

Barro Colorado Island

```
library(ppjssdm)
library(spatstat)
#> Loading required package: spatstat.data
#> Loading required package: nlme
#> Loading required package: rpart
#>
#> spatstat 1.62-2      (nickname: 'Shape-shifting lizard')
#> For an introduction to spatstat, type 'beginner'
remove(list = ls())

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

set.seed(1)
```

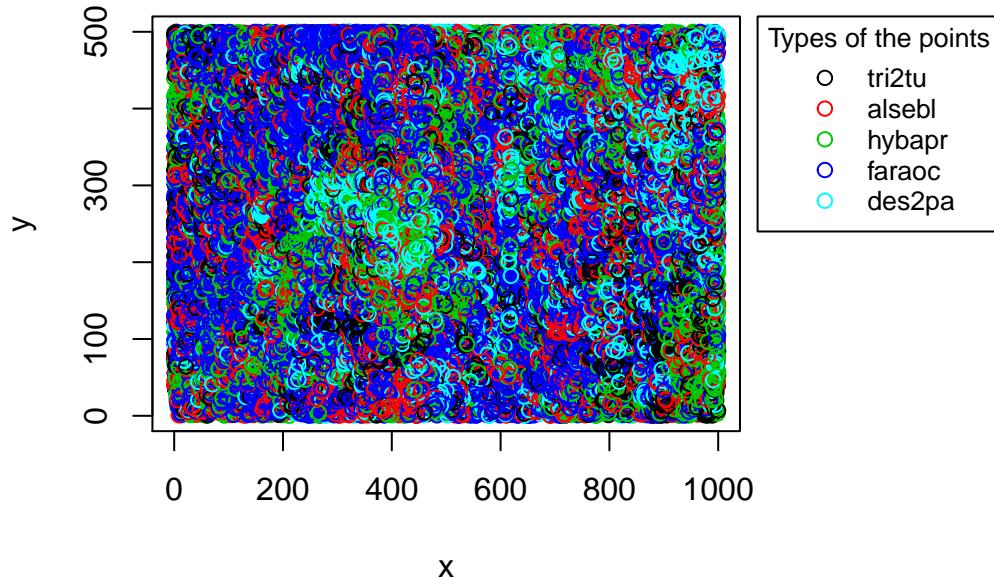
This vignette explains how to use the `ppjssdm` package with the Barro Colorado Island (BCI) dataset. We begin by loading the data with only the most prevalent species.

```
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



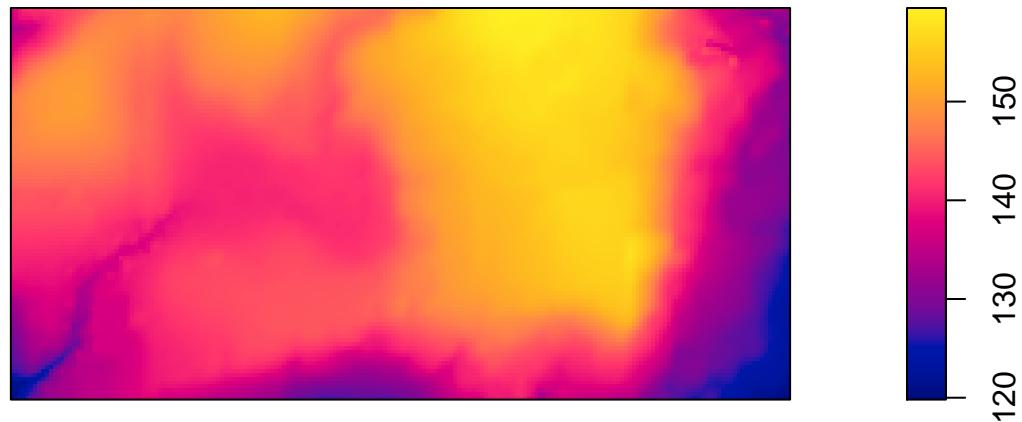
The BCI dataset also contains a series of environmental covariates. The easiest to obtain are the elevation level and the elevation gradient, since they are included in `spatstat`.

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

Plotting covariates maps is easy in `spatstat`.

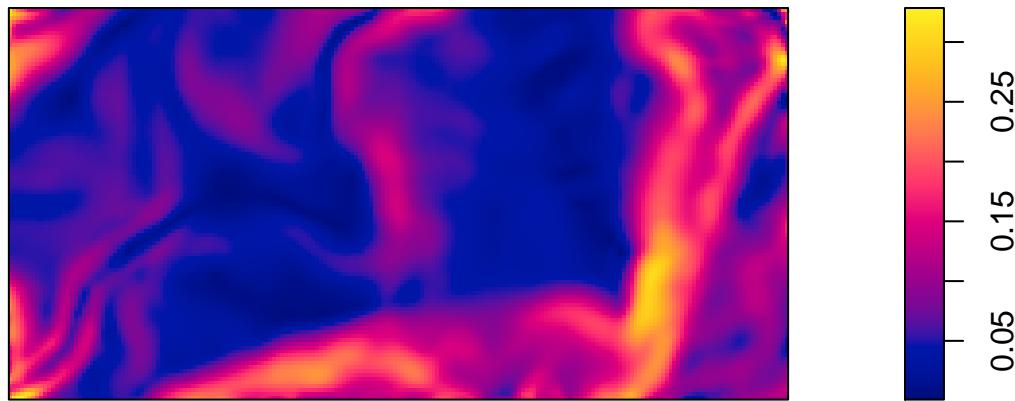
```
plot(covariates$elevation)
```

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)
```

