
## 10 vegetation.10             0        0                      0
## # ... with 52 more rows
```

Now let's investigate how well the species are represented.

1. What is the average proportion of the features held in protected areas (hint: `mean(x, na.rm = TRUE)`?
2. What is the average amount of land in km^2 that features are represented by protected areas?
3. What is the name of the feature with the greatest proportionate coverage by protected areas?
4. What is the name of the feature with the greatest aerial coverage by protected areas?
5. Do questions two and three have the same answer? If not, why could this be?

6. Is there a relationship between the total abundance of a feature and how well it is represented by protected areas (hint: `plot(abundances ~ relative_held)`)?
7. Are any features entirely missing from protected areas (hint: `sum(x == 0)`)?
8. If we set a target of 10% coverage by protected areas, how many features fail to meet this target (hint: `sum(relative_held >= target)`)?
9. If we set a target of 20% coverage by protected areas, how many features fail to meet this target?

1. `mean(repr_data$relative_held, na.rm = TRUE)`
2. `mean(repr_data$absolute_held_km2, na.rm = TRUE)`
3. `repr_data$feature[which.max(repr_data$relative_held)]`
4. `repr_data$feature[which.max(repr_data$absolute_held)]`
5. No, just because a vegetation class is widespread does not necessarily mean that it has the greatest overlap with protected areas. In fact, due to biases in the establishment of protected areas this can often be the case.
6. Yes, the largest protected areas tend to have the great representation (broadly speaking).
   See `plot(x = abundance_data$absolute_abundance, y = repr_data$relative_held)`
7. `sum(repr_data$absolute_held < 1e-10)` (floating point errors)
8. `sum(repr_data$relative_held > 0.1)`
9. `sum(repr_data$relative_held > 0.2)`

Chapter 5

Spatial prioritizations

5.1 Introduction

Here we will develop prioritizations to identify priority areas for protected area establishment. Its worth noting that prioritizr, Marxan, and Zonation are all decision *support* tools. This means that these tools are all designed to *help* you make decisions—they can't make decisions for you.

5.2 Starting out simple

To start things off, let's keep things simple. Let's create a prioritization using the minimum set problem formulation of the reserve selection problem. This problem will have 5% targets for each vegetation class and use the data in the `cost` column to specify acquisition costs. Although we strongly recommend using Gurobi to solve problems (`add_gurobi_solver`), we will use the lpsymphony solver in this workshop since it is much easier to install. The Gurobi solver is the fastest solver that prioritizr can use to generate solutions and is much, much, much faster than the lpsymphony solver (see here for Gurobi installation instructions).

```
# print planning unit data
print(pu_data)
```

```
## class       : SpatialPolygonsDataFrame
## features    : 1130
## extent      : 1080623, 1399989, -4840595, -4497092  (xmin, xmax, ymin, ymax)
## crs         : +proj=aea +lat_1=-18 +lat_2=-36 +lat_0=0 +lon_0=132 +x_0=0 +y_0=0 +ellp
## variables   : 6
## names       :   id,              cost, status, locked_in, locked_out, pa_status
## min values  :    1, 0.192488262910798,      0,         0,          0,         0
## max values  : 1130,  61.9272727272727,      2,         1,          1,         1
```

```
# make prioritization problem
p1 <- problem(pu_data, veg_data, cost_column = "cost") %>%
      add_min_set_objective() %>%
      add_relative_targets(0.05) %>% # 5% representation targets
      add_binary_decisions() %>%
      add_lpsymphony_solver(verbose = FALSE)

# print problem
print(p1)
```

```
## Conservation Problem
##   planning units: SpatialPolygonsDataFrame (1130 units)
##   cost:           min: 0.19249, max: 61.92727
##   features:       vegetation.1, vegetation.2, vegetation.3, ... (62 features)
##   objective:      Minimum set objective
##   targets:        Relative targets [targets (min: 0.05, max: 0.05)]
##   decisions:      Binary decision
##   constraints:    <none>
##   penalties:      <none>
##   portfolio:      default
##   solver:         Lpsymphony [first_feasible (0), gap (0.1), time_limit (-1), verbose
```

```
# solve problem
s1 <- solve(p1)

# print solution,
# the solution_1 column contains the solution values with binary values
# indicating if a planning unit was selected as a (1) priority area or (0) not
print(s1)
```

