Queensland rainforest

```r
library(ppjsdm)
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_qld.R")

set.seed(1)
```

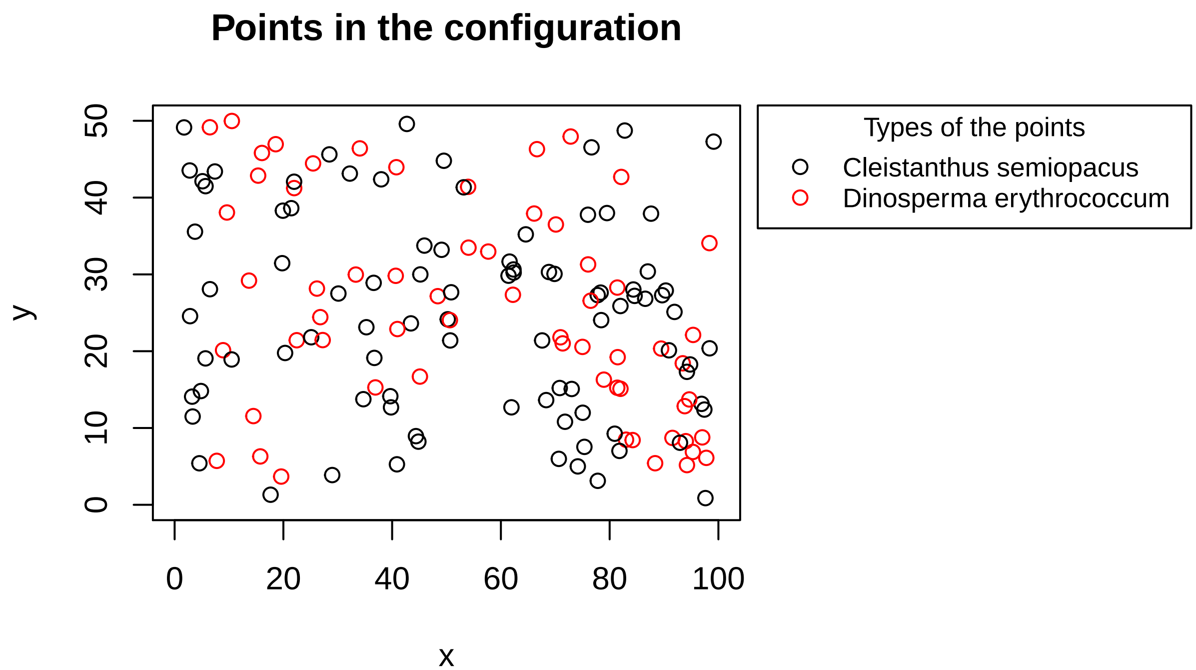
This vignette explains how to use the `ppjsdm` package with the Queensland rainforest dataset from CSIRO. We begin by loading the data with the most prevalent species.

```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)
```



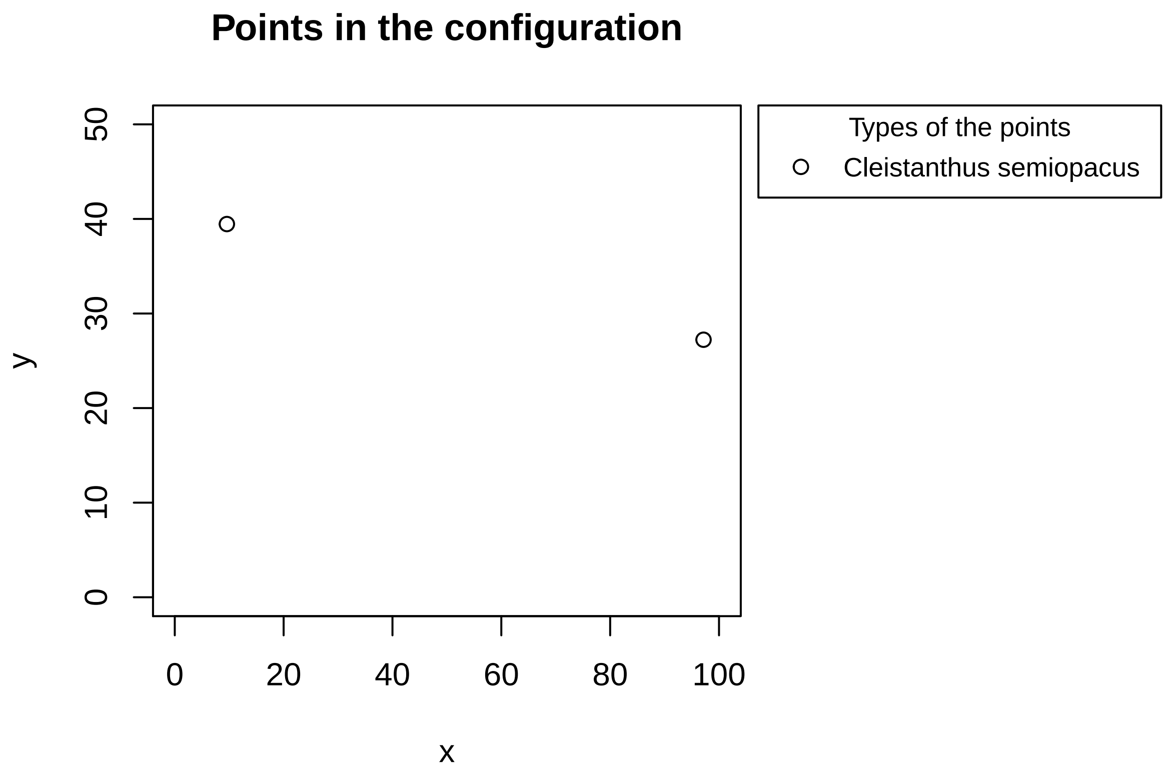
The function `gibbsm` fits a multivariate Gibbs point process to our dataset. For example,

```
fit <- ppjsdm::gibbsm(configuration, window = window)
#> log_lambda_1 log_lambda_2    alpha_1_1    alpha_1_2    alpha_2_2
#>    -3.978784    -4.431216    -3.936413     8.070406    -3.636435
```

