

# Barro Colorado Island

```
library(ppjsdm)
library(spatstat)
#> Loading required package: spatstat.data
#> Loading required package: nlme
#> Loading required package: rpart
#>
#> spatstat 1.63-0      (nickname: 'Space camouflage')
#> For an introduction to spatstat, type 'beginner'
remove(list = ls())

source("../R/get_bci.R")

set.seed(1)
```

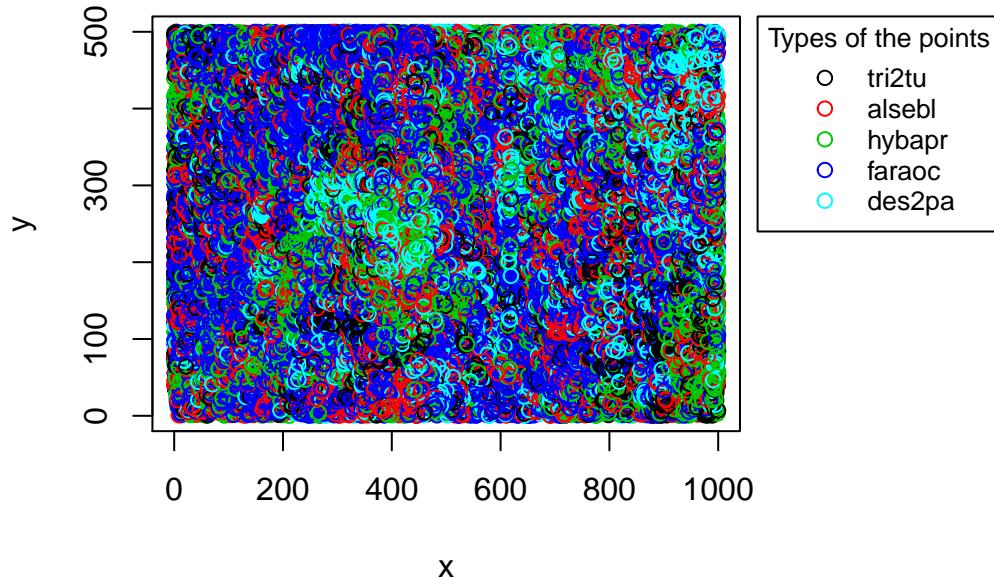
This vignette explains how to use the `ppjsdm` package with the Barro Colorado Island (BCI) dataset. We begin by loading the data with only the most prevalent species.

```
number_of_species <- 5
bci <- get_bci(prevalent = number_of_species)
configuration <- bci$configuration
window <- bci>window
```

The point configuration is plotted below.

```
par(mar = c(5, 4, 4, 13) + 0.1)
plot(configuration, window = window)
```

## Points in the configuration



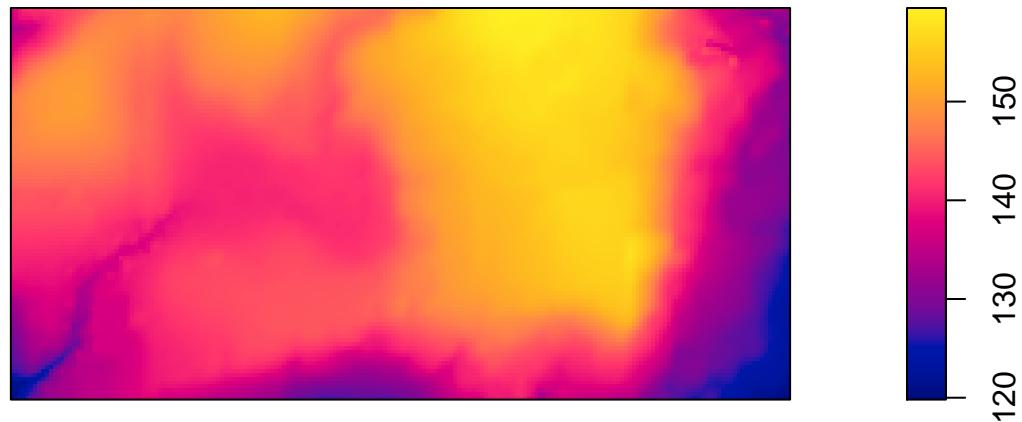
The BCI dataset also contains a series of environmental covariates. The easiest to obtain are the elevation level and the elevation gradient, since they are included in `spatstat`.

```
covariates <- list(elevation = spatstat.data::bei.extra$elev,
                    gradient = spatstat.data::bei.extra$grad)
```

Plotting covariates maps is easy in `spatstat`.

