Fithian et al. (2014) NSW

```
library(maptools)
#> Loading required package: sp
#> Checking rgeos availability: FALSE
#>      Note: when rgeos is not available, polygon geometry     computations in maptools depend on gpcl
#>      which has a restricted licence. It is disabled by default;
#>      to enable gpclib, type gpclibPermit()
library(ppjsdm)
#> Registered S3 method overwritten by 'spatstat':
#>   method     from
#>   print.boxx cli
library(raster)
library(sf)
#> Linking to GEOS 3.6.2, GDAL 2.2.3, PROJ 4.9.3
library(spatstat)
#> Loading required package: spatstat.data
#> Loading required package: nlme
#>
#> Attaching package: 'nlme'
#> The following object is masked from 'package:raster':
#>
#>     getData
#> Loading required package: rpart
#>
#> spatstat 1.64-0       (nickname: 'Susana Distancia')
#> For an introduction to spatstat, type 'beginner'
#>
#> Attaching package: 'spatstat'
#> The following objects are masked from 'package:raster':
#>
#>     area, rotate, shift
library(plot.matrix)
remove(list = ls())

source("../R/get_nsw.R")

set.seed(1)
```

This vignette explains how to use the `ppjsdm` package with the NSW dataset from Fithian et al. (2014). We begin by loading the data with only the most prevalent species.

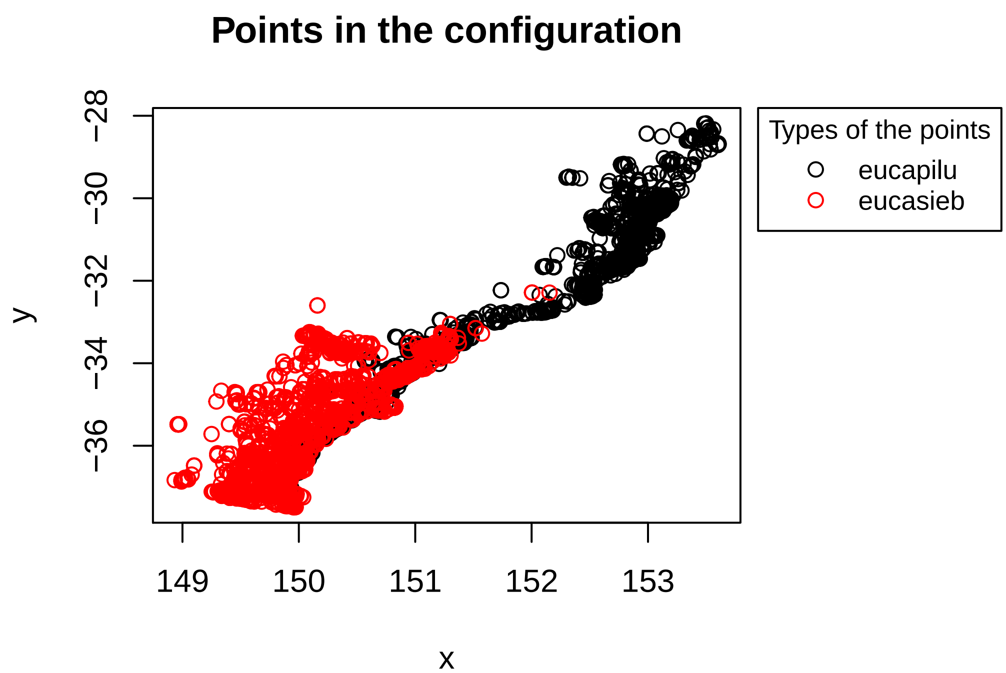
```
number_of_species <- 2 # Includes the most prevalent species from the plot

nsw <- get_nsw(prevalent = number_of_species)
configuration <- nsw$configuration
window <- nsw$window
covariates <- nsw$covariates
```

Some of the covariates give `NA` values at some locations in the configuration, so we have to remove these points

```r
for(covariate in append(covariates, list(window))) {
  ok <- inside.owin(x_coordinates(configuration), y_coordinates(configuration), covariate)
  configuration <- Configuration(x_coordinates(configuration)[ok],
                                 y_coordinates(configuration)[ok],
                                 types(configuration)[ok])
}
```

The point configuration is plotted below.

```r
print(configuration)
#> An S3 object representing a configuration.
#>
#> Number of points: 4913.
par(mar = c(5, 4, 4, 13) + 0.1)
plot(configuration, window = window)
```



The matrix `radii` defined below models interaction radii within a species (on the diagonal), and between species (outside the diagonal).

