Queensland rainforest

```r
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_qld.R")

set.seed(1)
```

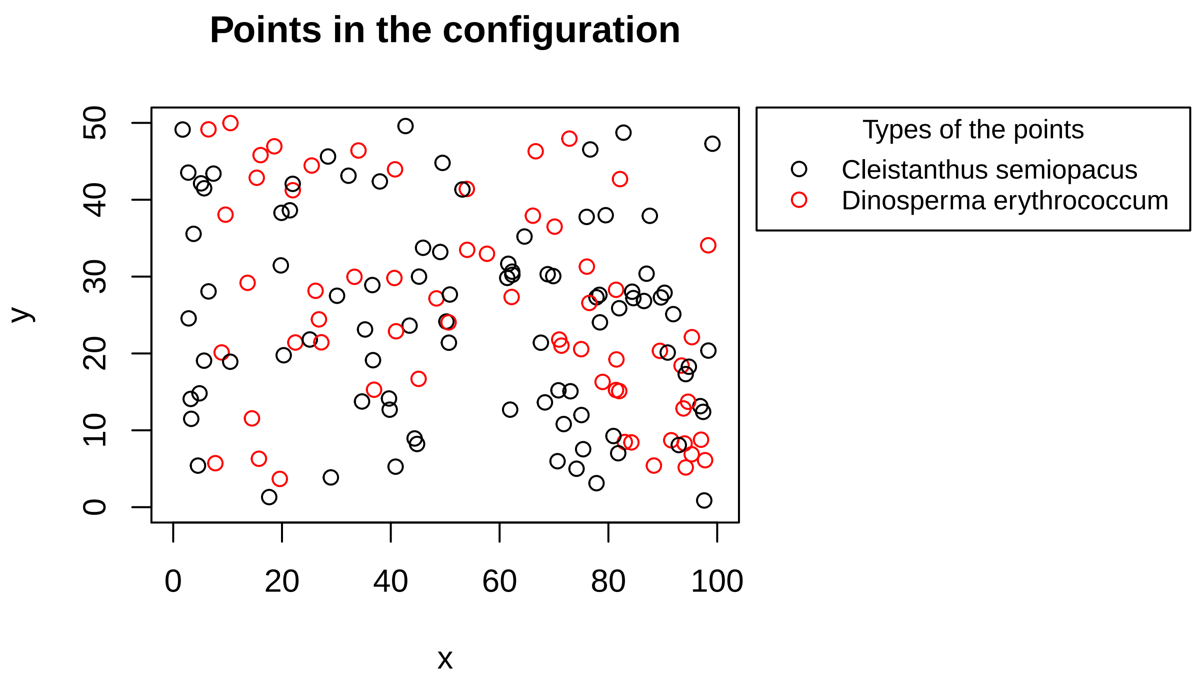
This vignette explains how to use the `ppjsdm` package with the Queensland rainforest dataset from CSIRO. We begin by loading the data with the most prevalent species.

```r
index_of_plot <- 3 # Between 1 and 20
year <- 2011 # Year of census
number_of_species <- 2 # Includes the most prevalent species from the plot

qld <- get_qld(index = index_of_plot,
               year = year,
               prevalent = number_of_species)
#> The chosen index corresponds to ep2.
configuration <- qld$configuration
window <- qld$window
```