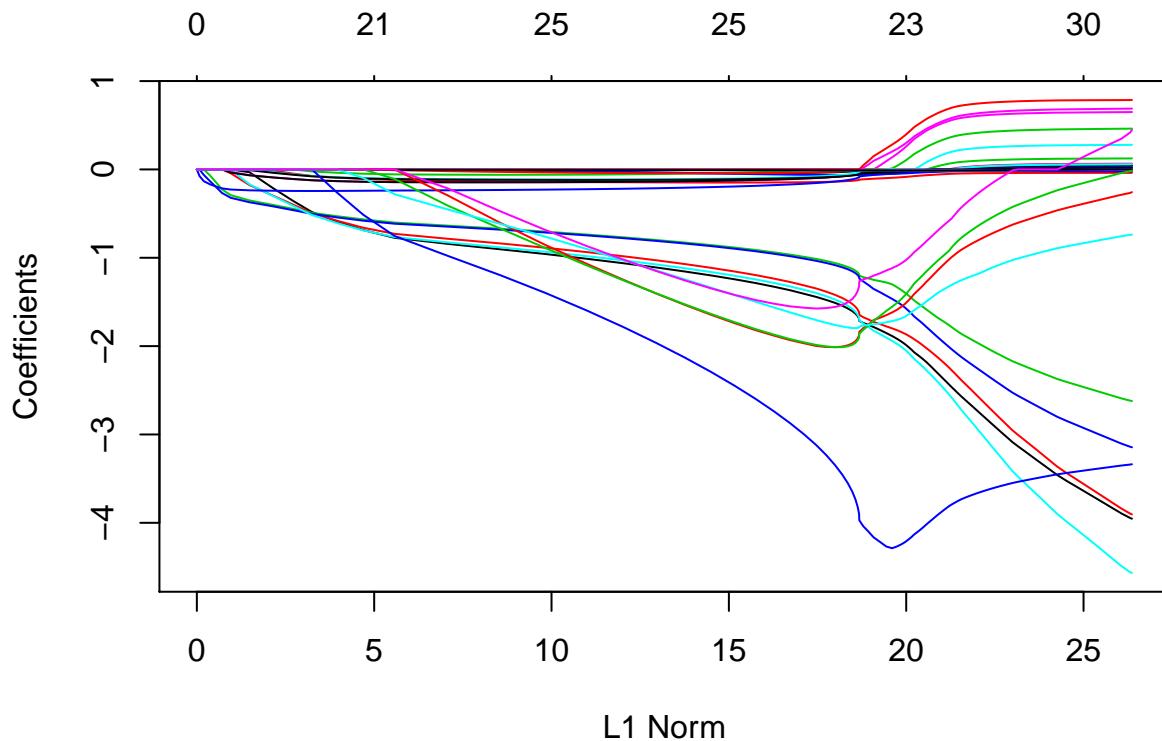
Fitting the model to the dataset is then quite easy.

```
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_lambda_1 -3.953972777
#> log_lambda_2 -3.904981202
#> log_lambda_3 -2.621940227
#> log_lambda_4 -3.145197644
#> log_lambda_5 -4.566250789
#> alpha_1_1      0.649761861
#> alpha_1_2      0.048498083
#> alpha_1_3     -0.038512917
#> alpha_1_4      0.124989213
#> alpha_1_5     -0.021565049
```

```

#> alpha_2_2      0.278521562
#> alpha_2_3      0.066105209
#> alpha_2_4      0.040104142
#> alpha_2_5      0.060004808
#> alpha_3_3      0.461968401
#> alpha_3_4      0.025013336
#> alpha_3_5      0.058752501
#> alpha_4_4      0.688677796
#> alpha_4_5      0.016030480
#> alpha_5_5      0.786396924
#> elevation_1    -0.003854742
#> elevation_2    -0.001472701
#> elevation_3    -0.005332725
#> elevation_4    -0.004568448
#> elevation_5    .
#> gradient_1     -0.256994952
#> gradient_2     -0.013801121
#> gradient_3     -3.337399621
#> gradient_4     -0.737481746
#> gradient_5     0.446657069
plot(fit$complete)

```



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