```
## class       : SpatialPolygonsDataFrame
## features    : 1130
## extent      : 1080623, 1399989, -4840595, -4497092  (xmin, xmax, ymin, ymax)
## crs         : +proj=aea +lat_1=-18 +lat_2=-36 +lat_0=0 +lon_0=132 +x_0=0 +y_0=0 +ellp
## variables   : 7
## names       :   id,              cost, status, locked_in, locked_out, pa_status, solu
## min values  :    1, 0.192488262910798,      0,         0,          0,         0,
## max values  : 1130,  61.9272727272727,      2,         1,          1,         1,
```

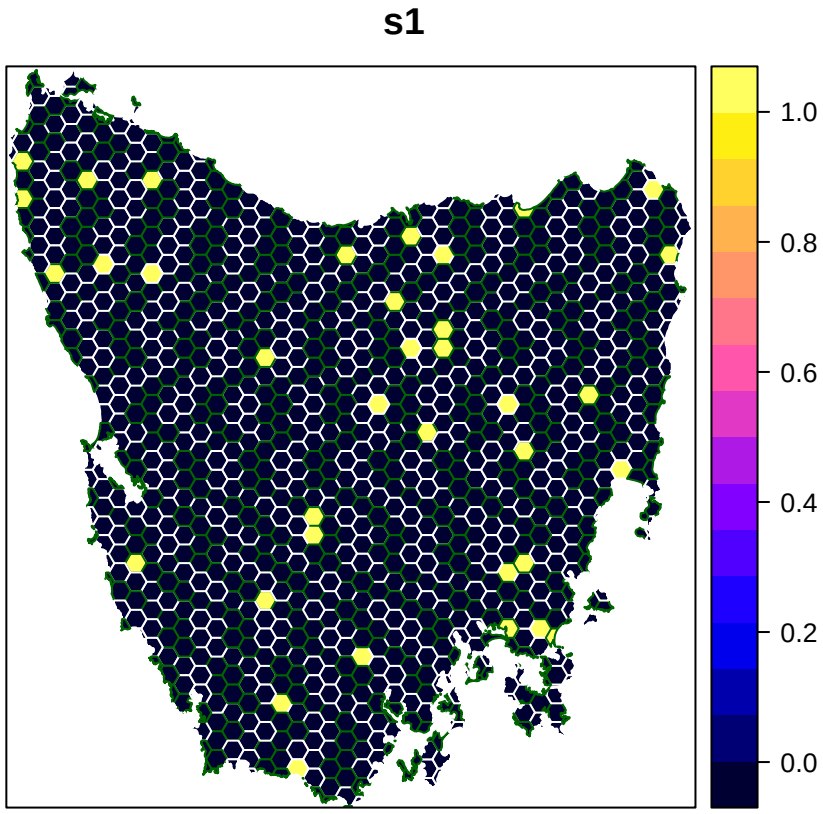
```
# calculate number of planning units selected in the prioritization
sum(s1$solution_1)
```

```
## [1] 36
```

```
# calculate total cost of the prioritization
sum(s1$solution_1 * s1$cost)
```