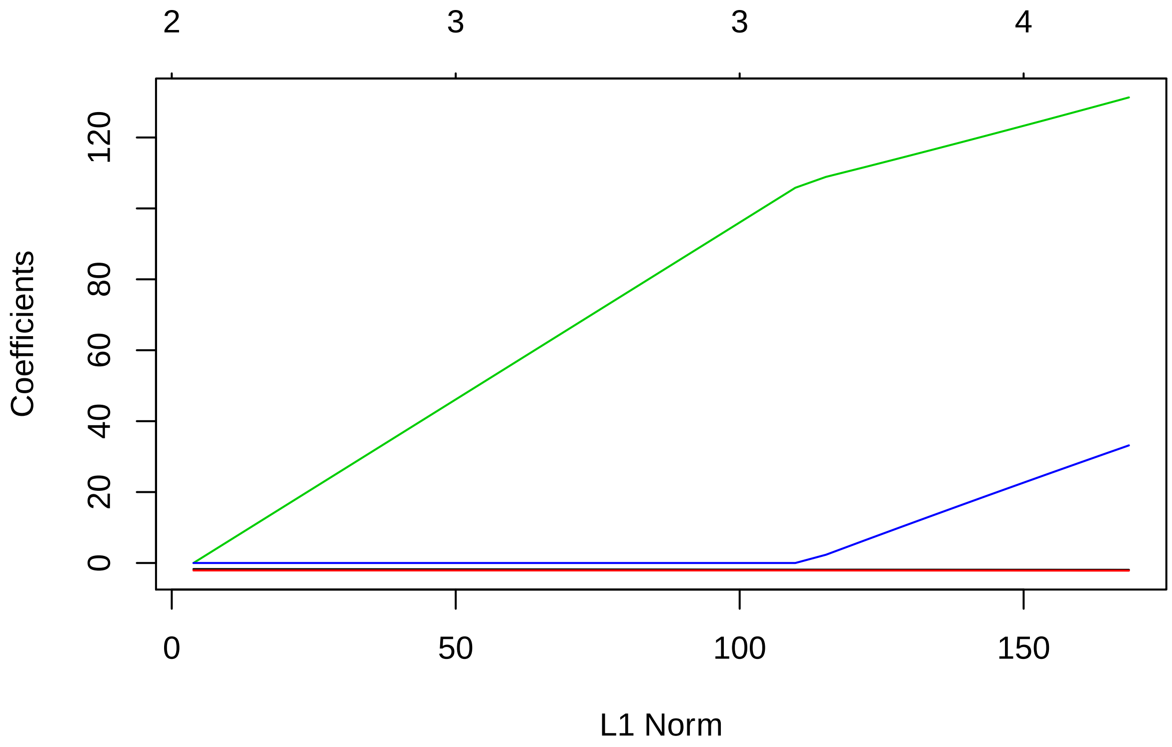
The point configuration is plotted below.

```r
par(mar = c(5, 4, 4, 13) + 0.1)
plot(configuration, window = window)
```



The function `gibbsm` fits a multivariate Gibbs point process to our dataset. For example,

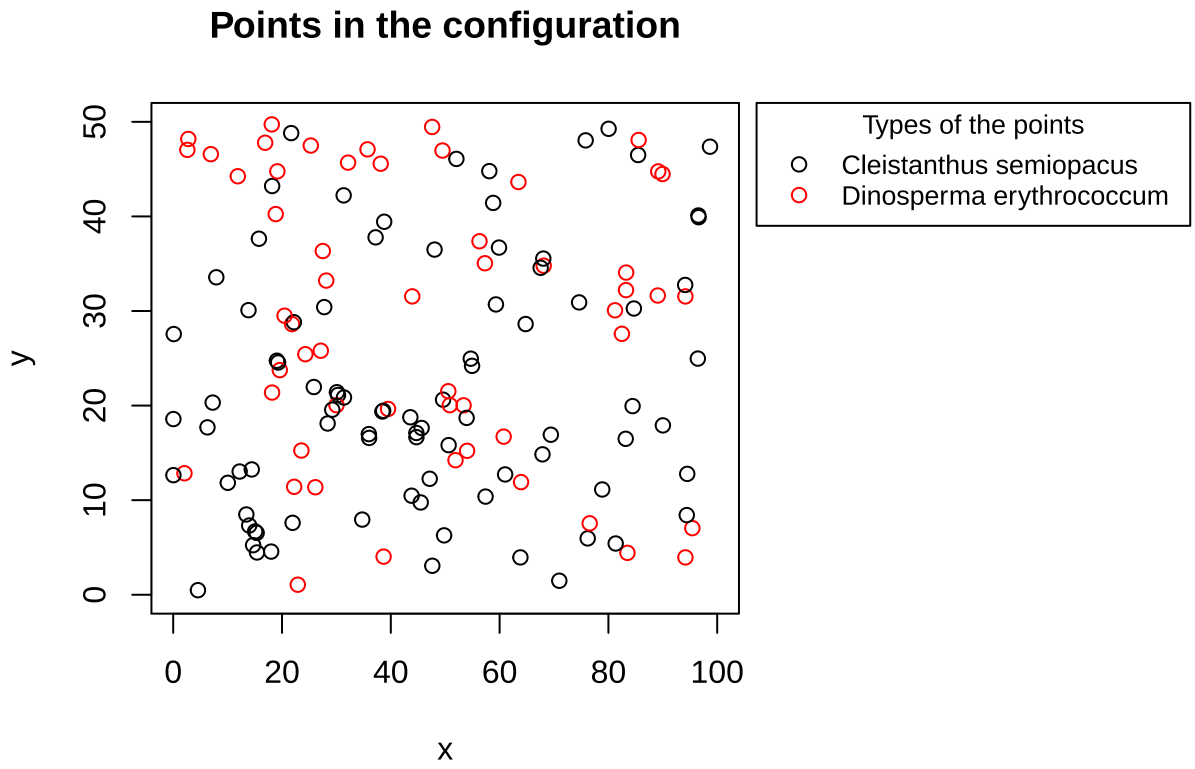
```
fit <- ppjsdm::gibbsm(configuration, window = window, use_glmnet = TRUE)
#> 6 x 1 sparse Matrix of class "dgCMatrix"
#>                         1
#> (Intercept)     .
#> log_lambda1   -4.221365
#> log_lambda2   -4.453533
#> alpha_1_1    131.300151
#> alpha_1_2       .
#> alpha_2_2     33.174667
plot(fit$complete)
```



