

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)
```

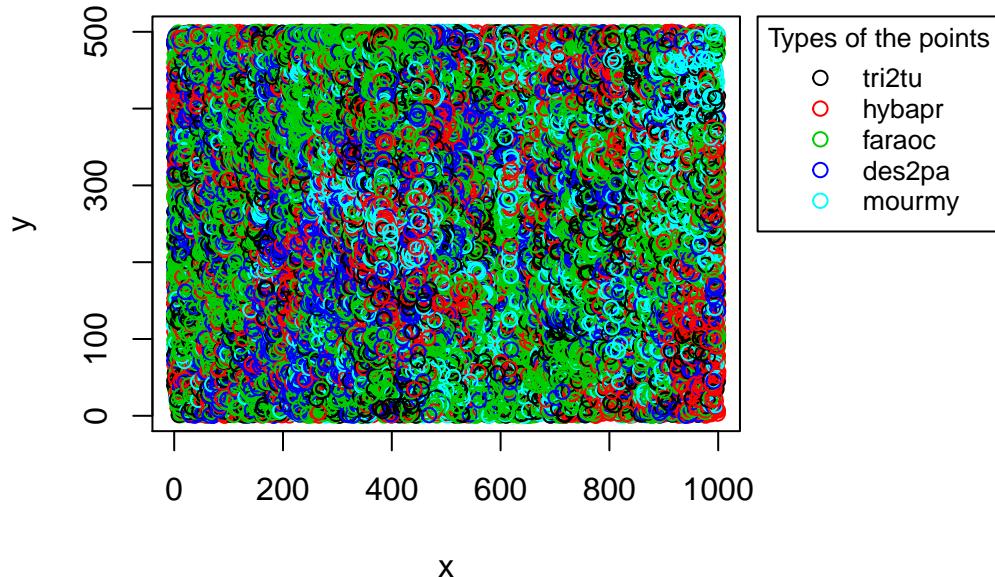
This vignette explains how to use the `ppjssdm` package with the Barro Colorado Island (BCI) dataset. We begin by loading the data with only the most prevalent species.

```
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



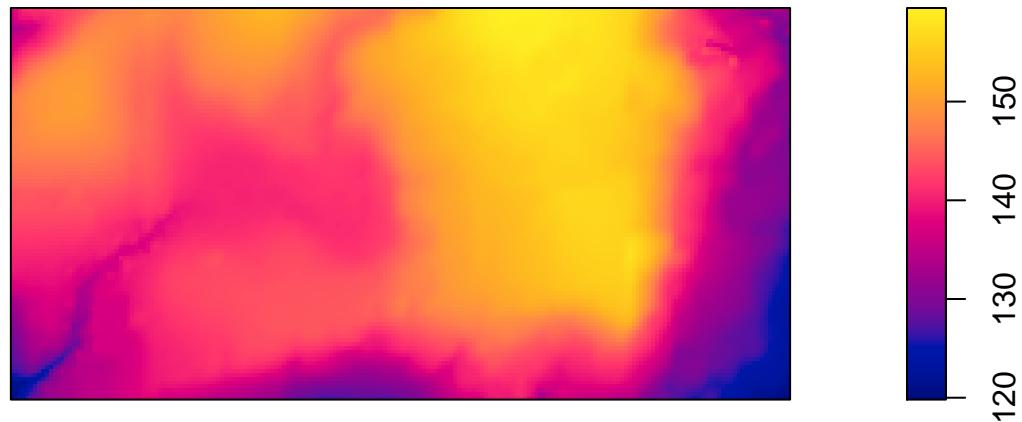
The BCI dataset also contains a series of environmental covariates. The easiest to obtain are the elevation level and the elevation gradient, since they are included in `spatstat`.

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

Plotting covariates maps is easy in `spatstat`.

