

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)
```

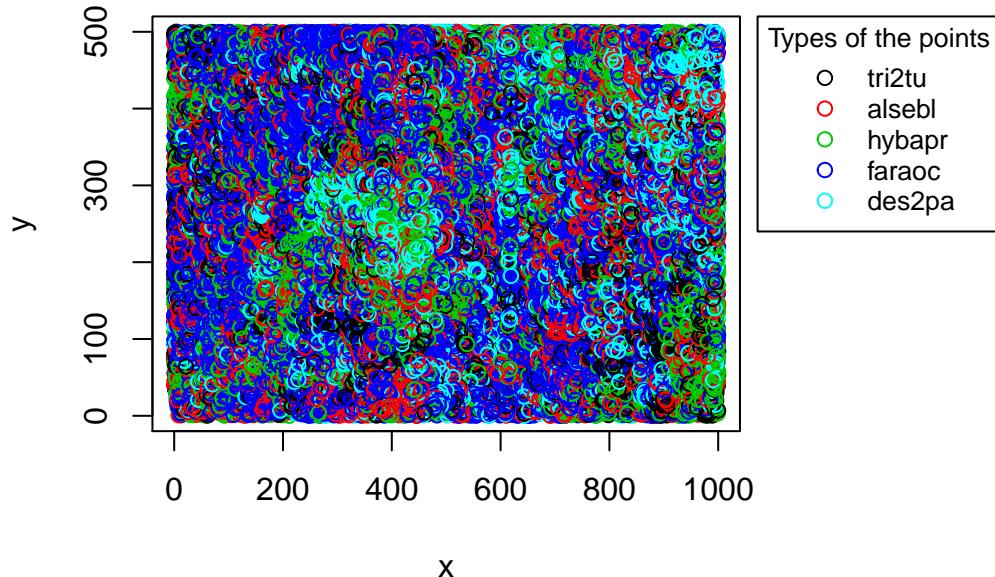
This vignette explains how to use the `ppjssdm` package with the Barro Colorado Island (BCI) dataset. We begin by loading the data with only the most prevalent species.

```
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



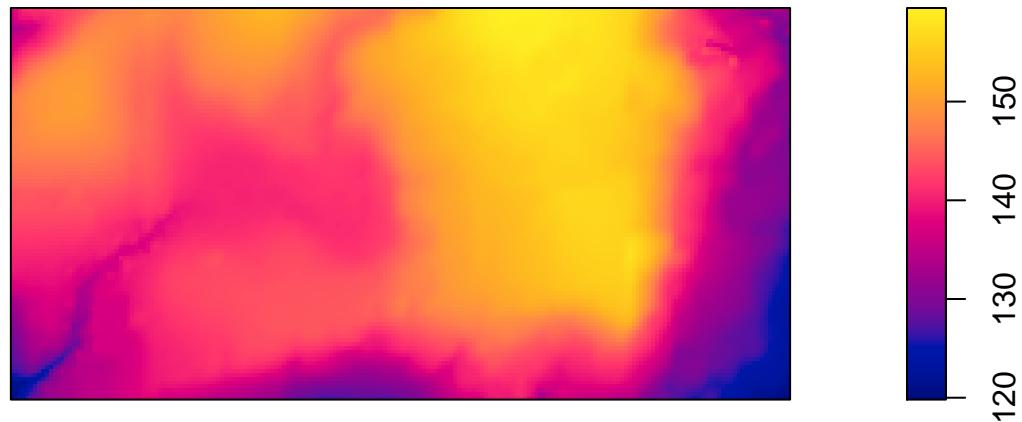
The BCI dataset also contains a series of environmental covariates. The easiest to obtain are the elevation level and the elevation gradient, since they are included in `spatstat`.

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

Plotting covariates maps is easy in `spatstat`.

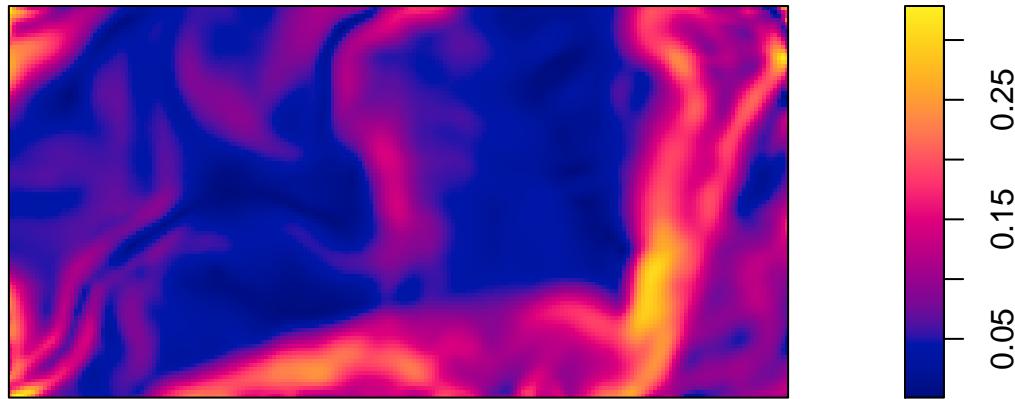
```
plot(covariates$elevation)
```

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 = FALSE)