```
## [1] 806.2393
```

```
# plot solution
spplot(s1, "solution_1", col = c("white", "darkgreen"), main = "s1")
```



Now let's examine the solution.

1. How many planing units were selected in the prioritization? What proportion of planning units were selected in the prioritization?
2. Is there a pattern in the spatial distribution of the priority areas?
3. Can you verify that all of the targets were met in the prioritization (hint: `feature_representation(p1, s1[, "solution_1"])`)?
4. What are limitations of this prioritization?

1. `sum(s1$solution_1)`
   `s1$solution_1)`
2. Yes, the planning units are generally spread out across most of the study area and they are not biased towards specific areas.
3. `all(feature_representation(p1, s1[, "solution_1"])$relative_held >= 0.2)`
4. This prioritization (i) does not account for existing protected areas, (ii) does not account for the spatial fragmentation of priority areas, or (iii) is not likely conserve enough habitat for each vegetation type (i.e. 5% is pretty small).

5.3 Adding complexity

Our first prioritization suffers many limitations, so let's add additional constraints to the problem to make it more useful. First, let's lock in planing units that are already inside protected areas.

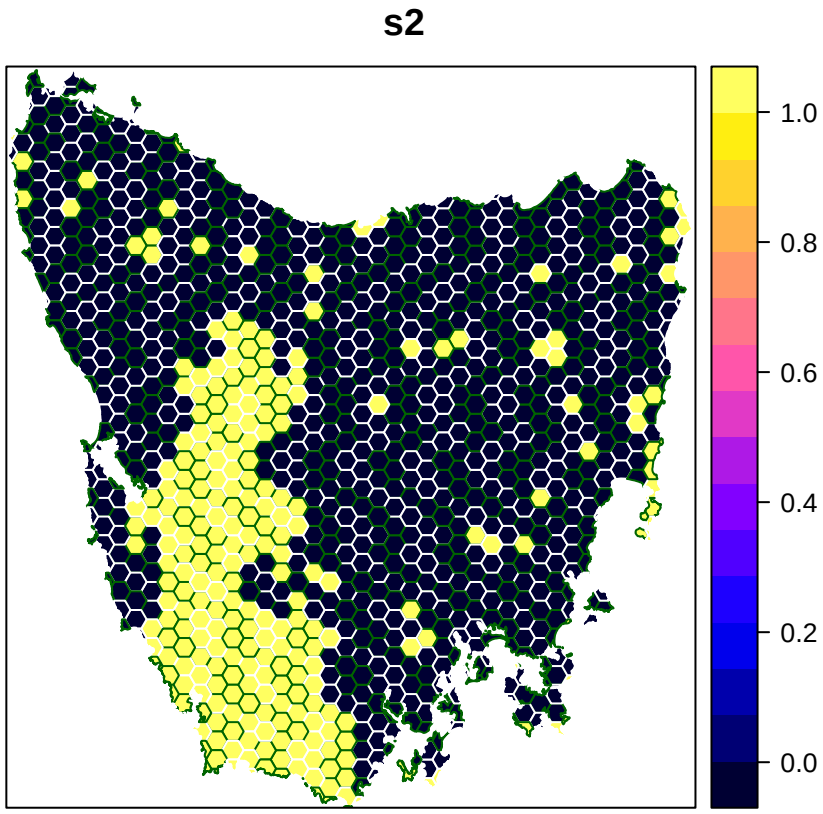
```
# make prioritization problem
p2 <- problem(pu_data, veg_data, cost_column = "cost") %>%
      add_min_set_objective() %>%
      add_relative_targets(0.05) %>%
      add_locked_in_constraints("locked_in") %>%
      add_binary_decisions() %>%
      add_lpsymphony_solver(verbose = FALSE)

# print problem
print(p2)
```

```
## Conservation Problem
##   planning units: SpatialPolygonsDataFrame (1130 units)
##   cost:           min: 0.19249, max: 61.92727
##   features:       vegetation.1, vegetation.2, vegetation.3, ... (62 features)
##   objective:      Minimum set objective
##   targets:        Relative targets [targets (min: 0.05, max: 0.05)]
##   decisions:      Binary decision
##   constraints:    <Locked in planning units [257 locked units]>
##   penalties:      <none>
##   portfolio:      default
##   solver:         Lpsymphony [first_feasible (0), gap (0.1), time_limit (-1), verbose
```

```
# solve problem
s2 <- solve(p2)

# plot solution
spplot(s2, "solution_1", col = c("white", "darkgreen"), main = "s2")
```



Let's pretend we talked to an expert on the vegetation communities in our study system and they recommended that a 20% target was needed. So, now let's set the targets to 20% of their total distribution in the study area.

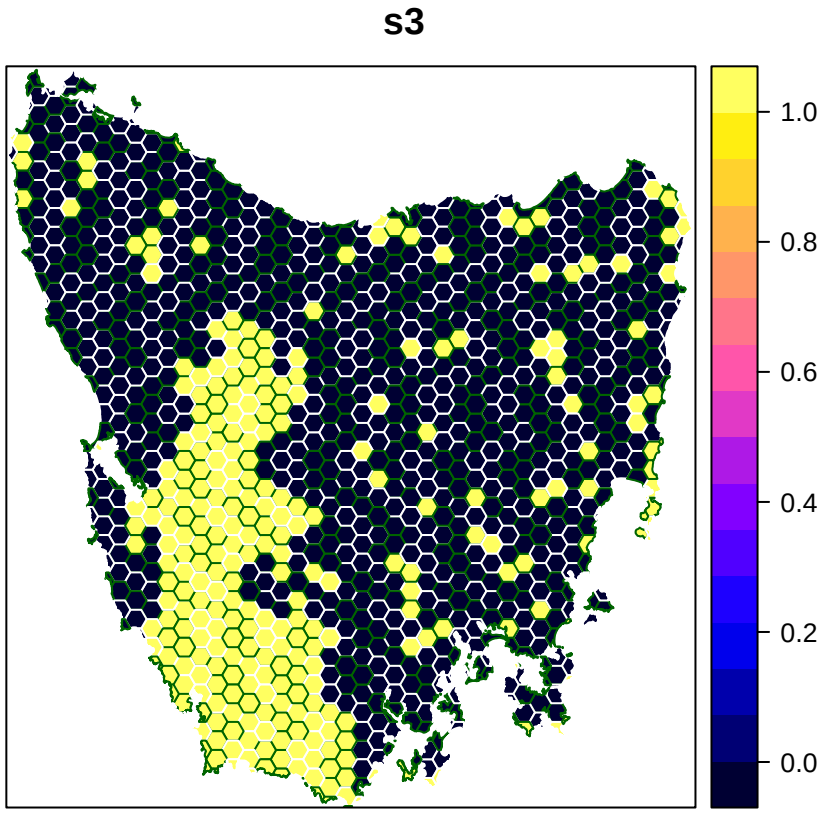
```
# make prioritization problem
p3 <- problem(pu_data, veg_data, cost_column = "cost") %>%
      add_min_set_objective() %>%
      add_relative_targets(0.2) %>%
      add_locked_in_constraints("locked_in") %>%
      add_binary_decisions() %>%
      add_lpsymphony_solver(verbose = FALSE)