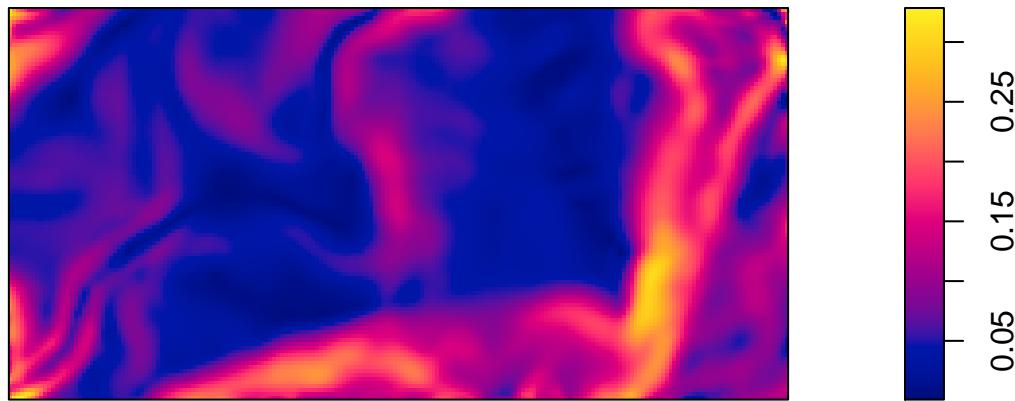
```
plot(covariates$elevation)
```

**covariates\$elevation**



```
plot(covariates$gradient)
```

## covariates\$gradient



The matrix `radii` defined below models interaction radii within a species (on the diagonal), and between species (outside the diagonal). One could play around with different interaction radii, but any homogeneous interaction radius of less than 10 m tends to work well.

```
radii <- matrix(3, number_of_species, number_of_species)
```

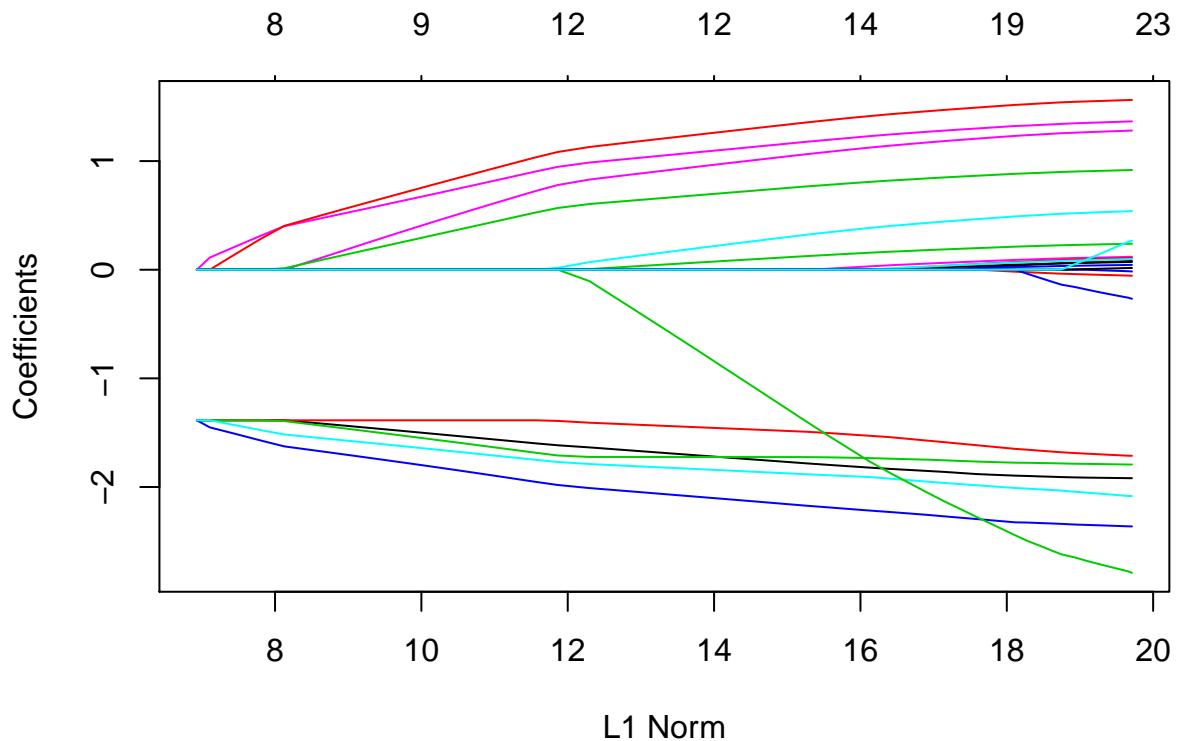
Fitting the model to the dataset is then quite easy.

```
fit <- ppjsdm::gibbsm(configuration,
                        window = window,
                        covariates = covariates,
                        model = "Geyer",
                        radius = radii,
                        use_glmnet = TRUE)
#> 31 x 1 sparse Matrix of class "dgCMatrix"
#>           1
#> (Intercept) .
#> log_lambda1 -4.53777871
#> log_lambda2 -4.09822285
#> log_lambda3 -3.42524025
#> log_lambda4 -3.82526277
#> log_lambda5 -4.53418255
#> alpha_1_1     1.28125919
#> alpha_1_2     0.08031431
#> alpha_1_3    -0.05575721
#> alpha_1_4     0.23935471
#> alpha_1_5    -0.01599904
```

```

#> alpha_2_2      0.53971175
#> alpha_2_3      0.11871960
#> alpha_2_4      0.07074299
#> alpha_2_5      0.10846987
#> alpha_3_3      0.91785298
#> alpha_3_4      0.04414910
#> alpha_3_5      0.09840173
#> alpha_4_4      1.36487525
#> alpha_4_5      0.01622990
#> alpha_5_5      1.56268408
#> elevation_1    .
#> elevation_2    .
#> elevation_3    .
#> elevation_4    .
#> elevation_5    .
#> gradient_1     .
#> gradient_2     .
#> gradient_3    -2.79013470
#> gradient_4    -0.26760149
#> gradient_5    0.26622727
plot(fit$complete)

```



```
plot(fit$cv)
```