#> log_lambda_1  log_lambda_2  log_lambda_3  log_lambda_4  log_lambda_5
#> -5.7277409098 -5.7836749482 -3.4094503456 -4.2993308091 -6.9275068129
#> elevation_1    elevation_2   elevation_3   elevation_4   elevation_5
#> 0.0080079426  0.0110758355 -0.0001983461  0.0030148716  0.0157764455
#> gradient_1     gradient_2   gradient_3   gradient_4   gradient_5
#> 0.4235175948  0.6981198584 -2.9979090270 -0.2555045945  1.4368522555
#> alpha_1_1       alpha_1_2    alpha_1_3    alpha_1_4    alpha_1_5
#> 0.6510289400  0.0461869051 -0.0389138595  0.1257516224 -0.0320022479
#> alpha_2_2       alpha_2_3    alpha_2_4    alpha_2_5    alpha_3_3
#> 0.2767581525  0.0682817718  0.0406706629  0.0533307853  0.4701810433
#> alpha_3_4       alpha_3_5    alpha_4_4    alpha_4_5    alpha_5_5
#> 0.0284665590  0.0594735848  0.6962325039  0.0140366978  0.7795761495

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
#> -1.1751  -0.7355  -0.5716  -0.4259   2.3577
#>
#> Coefficients:
#>             Estimate Std. Error z value Pr(>|z|)
#> log_lambda_1 -5.7277409  0.2409661 -23.770 < 2e-16 ***
#> log_lambda_2 -5.7836749  0.2161062 -26.763 < 2e-16 ***
#> log_lambda_3 -3.4094503  0.1473532 -23.138 < 2e-16 ***
#> log_lambda_4 -4.2993308  0.1419765 -30.282 < 2e-16 ***
#> log_lambda_5 -6.9275068  0.2245189 -30.855 < 2e-16 ***
#> elevation_1   0.0080079  0.0016197   4.944 7.65e-07 ***
#> elevation_2   0.0110758  0.0014541   7.617 2.59e-14 ***
#> elevation_3   -0.0001983  0.0009906  -0.200 0.841300
#> elevation_4   0.0030149  0.0009525   3.165 0.001550 **
#> elevation_5   0.0157764  0.0015038  10.491 < 2e-16 ***
#> gradient_1    0.4235176  0.2203671   1.922 0.054622 .
#> gradient_2    0.6981199  0.1938549   3.601 0.000317 ***
#> gradient_3   -2.9979090  0.1515800 -19.778 < 2e-16 ***
#> gradient_4   -0.2555046  0.1317110  -1.940 0.052393 .
#> gradient_5    1.4368523  0.2021358   7.108 1.17e-12 ***
#> alpha_1_1     0.6510289  0.0150188  43.348 < 2e-16 ***
#> alpha_1_2     0.0461869  0.0110891   4.165 3.11e-05 ***
#> alpha_1_3    -0.0389139  0.0087432  -4.451 8.56e-06 ***
#> alpha_1_4     0.1257516  0.0078510  16.017 < 2e-16 ***
#> alpha_1_5    -0.0320022  0.0118546  -2.700 0.006943 **
#> alpha_2_2     0.2767582  0.0136119  20.332 < 2e-16 ***
#> alpha_2_3     0.0682818  0.0077556   8.804 < 2e-16 ***
#> alpha_2_4     0.0406707  0.0073262   5.551 2.83e-08 ***
#> alpha_2_5     0.0533308  0.0103739   5.141 2.74e-07 ***
#> alpha_3_3     0.4701810  0.0092044  51.082 < 2e-16 ***
#> alpha_3_4     0.0284666  0.0059035   4.822 1.42e-06 ***
#> alpha_3_5     0.0594736  0.0080332   7.403 1.33e-13 ***
#> alpha_4_4     0.6962325  0.0089376  77.899 < 2e-16 ***
#> alpha_4_5     0.0140367  0.0076052   1.846 0.064941 .
#> alpha_5_5     0.7795761  0.0133965  58.193 < 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: 1409270  on 424040  degrees of freedom
#> Residual deviance: 406237  on 424010  degrees of freedom
#> AIC: 406297
#>
#> Number of Fisher Scoring iterations: 4

```