# print problem
print(p3)
```

```
## Conservation Problem
##   planning units: SpatialPolygonsDataFrame (1130 units)
##   cost:           min: 0.19249, max: 61.92727
##   features:       vegetation.1, vegetation.2, vegetation.3, ... (62 features)
##   objective:      Minimum set objective
##   targets:        Relative targets [targets (min: 0.2, max: 0.2)]
##   decisions:      Binary decision
##   constraints:    <Locked in planning units [257 locked units]>
##   penalties:      <none>
##   portfolio:      default
##   solver:         Lpsymphony [first_feasible (0), gap (0.1), time_limit (-1), verbose
```

```r
# solve problem
s3 <- solve(p3)

# plot solution
spplot(s3, "solution_1", col = c("white", "darkgreen"), main = "s3")
```



Next, let's lock out highly degraded areas.

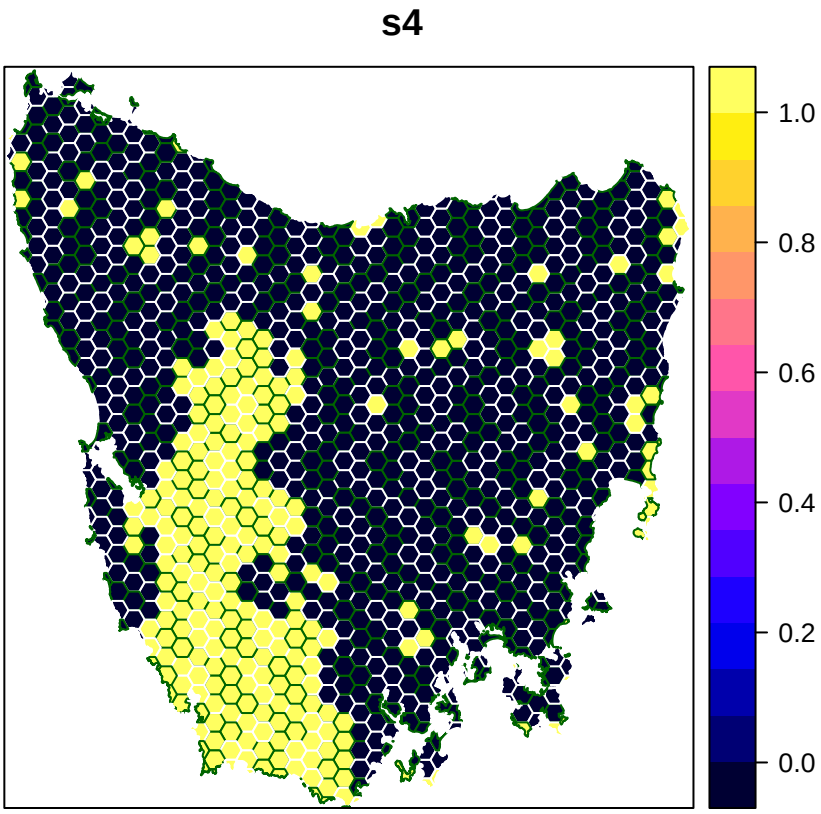
```
# make prioritization problem
p4 <- problem(pu_data, veg_data, cost_column = "cost") %>%
      add_min_set_objective() %>%
      add_relative_targets(0.05) %>%
      add_locked_in_constraints("locked_in") %>%
      add_locked_out_constraints("locked_out") %>%
      add_binary_decisions() %>%
      add_lpsymphony_solver(verbose = FALSE)

