

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)
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 1.63-0 (nickname: 'Space camouflage')
#> For an introduction to spatstat, type 'beginner'
#>
#> Attaching package: 'spatstat'
#> The following objects are masked from 'package:raster':
#>
#>   area, rotate, shift
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
```

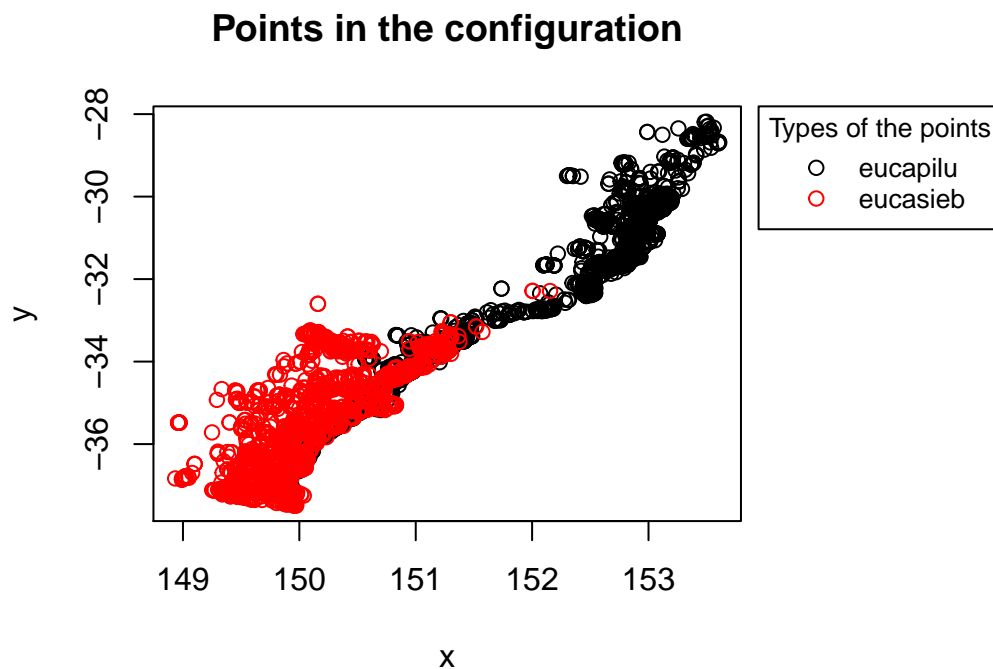
Some of the covariates give NA values at some locations in the configuration, so we have to remove these points

```
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.

```
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).

```
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"
```

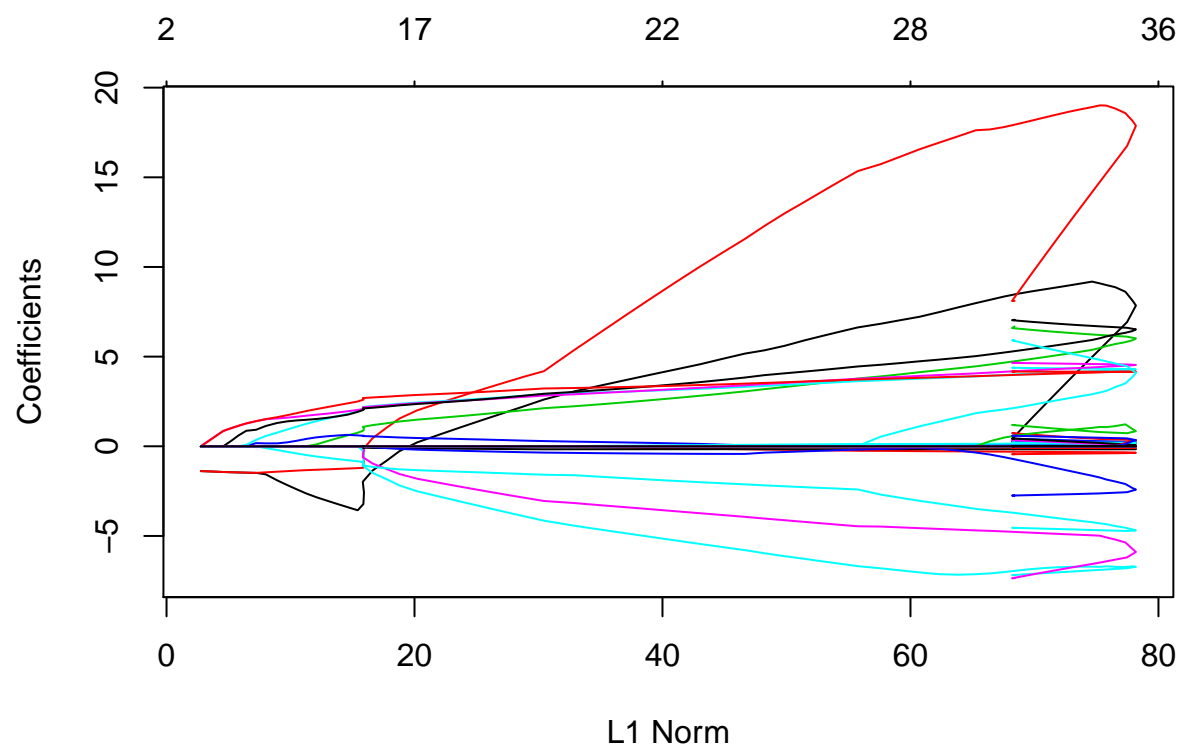
Fitting the model to the dataset is then quite easy.

```
fit <- ppjsdm::gibbsm(configuration,
                      window = window,
                      covariates = covariates,
                      model = model,
                      medium_range_model = medium_range_model,
```

```

        short_range = short_range,
        medium_range = medium_range,
        long_range = long_range,
        use_glmnet = TRUE)
#> 39 x 1 sparse Matrix of class "dgCMatrix"
#>           1
#> (Intercept) .
#> log_lambda1 6.691550e+00
#> log_lambda2 1.440687e+01
#> alpha_1_1   6.684091e+00
#> alpha_1_2   6.242880e-02
#> alpha_2_2   4.386132e+00
#> gamma_1_1   4.659356e+00
#> gamma_1_2   7.058539e+00
#> gamma_2_2   4.173006e+00
#> bc02_1      -1.067341e-01
#> bc02_2       4.301501e-01
#> bc04_1      -7.186190e+00
#> bc04_2      -7.358519e+00
#> bc05_1       1.901697e-02
#> bc05_2      -4.409896e-01
#> bc12_1       7.228977e-03
#> bc12_2      .
#> bc14_1       2.655619e-01
#> bc14_2       2.086023e-01
#> bc21_1       3.428696e-01
#> bc21_2       4.368892e-01
#> bc32_1       7.312548e-01
#> bc32_2       1.189161e+00
#> bc33_1       5.876227e-01
#> bc33_2       5.910044e+00
#> mvbf_1      -1.518058e-02
#> mvbf_2      -1.549144e-01
#> rjja_1      -3.832016e-02
#> rjja_2      -2.326913e-02
#> rsea_1      -2.747255e+00
#> rsea_2      -4.546395e+00
#> rugg_1      -2.205302e-02
#> rugg_2      .
#> subs_1      -7.174033e-02
#> subs_2       1.603860e-02
#> twmd_1      -1.864165e-04
#> twmd_2      -3.094481e-04
#> twmx_1      -1.767750e-05
#> twmx_2      -6.435004e-05
plot(fit$complete)

```



```
plot(fit$cv)
```