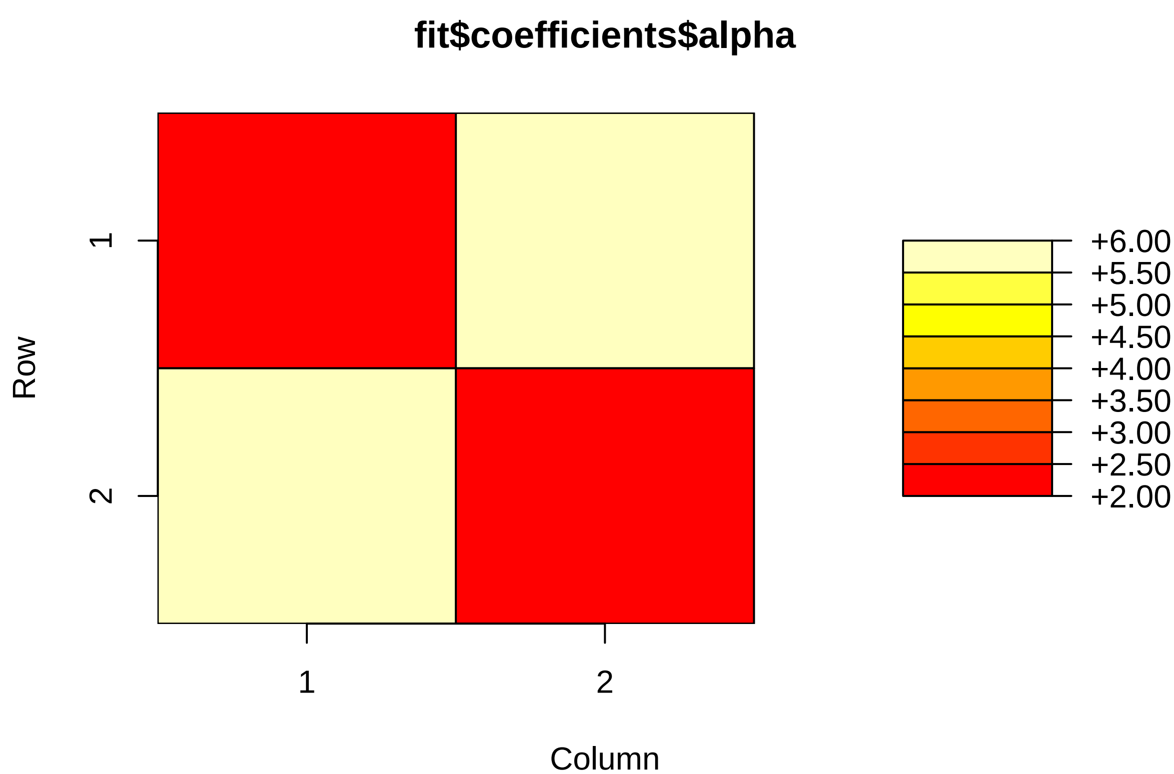
```r
short_range <- matrix(0.0005, number_of_species, number_of_species)
medium_range <- diag(0.0005, number_of_species)
long_range <- medium_range + diag(0.001, number_of_species)

model <- "Geyer"
medium_range_model <- "Geyer"
```

Fitting the model to the dataset is then quite easy.

