

# Barro Colorado Island

```
library(ppjsdm)
#> Registered S3 method overwritten by 'spatstat':
#>   method      from
#> print.boxx cli
library(spatstat)
#> Loading required package: spatstat.data
#> Loading required package: nlme
#> Loading required package: rpart
#>
#> spatstat 1.64-0      (nickname: 'Susana Distancia')
#> For an introduction to spatstat, type 'beginner'
#>
#> Attaching package: 'spatstat'
#> The following object is masked from 'package:ppjsdm':
#>
#>      marks
library(plot.matrix)
remove(list = ls())

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

set.seed(1)
```

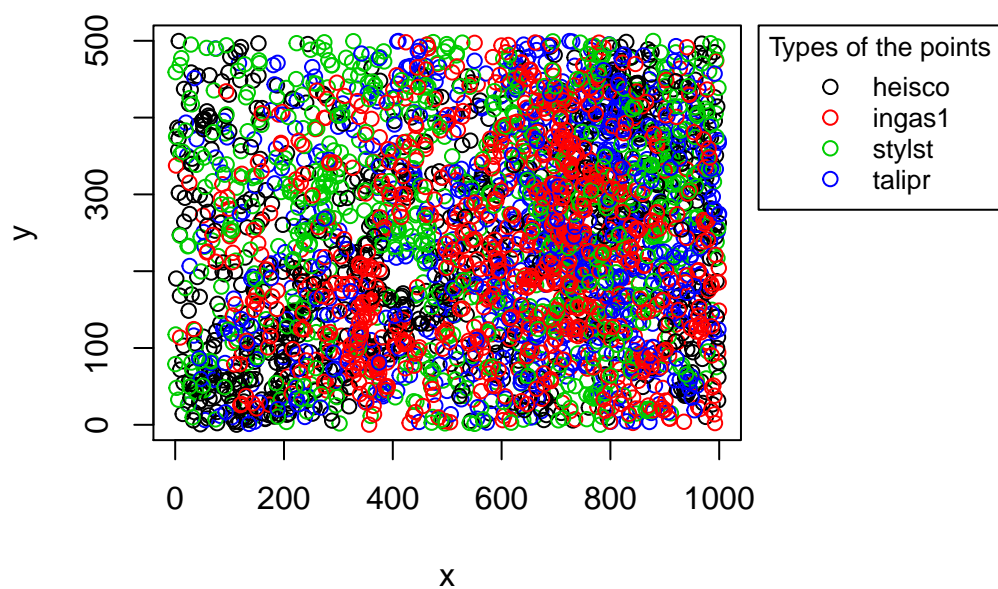
This vignette explains how to use the `ppjsdm` package with the Barro Colorado Island (BCI) dataset. We begin by loading the data with only the most prevalent species.

```
number_of_species <- 4
bci <- get_bci(least_prevalent = 50, most_prevalent = 50 + number_of_species - 1)
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



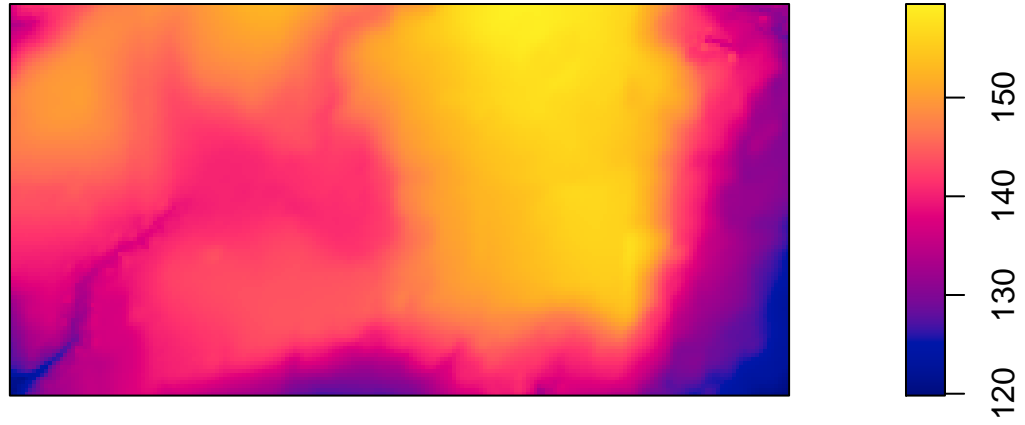
The BCI dataset also contains a series of environmental covariates. The easiest to obtain are the elevation level and the elevation gradient, since they are included in `spatstat`.

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

Plotting covariates maps is easy in `spatstat`.

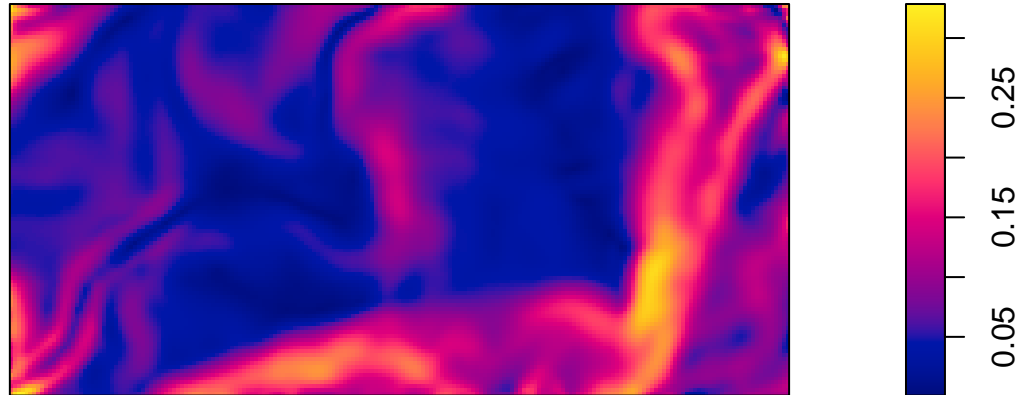
```
plot(covariates$elevation)
```

**covariates\$elevation**



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

## covariates\$gradient



The matrix `short_range` defined below models short range 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 10m tends to work well.

