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 1.62-2       (nickname: 'Shape-shifting lizard')
#> 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)
```

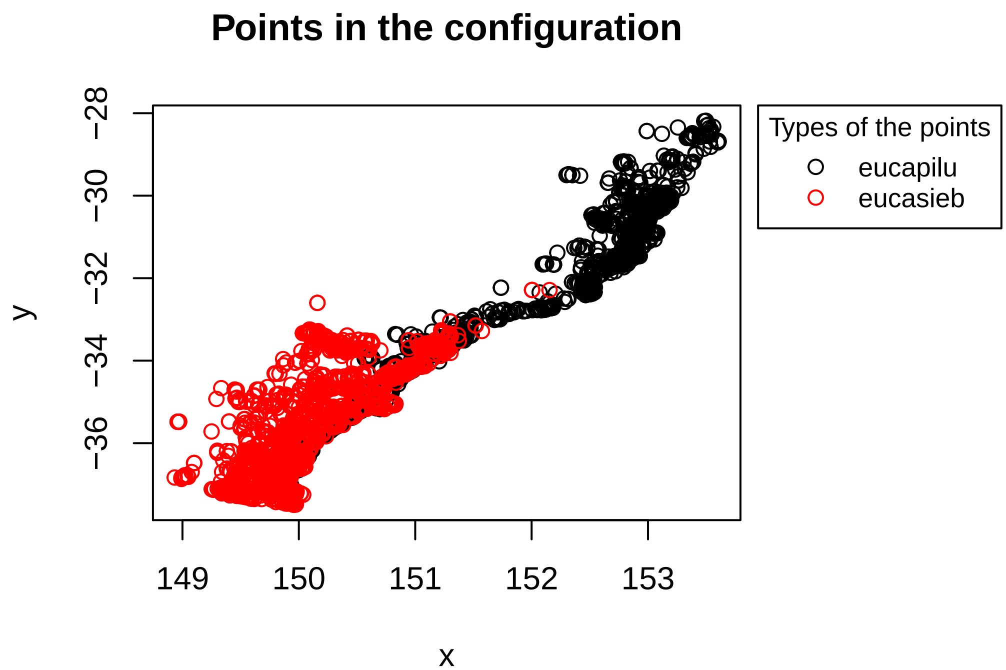
This vignette explains how to use the `ppjsdm` package with the NSW dataset from Fithian et al. (2014). We begin by loading the data with only the most prevalent species.

```
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
```

The point configuration is plotted below.

```
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).

```
radii <- matrix(0.1, 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  unnamed_covariate1_1
#>            5.529328e+00            1.589754e+01         -3.955523e-01
#>   unnamed_covariate1_2  unnamed_covariate2_1  unnamed_covariate2_2
#>            1.310175e-01           -1.625017e+00         -9.397341e-01
#>   unnamed_covariate3_1  unnamed_covariate3_2  unnamed_covariate4_1
#>           -5.710862e-02           -1.855167e-01          4.580865e-03
#>   unnamed_covariate4_2  unnamed_covariate5_1  unnamed_covariate5_2
#>           -1.371843e-03            1.251534e-01         -1.679067e-01
#>   unnamed_covariate6_1  unnamed_covariate6_2  unnamed_covariate7_1
#>            1.825983e-01           -2.903524e-01          1.418842e+00
#>   unnamed_covariate7_2  unnamed_covariate8_1  unnamed_covariate8_2
#>            5.766286e-01            1.403485e-01          1.033571e+01
#>   unnamed_covariate9_1  unnamed_covariate9_2 unnamed_covariate10_1
#>           -3.045413e-02           -8.838308e-02         -2.718107e-02
#> unnamed_covariate10_2 unnamed_covariate11_1 unnamed_covariate11_2
#>           -8.712071e-03           -1.228389e+00         -5.198815e+00
#> unnamed_covariate12_1 unnamed_covariate12_2 unnamed_covariate13_1
```

```
#>          -1.988137e-02          -3.962883e-03          -4.126264e-02
#> unnamed_covariate13_2 unnamed_covariate14_1 unnamed_covariate14_2
#>           1.656442e-02          -2.139818e-04          -2.395632e-04
#> unnamed_covariate15_1 unnamed_covariate15_2               alpha_1_1
#>          -2.233812e-05          -7.133730e-05           2.434970e+00
#>              alpha_1_2              alpha_2_2
#>           1.647519e-01           2.980384e+00
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
#> -2.2923  -0.0911  -0.0411  -0.0148   4.0261
#>
#> Coefficients:
#>                         Estimate Std. Error z value Pr(>|z|)
#> log_lambda_1           5.529e+00  3.557e+00   1.554  0.12010