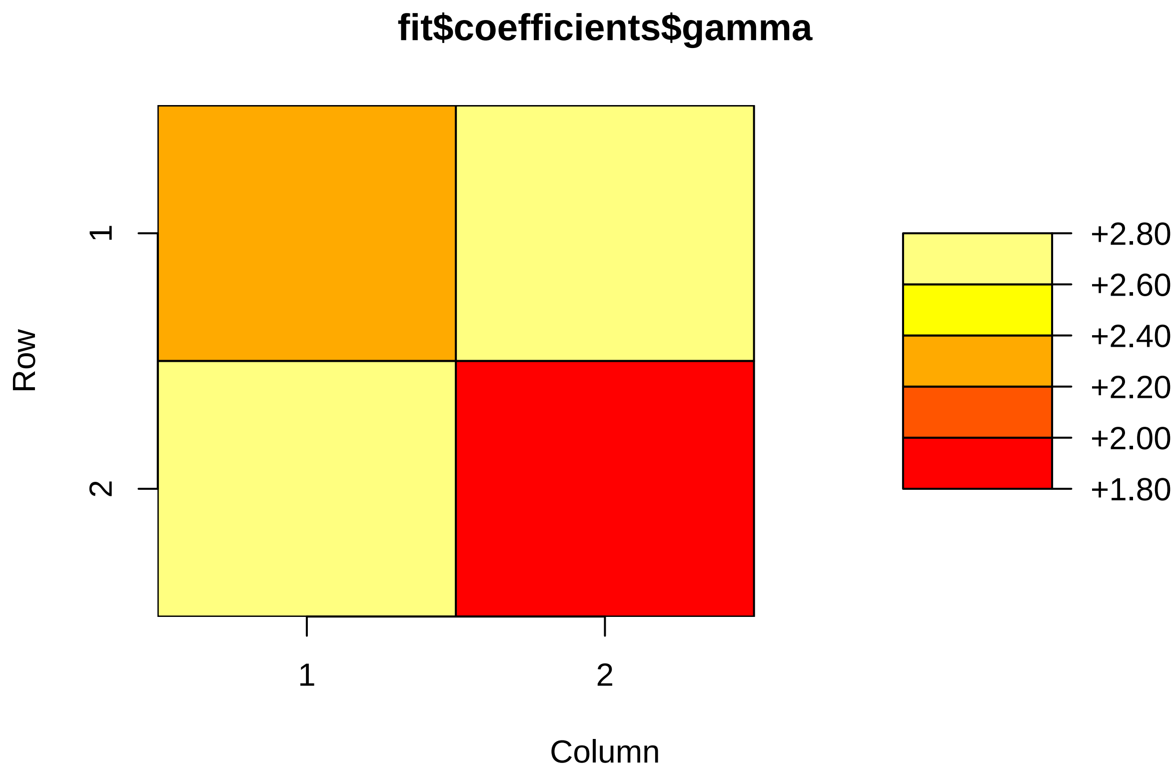
```r
fit <- ppjsdm::gibbsm(configuration,
                      window = window,
```

```r
                      covariates = covariates,
                      model = model,
                      medium_range_model = medium_range_model,
                      short_range = short_range,
                      medium_range = medium_range,
                      long_range = long_range,
                      use_glmnet = FALSE)
#> $beta0
#> [1] -18.07506 -15.07602
#>
#> $alpha
#>          [,1]     [,2]
#> [1,] 2.470980 5.729179
#> [2,] 5.729179 2.307864
#>
#> $gamma
#>          [,1]     [,2]
#> [1,] 2.245845 2.645886
#> [2,] 2.645886 1.911686
#>
#> $beta
#>            [,1]       [,2]       [,3]        [,4]      [,5]     [,6]     [,7]
#> [1,] 0.03764802  -8.798701 -0.0824624 0.011630528 0.2522793 1.350746 2.290461
#> [2,] 0.96882247 -10.505647 -0.6739432 0.001593084 0.2294329 1.594836 3.286275
#>           [,8]        [,9]       [,10]     [,11]         [,12]       [,13]
#> [1,] 0.6760066 -0.01264236 -0.05280978 -2.968373 -0.0210053088 -0.06999104
#> [2,] 8.5927147 -0.15798598 -0.02242382 -3.861317  0.0005320236  0.01106579
#>              [,14]         [,15]
#> [1,] -0.0001972805 -9.819659e-06
#> [2,] -0.0002969501 -8.086017e-05
print(fit$coefficients)
#> $beta0
#> [1] -18.07506 -15.07602
#>
#> $alpha
#>          [,1]     [,2]
#> [1,] 2.470980 5.729179
#> [2,] 5.729179 2.307864
#>
#> $gamma
#>          [,1]     [,2]
#> [1,] 2.245845 2.645886
#> [2,] 2.645886 1.911686
#>
#> $beta
#>            [,1]       [,2]       [,3]        [,4]      [,5]     [,6]     [,7]
#> [1,] 0.03764802  -8.798701 -0.0824624 0.011630528 0.2522793 1.350746 2.290461
#> [2,] 0.96882247 -10.505647 -0.6739432 0.001593084 0.2294329 1.594836 3.286275
#>           [,8]        [,9]       [,10]     [,11]         [,12]       [,13]
#> [1,] 0.6760066 -0.01264236 -0.05280978 -2.968373 -0.0210053088 -0.06999104
#> [2,] 8.5927147 -0.15798598 -0.02242382 -3.861317  0.0005320236  0.01106579
#>              [,14]         [,15]
#> [1,] -0.0001972805 -9.819659e-06
```

```r
#> [2,] -0.0002969501 -8.086017e-05
#>
#> $short_range
#>        [,1]  [,2]
#> [1,] 5e-04 5e-04
#> [2,] 5e-04 5e-04
#>
#> $medium_range
#>        [,1]  [,2]
#> [1,] 5e-04 0e+00
#> [2,] 0e+00 5e-04
#>
#> $long_range
#>         [,1]   [,2]
#> [1,] 0.0015 0.0000
#> [2,] 0.0000 0.0015
par(mar = c(5.1, 5.1, 4.1, 4.1))
plot(fit$coefficients$alpha)
```




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




```r
print(fit$aic)
#> [1] 12131.32
print(fit$bic)
#> [1] 12439.4
```