```
short_range <- matrix(10, number_of_species, number_of_species)
medium_range <- matrix(20, number_of_species, number_of_species)
long_range <- matrix(40, number_of_species, number_of_species)
```

Fitting the model to the dataset is then quite easy.

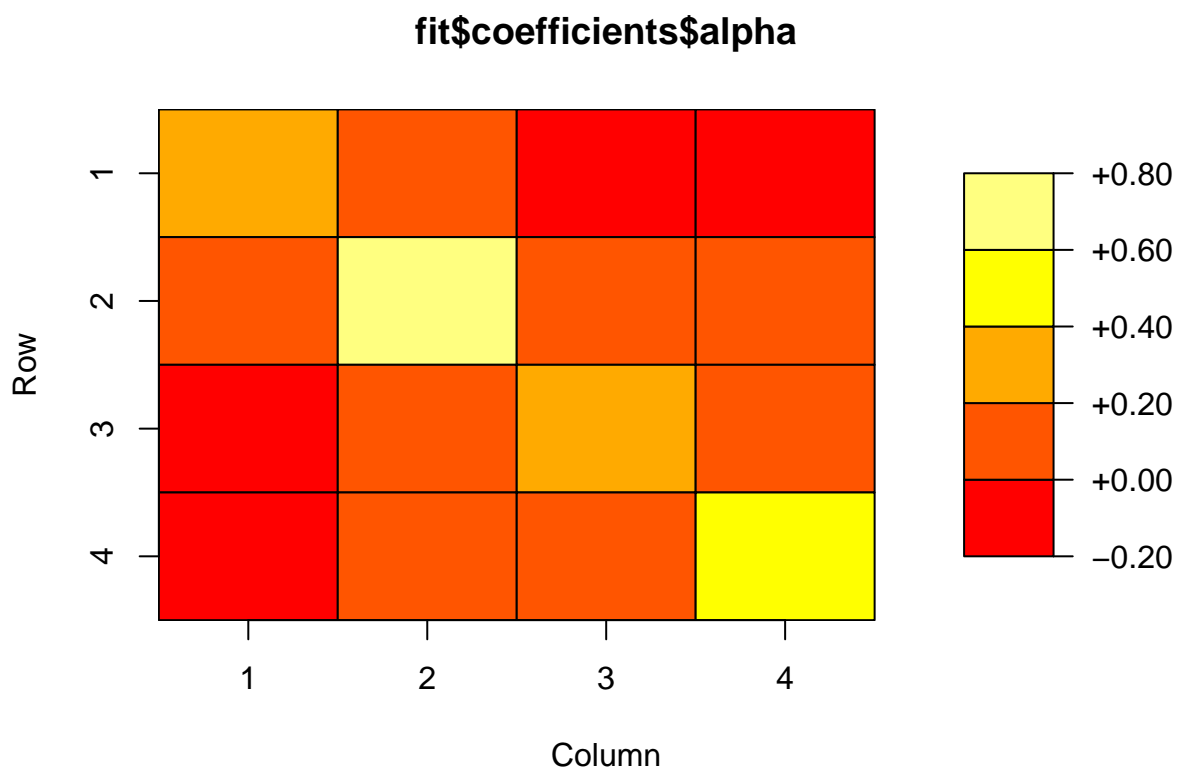
```
tm <- Sys.time()
fit <- ppjsdm::gibbsm(configuration,
  window = window,
  covariates = covariates,
  model = "square_exponential",
  medium_range_model = "square_exponential",
  short_range = short_range,
  medium_range = medium_range,
  long_range = long_range,
  use_glmnet = FALSE)