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.

```
lambda <- exp(fit$coefficients[1:number_of_species])
alpha <- matrix(c(fit$coefficients[3],
                  fit$coefficients[4],
                  fit$coefficients[4],
                  fit$coefficients[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.

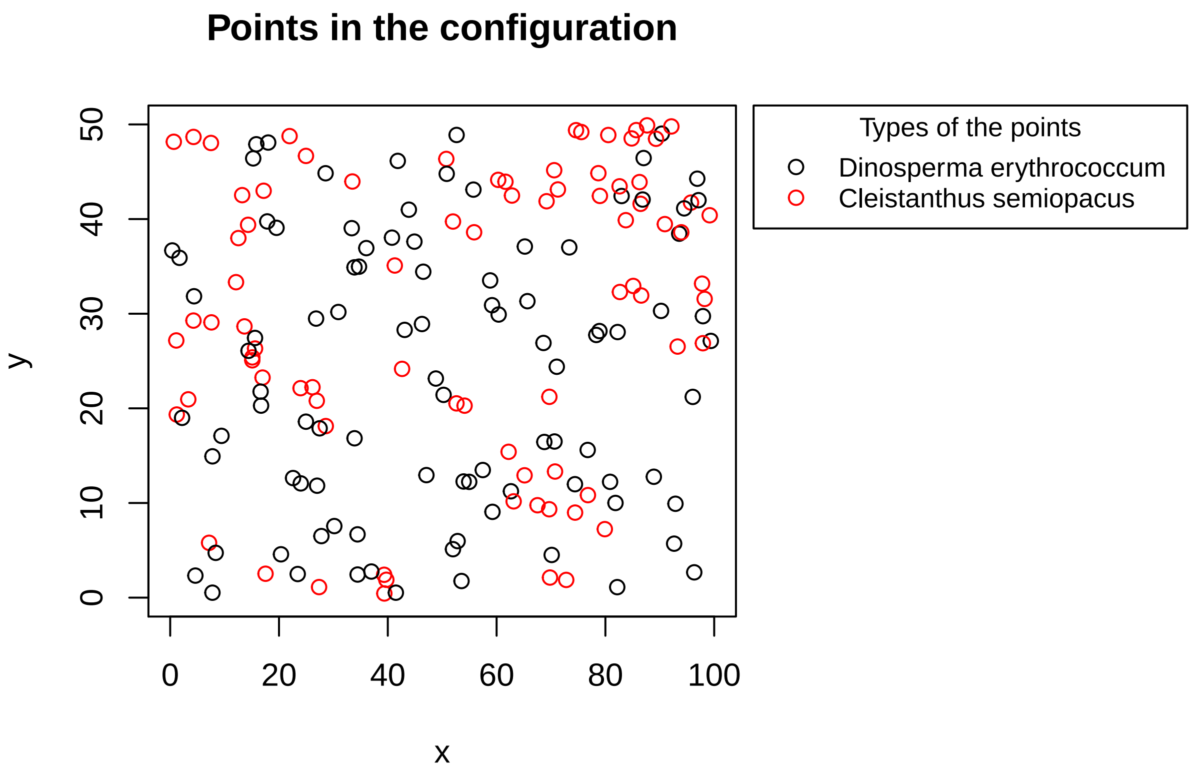
```
fit <- ppjsdm::gibbsm(configuration, window = window, model = "Geyer", radius = radii)
#> log_lambda_1 log_lambda_2    alpha_1_1    alpha_1_2    alpha_2_2
#>  -4.22694003  -4.85656953   0.16730695   0.02636396   0.49504414
summary(fit)
#>
#> Call:
#> glm(formula = as.formula(gibbsm_data$formula), family = binomial(),
#>     data = as.data.frame(gibbsm_data$data))
#>
#> Deviance Residuals:
#>     Min       1Q   Median       3Q      Max
#> -0.6315  -0.5781  -0.5220  -0.3920   2.2930
#>
#> Coefficients:
#>              Estimate Std. Error z value Pr(>|z|)
#> log_lambda_1 -4.22694    0.21507 -19.654  < 2e-16 ***
#> log_lambda_2 -4.85657    0.24659 -19.695  < 2e-16 ***
#> alpha_1_1     0.16731    0.14357   1.165  0.24388
#> alpha_1_2     0.02636    0.11261   0.234  0.81489
```

```
#> alpha_2_2     0.49504    0.17740   2.791  0.00526 **
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> (Dispersion parameter for binomial family taken to be 1)
#>
#>     Null deviance: 4824.57  on 1151  degrees of freedom
#> Residual deviance:  880.46  on 1146  degrees of freedom
#> AIC: 890.46
#>
#> Number of Fisher Scoring iterations: 5
```

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

```
lambda <- exp(fit$coefficients[1:number_of_species])
alpha <- matrix(c(fit$coefficients[3],
                  fit$coefficients[4],
                  fit$coefficients[4],
                  fit$coefficients[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)),
                       steps = 1000000)
```

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


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