

# 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)
```

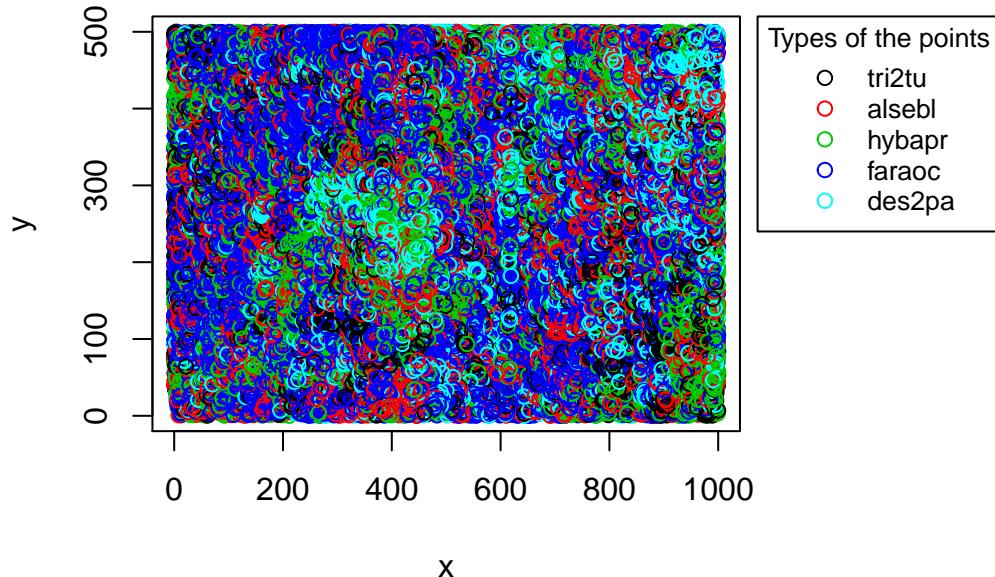
This vignette explains how to use the `ppjsdm` package with the Barro Colorado Island (BCI) dataset. We begin by loading the data with only the most prevalent species.

```
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



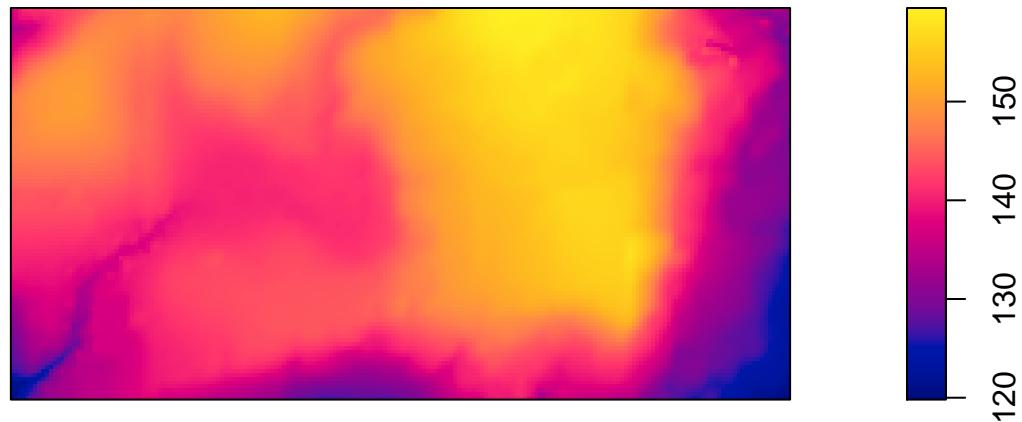
The BCI dataset also contains a series of environmental covariates. The easiest to obtain are the elevation level and the elevation gradient, since they are included in `spatstat`.

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

Plotting covariates maps is easy in `spatstat`.