print(Sys.time() - tm)
#> Time difference of 4.221825 mins
print(fit$coefficients)
#> $beta0
#> [1] -5.702813 -10.186507 -4.986499 -10.727998
#>
#> $alpha
```

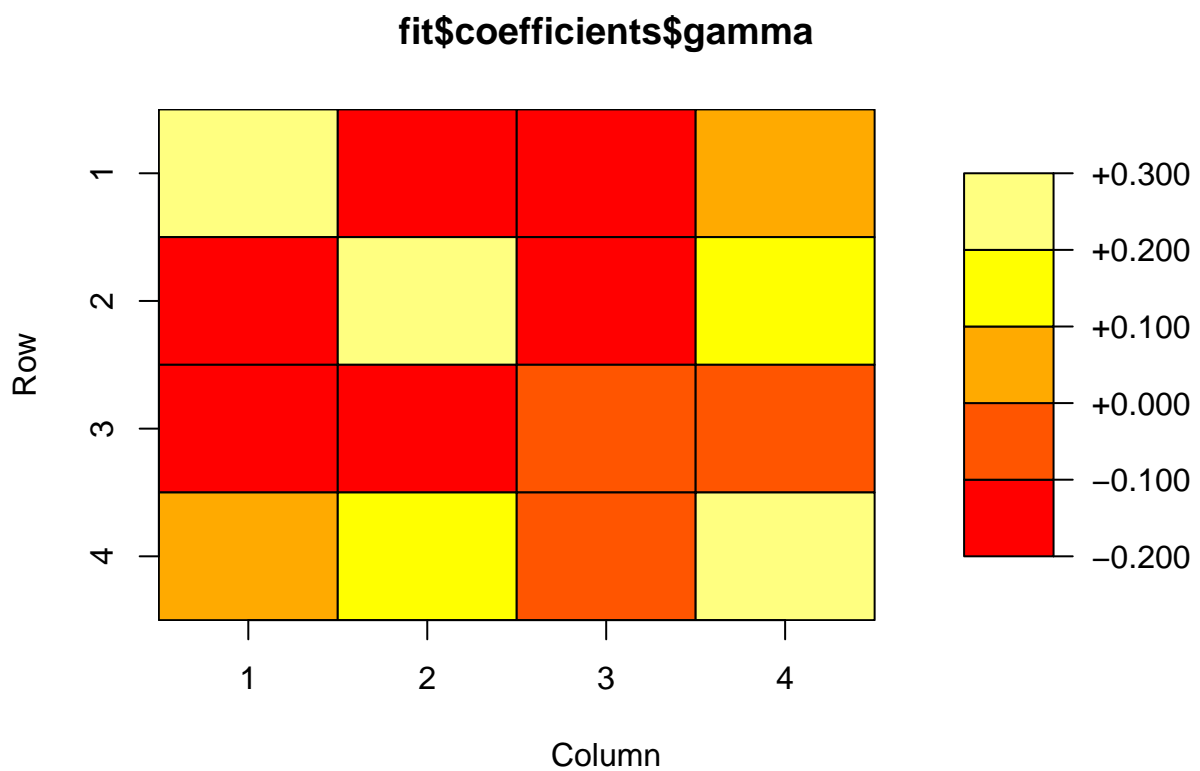
```

#>           [,1]      [,2]      [,3]      [,4]
#> [1,] 0.33131696 0.08664114 -0.03860860 -0.01466829
#> [2,] 0.08664114 0.73664460 0.03386179 0.10122725
#> [3,] -0.03860860 0.03386179 0.28899282 0.15913165
#> [4,] -0.01466829 0.10122725 0.15913165 0.41523899
#>
#> $gamma
#>           [,1]      [,2]      [,3]      [,4]
#> [1,] 0.29765179 -0.1066259 -0.10993179 0.02123073
#> [2,] -0.10662590 0.2664075 -0.13612367 0.11918027
#> [3,] -0.10993179 -0.1361237 -0.09477362 -0.02017127
#> [4,] 0.02123073 0.1191803 -0.02017127 0.25231364
#>
#> $beta
#>           [,1]      [,2]
#> [1,] -0.008904305 0.442801492
#> [2,] 0.018250708 -0.878159790
#> [3,] -0.007623592 -0.009519699
#> [4,] 0.020026593 -0.100391594
#>
#> $short_range
#>           [,1] [,2] [,3] [,4]
#> [1,] 10 10 10 10
#> [2,] 10 10 10 10
#> [3,] 10 10 10 10
#> [4,] 10 10 10 10
#>
#> $medium_range
#>           [,1] [,2] [,3] [,4]
#> [1,] 20 20 20 20
#> [2,] 20 20 20 20
#> [3,] 20 20 20 20
#> [4,] 20 20 20 20
#>
#> $long_range
#>           [,1] [,2] [,3] [,4]
#> [1,] 40 40 40 40
#> [2,] 40 40 40 40
#> [3,] 40 40 40 40
#> [4,] 40 40 40 40
par(mar = c(5.1, 5.1, 4.1, 4.1))
plot(fit$coefficients$alpha)

```



```
plot(fit$coefficients$gamma)
```



```
print(fit$aic)
#> [1] 6946.821
print(fit$bic)
#> [1] 7158.711
```