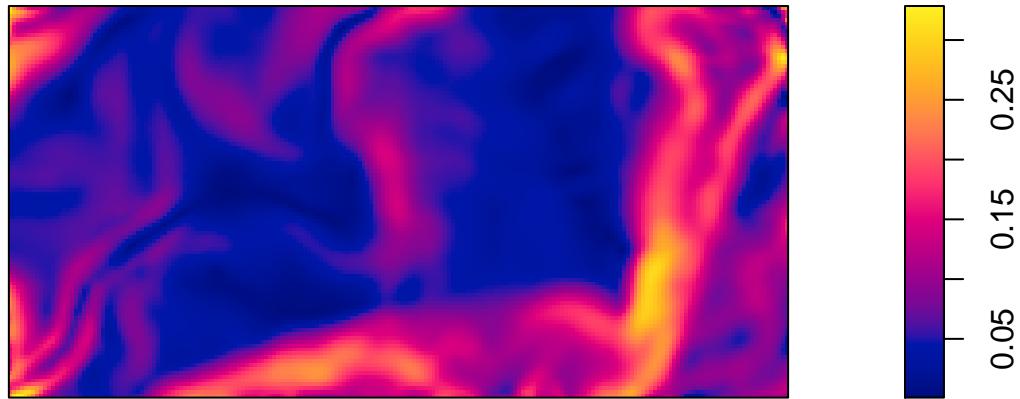
```
plot(covariates$elevation)
```

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 =
#> log_lambda_1 log_lambda_2 log_lambda_3 log_lambda_4 log_lambda_5
#> -5.9628027361 -3.4655194455 -4.3152154574 -3.6564479294 -6.9839304922
#> elevation_1 elevation_2 elevation_3 elevation_4 elevation_5
#> 0.0121602649 -0.0002175948 0.0034124632 -0.0052379576 0.0160378653
#> gradient_1 gradient_2 gradient_3 gradient_4 gradient_5
#> 0.8595554342 -2.8203610409 -0.2373517573 -4.0508777054 1.5431576436
#> alpha_1_1 alpha_1_2 alpha_1_3 alpha_1_4 alpha_1_5
#> 0.2703346927 0.0704938756 0.0348711638 0.0976643476 0.0505956807
#> alpha_2_2 alpha_2_3 alpha_2_4 alpha_2_5 alpha_3_3
#> 0.4638755291 0.0183693533 0.0954763018 0.0683413545 0.7089318858
#> alpha_3_4 alpha_3_5 alpha_4_4 alpha_4_5 alpha_5_5
#> 0.0476588440 0.0112733889 0.5651416862 -0.0210046347 0.7769550009
summary(fit)
#>
#> Call:
#> glm(formula = as.formula(gibbsm_data$formula), family = binomial(),
#>      data = as.data.frame(gibbsm_data$data))
#>
```

```

#> Deviance Residuals:
#>      Min     1Q Median     3Q    Max
#> -1.1973 -0.7351 -0.5816 -0.4284 2.3599
#>
#> Coefficients:
#>             Estimate Std. Error z value Pr(>|z|)
#> log_lambda_1 -5.9628027 0.2165725 -27.533 < 2e-16 ***
#> log_lambda_2 -3.4655194 0.1477635 -23.453 < 2e-16 ***
#> log_lambda_3 -4.3152155 0.1423789 -30.308 < 2e-16 ***
#> log_lambda_4 -3.6564479 0.2753348 -13.280 < 2e-16 ***
#> log_lambda_5 -6.9839305 0.2244785 -31.112 < 2e-16 ***
#> elevation_1   0.0121603 0.0014539  8.364 < 2e-16 ***
#> elevation_2  -0.0002176 0.0009910 -0.220 0.826197
#> elevation_3   0.0034125 0.0009537  3.578 0.000346 ***
#> elevation_4  -0.0052380 0.0018502 -2.831 0.004640 **
#> elevation_5   0.0160379 0.0015017 10.679 < 2e-16 ***
#> gradient_1    0.8595554 0.1950754  4.406 1.05e-05 ***
#> gradient_2   -2.8203610 0.1521848 -18.532 < 2e-16 ***
#> gradient_3   -0.2373518 0.1323404 -1.793 0.072894 .
#> gradient_4  -4.0508777 0.2873984 -14.095 < 2e-16 ***
#> gradient_5   1.5431576 0.2034918  7.583 3.37e-14 ***
#> alpha_1_1     0.2703347 0.0135859 19.898 < 2e-16 ***
#> alpha_1_2     0.0704939 0.0077719  9.070 < 2e-16 ***
#> alpha_1_3     0.0348712 0.0073201  4.764 1.90e-06 ***
#> alpha_1_4     0.0976643 0.0119051  8.204 2.33e-16 ***
#> alpha_1_5     0.0505957 0.0103680  4.880 1.06e-06 ***
#> alpha_2_2     0.4638755 0.0092090 50.372 < 2e-16 ***
#> alpha_2_3     0.0183694 0.0058969  3.115 0.001839 **
#> alpha_2_4     0.0954763 0.0090460 10.554 < 2e-16 ***
#> alpha_2_5     0.0683414 0.0080185  8.523 < 2e-16 ***
#> alpha_3_3     0.7089319 0.0089299 79.389 < 2e-16 ***
#> alpha_3_4     0.0476588 0.0086676  5.499 3.83e-08 ***
#> alpha_3_5     0.0112734 0.0075956  1.484 0.137757
#> alpha_4_4     0.5651417 0.0177707 31.802 < 2e-16 ***
#> alpha_4_5   -0.0210046 0.0131080 -1.602 0.109061
#> alpha_5_5     0.7769550 0.0133834 58.054 < 2e-16 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> (Dispersion parameter for binomial family taken to be 1)
#>
#> Null deviance: 1384482 on 415770 degrees of freedom
#> Residual deviance: 398558 on 415740 degrees of freedom
#> AIC: 398618
#>
#> Number of Fisher Scoring iterations: 4

```