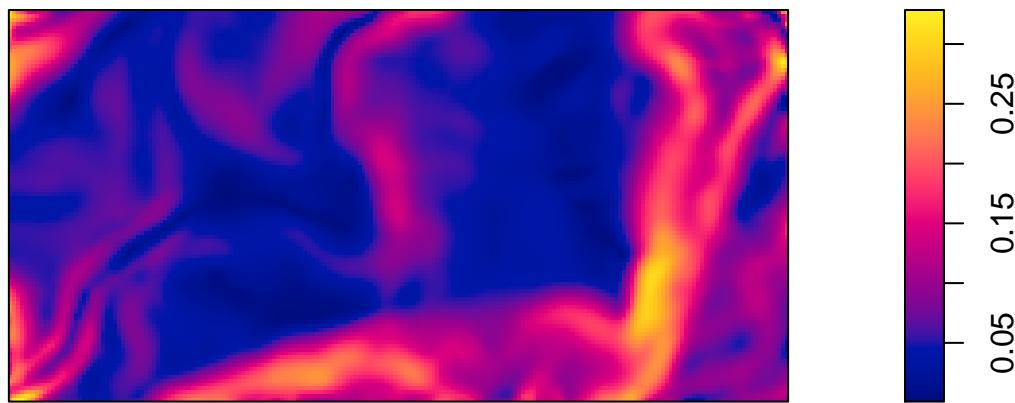
```
plot(covariates$elevation)
```

**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)
```

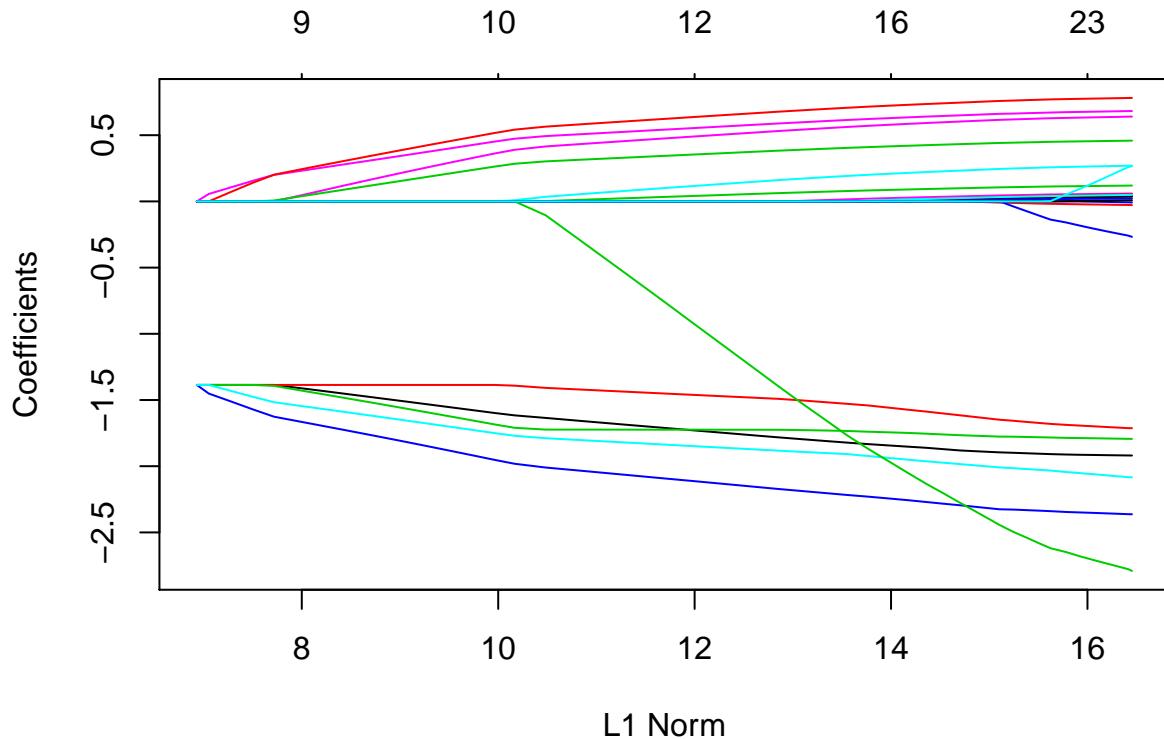
Fitting the model to the dataset is then quite easy.

```
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 -4.537778713
#> log_lambda2 -4.098222849
#> log_lambda3 -3.425240246
#> log_lambda4 -3.825262766
#> log_lambda5 -4.534182546
#> alpha_1_1 0.640629597
#> alpha_1_2 0.040157155
#> alpha_1_3 -0.027878603
#> alpha_1_4 0.119677355
#> alpha_1_5 -0.007999519
```

```

#> alpha_2_2    0.269855876
#> alpha_2_3    0.059359800
#> alpha_2_4    0.035371494
#> alpha_2_5    0.054234935
#> alpha_3_3    0.458926490
#> alpha_3_4    0.022074551
#> alpha_3_5    0.049200865
#> alpha_4_4    0.682437625
#> alpha_4_5    0.008114952
#> alpha_5_5    0.781342039
#> elevation_1   .
#> elevation_2   .
#> elevation_3   .
#> elevation_4   .
#> elevation_5   .
#> gradient_1   .
#> gradient_2   .
#> gradient_3   -2.790134698
#> gradient_4   -0.267601491
#> gradient_5   0.266227274
plot(fit$complete)

```



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

