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)
```

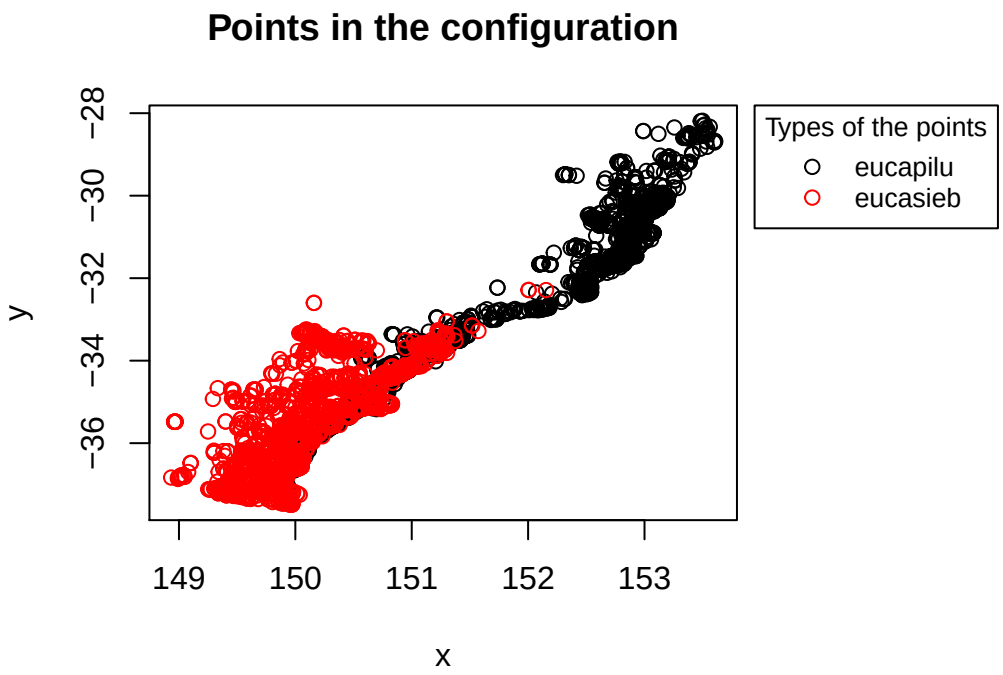
This vignette explains how to use the `ppjsdm` package with the NSW dataset from Fithian et al. (2014). We begin by loading the data with only the most prevalent species.

```
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 =
#>   log_lambda_1   log_lambda_2  covariates1_1  covariates1_2  covariates2_1
#>   5.529328e+00   1.589754e+01  -3.955523e-01   1.310175e-01  -1.625017e+00
#>  covariates2_2  covariates3_1  covariates3_2  covariates4_1  covariates4_2
#>  -9.397341e-01  -5.710862e-02  -1.855167e-01   4.580865e-03  -1.371843e-03
#>  covariates5_1  covariates5_2  covariates6_1  covariates6_2  covariates7_1
#>   1.251534e-01  -1.679067e-01   1.825983e-01  -2.903524e-01   1.418842e+00
#>  covariates7_2  covariates8_1  covariates8_2  covariates9_1  covariates9_2
#>   5.766286e-01   1.403485e-01   1.033571e+01  -3.045413e-02  -8.838308e-02
#> covariates10_1 covariates10_2 covariates11_1 covariates11_2 covariates12_1
#>  -2.718107e-02  -8.712071e-03  -1.228389e+00  -5.198815e+00  -1.988137e-02
#> covariates12_2 covariates13_1 covariates13_2 covariates14_1 covariates14_2
#>  -3.962883e-03  -4.126264e-02   1.656442e-02  -2.139818e-04  -2.395632e-04
#> covariates15_1 covariates15_2      alpha_1_1      alpha_1_2      alpha_2_2
#>  -2.233812e-05  -7.133730e-05   2.434970e+00   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 ***
#> covariates1_1  -3.956e-01  9.335e-02  -4.237 2.26e-05 ***
#> covariates1_2   1.310e-01  9.011e-02   1.454  0.14597
#> covariates2_1  -1.625e+00  7.440e-01  -2.184  0.02895 *
#> covariates2_2  -9.397e-01  6.076e-01  -1.547  0.12194
#> covariates3_1  -5.711e-02  4.238e-02  -1.348  0.17781
#> covariates3_2  -1.855e-01  4.728e-02  -3.924 8.72e-05 ***
#> covariates4_1   4.581e-03  7.435e-04   6.161 7.21e-10 ***
#> covariates4_2  -1.372e-03  1.115e-03  -1.231  0.21848
#> covariates5_1   1.252e-01  4.073e-02   3.073  0.00212 **
#> covariates5_2  -1.679e-01  3.243e-02  -5.178 2.24e-07 ***
#> covariates6_1   1.826e-01  1.420e-01   1.286  0.19853
#> covariates6_2  -2.904e-01  1.443e-01  -2.012  0.04417 *
#> covariates7_1   1.419e+00  9.811e-01   1.446  0.14814
#> covariates7_2   5.766e-01  8.644e-01   0.667  0.50474
#> covariates8_1   1.403e-01  7.340e-01   0.191  0.84836
#> covariates8_2   1.034e+01  1.250e+00   8.271  < 2e-16 ***
#> covariates9_1  -3.045e-02  1.717e-02  -1.774  0.07605 .
#> covariates9_2  -8.838e-02  2.857e-02  -3.093  0.00198 **
#> covariates10_1 -2.718e-02  3.979e-03  -6.831 8.41e-12 ***
#> covariates10_2 -8.712e-03  4.095e-03  -2.128  0.03336 *
#> covariates11_1 -1.228e+00  5.740e-01  -2.140  0.03234 *
#> covariates11_2 -5.199e+00  7.214e-01  -7.207 5.73e-13 ***
#> covariates12_1 -1.988e-02  2.136e-03  -9.309  < 2e-16 ***
#> covariates12_2 -3.963e-03  1.441e-03  -2.751  0.00594 **
#> covariates13_1 -4.126e-02  1.327e-02  -3.109  0.00188 **
#> covariates13_2  1.656e-02  1.453e-02   1.140  0.25433
#> covariates14_1 -2.140e-04  3.649e-05  -5.864 4.51e-09 ***
#> covariates14_2 -2.396e-04  4.048e-05  -5.918 3.25e-09 ***
#> covariates15_1 -2.234e-05  1.369e-05  -1.632  0.10270
#> covariates15_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
```