By default, the function fits the model that was introduced in the ARC grant [TODO: Add reference]. This model has many drawbacks, the most important of which is that the model with the fitted values is degenerate, as can be seen by drawing from the model.

```
coefs <- fit$coefficients[-1]
lambda <- exp(coefs[1:2])
alpha <- matrix(c(coefs[3],
                  coefs[4],
                  coefs[4],
                  coefs[5]),
                ncol = number_of_species,
                nrow = number_of_species)
draw <- ppjsdm::rgibbs(window = window,
                       alpha = alpha,
                       lambda = lambda,
                       types = levels(types(configuration)),
                       steps = 1000000)
```

```
par(mar = c(5, 4, 4, 13) + 0.1)
plot(draw, window = window)
```

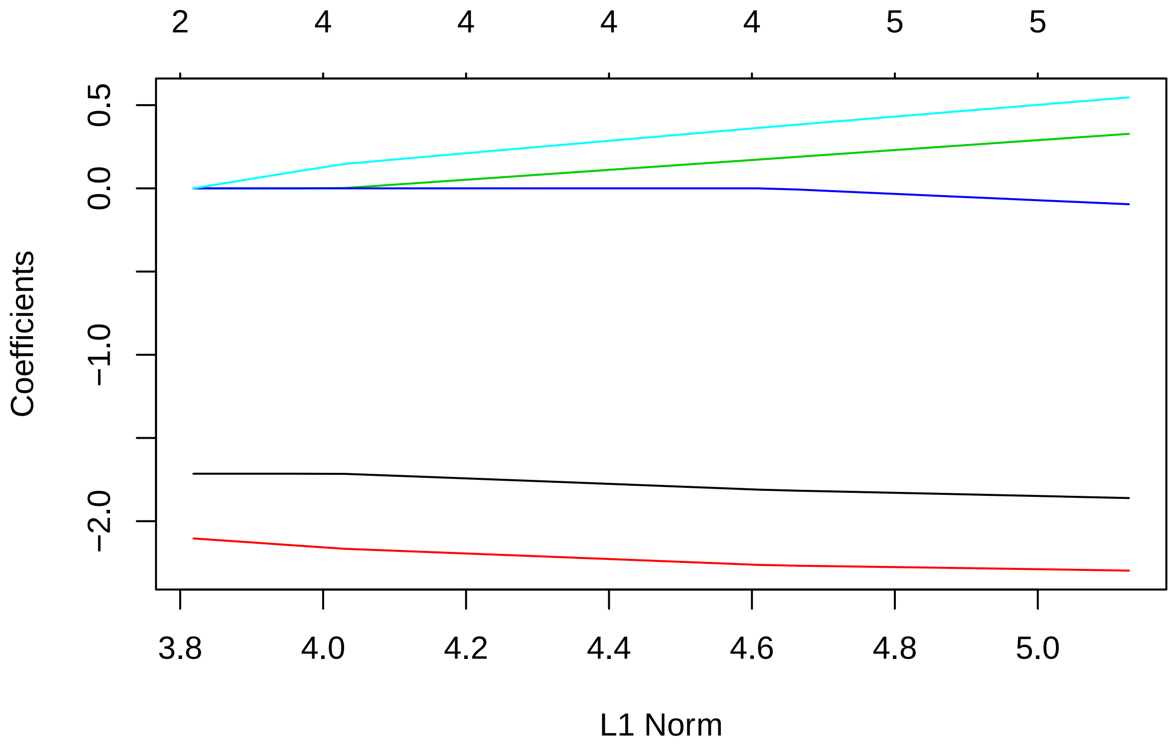


The Geyer model is better suited to most situations, but the user needs to specify some additional parameters before the fitting may take place.

```
radii <- matrix(5, number_of_species, number_of_species)
```

The matrix `radii` models interaction radii within a species, and between species. An interaction radius of 5 gives good results in the fitting procedure.