#> log_lambda_2           1.590e+01  3.325e+00   4.781 1.74e-06 ***
#> unnamed_covariate1_1  -3.956e-01  9.335e-02  -4.237 2.26e-05 ***
#> unnamed_covariate1_2   1.310e-01  9.011e-02   1.454  0.14597
#> unnamed_covariate2_1  -1.625e+00  7.440e-01  -2.184  0.02895 *
#> unnamed_covariate2_2  -9.397e-01  6.076e-01  -1.547  0.12194
#> unnamed_covariate3_1  -5.711e-02  4.238e-02  -1.348  0.17781
#> unnamed_covariate3_2  -1.855e-01  4.728e-02  -3.924 8.72e-05 ***
#> unnamed_covariate4_1   4.581e-03  7.435e-04   6.161 7.21e-10 ***
#> unnamed_covariate4_2  -1.372e-03  1.115e-03  -1.231  0.21848
#> unnamed_covariate5_1   1.252e-01  4.073e-02   3.073  0.00212 **
#> unnamed_covariate5_2  -1.679e-01  3.243e-02  -5.178 2.24e-07 ***
#> unnamed_covariate6_1   1.826e-01  1.420e-01   1.286  0.19853
#> unnamed_covariate6_2  -2.904e-01  1.443e-01  -2.012  0.04417 *
#> unnamed_covariate7_1   1.419e+00  9.811e-01   1.446  0.14814
#> unnamed_covariate7_2   5.766e-01  8.644e-01   0.667  0.50474
#> unnamed_covariate8_1   1.403e-01  7.340e-01   0.191  0.84836
#> unnamed_covariate8_2   1.034e+01  1.250e+00   8.271  < 2e-16 ***
#> unnamed_covariate9_1  -3.045e-02  1.717e-02  -1.774  0.07605 .
#> unnamed_covariate9_2  -8.838e-02  2.857e-02  -3.093  0.00198 **
#> unnamed_covariate10_1 -2.718e-02  3.979e-03  -6.831 8.41e-12 ***
#> unnamed_covariate10_2 -8.712e-03  4.095e-03  -2.128  0.03336 *
#> unnamed_covariate11_1 -1.228e+00  5.740e-01  -2.140  0.03234 *
#> unnamed_covariate11_2 -5.199e+00  7.214e-01  -7.207 5.73e-13 ***
#> unnamed_covariate12_1 -1.988e-02  2.136e-03  -9.309  < 2e-16 ***
#> unnamed_covariate12_2 -3.963e-03  1.441e-03  -2.751  0.00594 **
#> unnamed_covariate13_1 -4.126e-02  1.327e-02  -3.109  0.00188 **
#> unnamed_covariate13_2  1.656e-02  1.453e-02   1.140  0.25433
#> unnamed_covariate14_1 -2.140e-04  3.649e-05  -5.864 4.51e-09 ***
#> unnamed_covariate14_2 -2.396e-04  4.048e-05  -5.918 3.25e-09 ***
#> unnamed_covariate15_1 -2.234e-05  1.369e-05  -1.632  0.10270
#> unnamed_covariate15_2 -7.134e-05  1.421e-05  -5.021 5.15e-07 ***
#> alpha_1_1              2.435e+00  1.250e-01  19.482  < 2e-16 ***
#> alpha_1_2              1.648e-01  4.224e-02   3.900 9.62e-05 ***
```

```
#> alpha_2_2              2.980e+00  1.297e-01  22.987  < 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: 61921  on 24550  degrees of freedom
#> Residual deviance: 11014  on 24515  degrees of freedom
#>   (50 observations deleted due to missingness)
#> AIC: 11084
#>
#> Number of Fisher Scoring iterations: 8
```