# print problem
print(p4)
```

```
## Conservation Problem
##   planning units: SpatialPolygonsDataFrame (1130 units)
##   cost:           min: 0.19249, max: 61.92727
##   features:       vegetation.1, vegetation.2, vegetation.3, ... (62 features)
##   objective:      Minimum set objective
##   targets:        Relative targets [targets (min: 0.05, max: 0.05)]
##   decisions:      Binary decision
##   constraints:    <Locked out planning units [51 locked units]
##                    Locked in planning units [257 locked units]>
##   penalties:      <none>
##   portfolio:      default
##   solver:         Lpsymphony [first_feasible (0), gap (0.1), time_limit (-1), verbose
```

```
# solve problem
s4 <- solve(p4)

# plot solution
spplot(s4, "solution_1", col = c("white", "darkgreen"), main = "s4")
```



Now, let's compare the solutions.

1. What is the cost of the planning units selected in `s2`, `s3`, and `s4`?
2. How many planning units are in `s2`, `s3`, and `s4`?
3. Do the solutions with more planning units have a greater cost? Why or why not?
4. Why does the first solution (`s1`) cost less than the second solution with protected areas locked into the solution (`s2`)?
5. Why does the third solution (`s3`) cost less than the fourth solution solution with highly degraded areas locked out (`s4`)?
6. What happens if you specify targets that exceed the total amount of vegetation in the study area? You can do this by rerunning the code to make `p4` with `add_absolute_targets(1000)` instead of `add_relative_targets(0.2)` and generating a new solution?

1. ```
   sum(s2$cost * s2$solution_1)
   sum(s3$cost * s3$solution_1)
   sum(s4$cost * s4$solution_1)
   ```
2. ```
   sum(s2$solution_1)
   sum(s3$solution_1)
   sum(s4$solution_1)
   ```

3. No, just because a solution a solution has more planning units does not mean that it will cost less.
4. This is because the planning units covered by existing protected areas have a non-zero cost and locking in these planning units introduces inefficiencies into the solution. This is very common in real-world conservation prioritizations because existing protected areas are often in places that do little to benefit biodiversity [Fuller et al., 2010].
5. This is because some of the planning units that are highly degraded – based on just the planning unit costs and vegetation data – provide cost-efficient opportunities for meeting the targets and excluding them from the reserve selection process means that other more costly planning units are needed to meet the targets.
6. We get an error message stating the the problem is infeasible because there is no valid solution—even if we selected all the planning units the study area we would still not meet the targets.

Chapter 6

Budget limited prioritizations

The Conventional on Biological Diversity (https://www.cbd.int) mandates that signatories – including Australia – should have at least 17% of their land and 10% of their oceans covered by protected areas (or other effective area-based conservation measures) by 2020. But is 17% coverage enough to adequately conserve biodiversity? Well, let's calculate the percentage of land secured in priority areas.

```
# calculate area for each planning unit in km^2
pu_data$area_km2 <-
  pu_data %>%
  gArea(byid = TRUE) %>%
  set_units(m^2) %>%
  set_units(km^2)

# calculate proportion of land covered by existing protected areas
sum(pu_data$pa_status * pu_data$area_km2) / sum(pu_data$area_km2)
```

```
## 0.2220554 [1]
```

```
# calculate proportion of land covered by prioritization
sum(s4$solution_1 * pu_data$area_km2) / sum(pu_data$area_km2)
```

```
## 0.2395804 [1]
```

We can see that the answer is no. If additional protected areas were established to ensure adequate representation of the 62 vegetation communities for minimal cost, then we would need at least 23.96% of Tasmania covered by protected areas. So, one question could be where should the Australian government establish new protected areas to increase representation of vegetation

what if the Australian government

If the Australian government wanted to expand the protected area system to increase protected area coverage of as many vegetation communities as possible without exceeding the 17% threshold,

Chapter 7

Irreplaceability

TODO.

Chapter 8

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