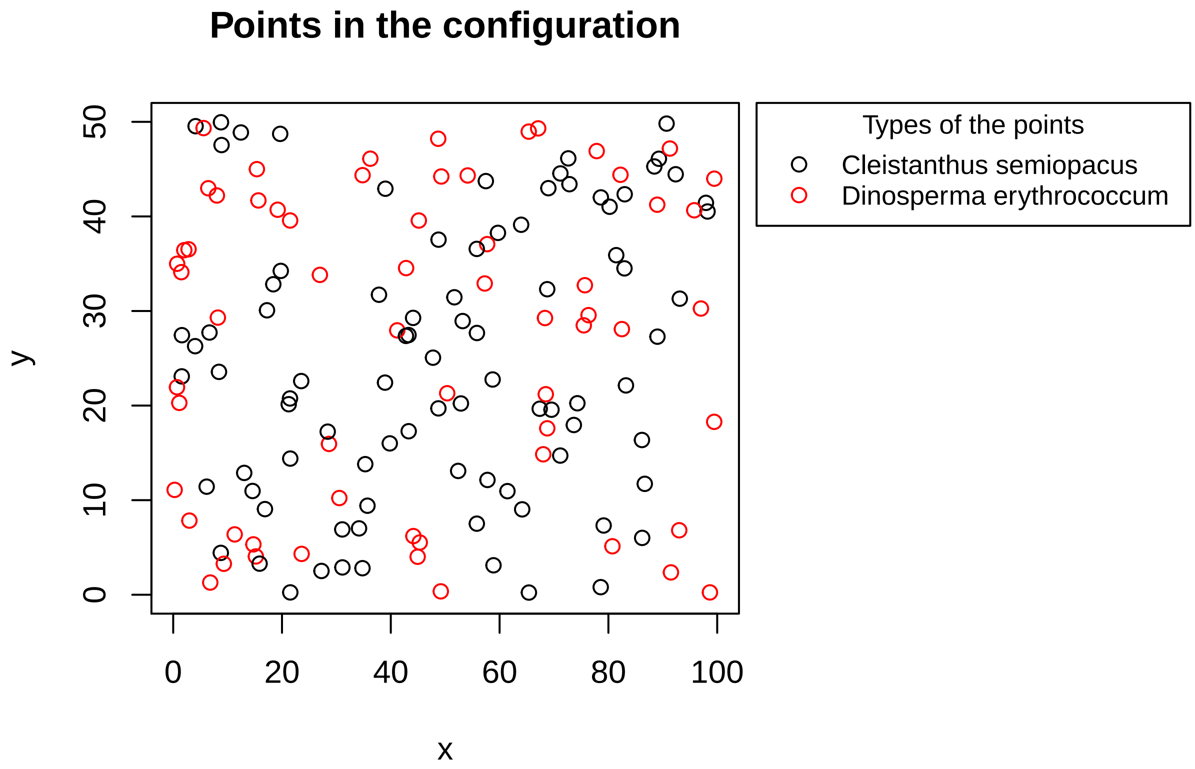
```
fit <- ppjsdm::gibbsm(configuration,
                      window = window,
                      model = "Geyer",
                      radius = radii,
                      use_glmnet = TRUE)
#> 6 x 1 sparse Matrix of class "dgCMatrix"
#>                       1
#> (Intercept)  .
#> log_lambda1 -4.16370564
#> log_lambda2 -4.59967424
#> alpha_1_1    0.32741334
#> alpha_1_2   -0.09547898
#> alpha_2_2    0.54641222
plot(fit$complete)
```



Note that in this case the model is not degenerate; indeed we can sample from it as follows.

```
coefs <- fit$coefficients[-1]
lambda <- exp(coefs[1:2])
alpha <- matrix(c(coefs[3],
                  coefs[4],
                  coefs[4],
                  coefs[5]),
                ncol = number_of_species,
                nrow = number_of_species)
draw <- ppjsdm::rgibbs(window = window,
                       alpha = alpha,
                       lambda = lambda,
                       model = "Geyer",
                       radius = radii,
                       types = levels(types(configuration)))
```

```
par(mar = c(5, 4, 4, 13) + 0.1)
plot(draw, window = window)
```


Points in the configuration
y
50
40
30
20
10
0
x
0
20
40
60
80
100
Types of the points
○ Cleistanthus semiopacus
○ Dinosperma erythrococcum