

KSBound: Kernel Stick-Breaking Prior Distribution for Spatial Boundary Detection

KSBound_Example

[1] Simulate data from the proposed model:

- Setting the reproducibility seed and initializing packages for data simulation:

```
set.seed(8845)

library(KSBound)
library(mnormt) #Multivariate normal distribution

## Warning: package 'mnormt' was built under R version 4.3.0
library(fields)

## Warning: package 'fields' was built under R version 4.3.1
## Loading required package: spam
## Warning: package 'spam' was built under R version 4.3.1
## Spam version 2.9-1 (2022-08-07) is loaded.
## Type 'help( Spam)' or 'demo( spam)' for a short introduction
## and overview of this package.
## Help for individual functions is also obtained by adding the
## suffix '.spam' to the function name, e.g. 'help( chol.spam)'.
##
## Attaching package: 'spam'
## The following objects are masked from 'package:base':
##
##      backsolve, forwardsolve
## Loading required package: viridis
## Warning: package 'viridis' was built under R version 4.3.1
## Loading required package: viridisLite
## Warning: package 'viridisLite' was built under R version 4.3.1
##
## Try help(fields) to get started.
```

- Creating a Grid:

```
n.space<-7
x.easting<-1:n.space
x.northing<-1:n.space
Grid<-expand.grid(x.easting,
                  x.northing)
K<-nrow(Grid)

distance<-as.matrix(dist(Grid))
W<-array(0, c(K,K))
W[distance == 1]<-1 #Rook definition
diag(W)<-0
```

- Simulating Data:

```

offset<-rep(0,
            times = nrow(W))
trials<-rep(50,
            times = nrow(W))

beta_true<-c(-1.50,
             -0.35)

#Design Matrix
x<-matrix(1,
          nrow = nrow(W),
          ncol = 2)
x[,2]<-scale(rnorm(n = nrow(W)))

#Simulating the Data
phi<-rep(0,
        times = nrow(W))

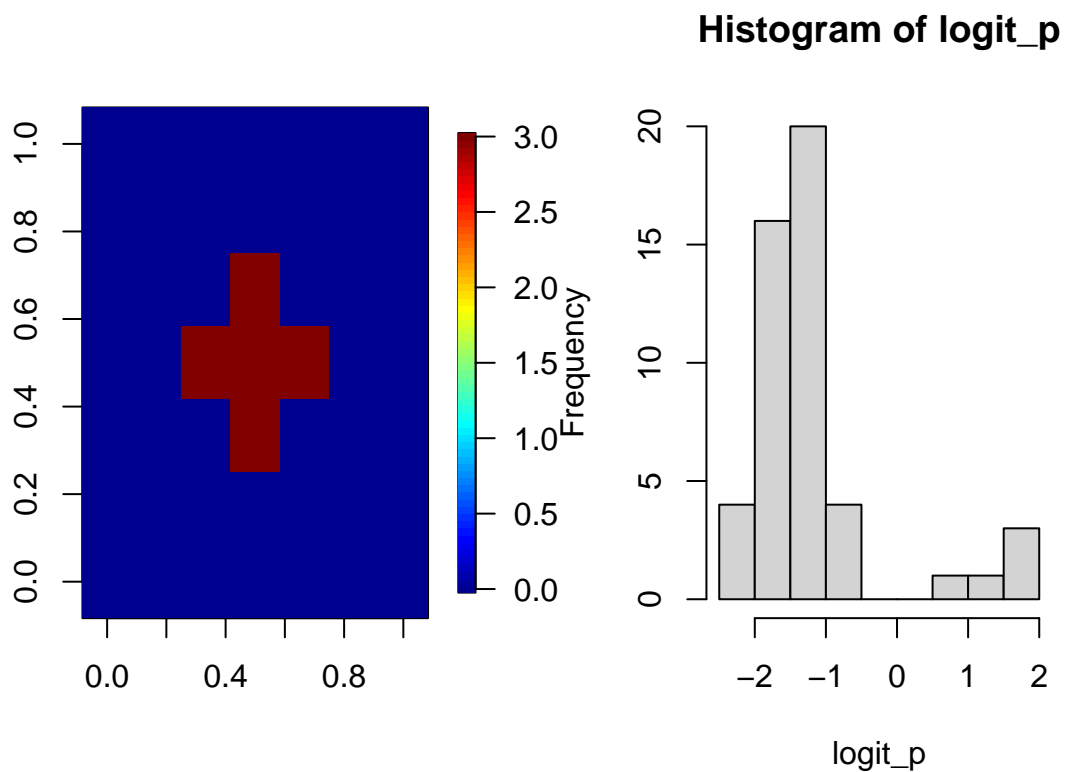
center<-25
phi[W[center,] == 1]<-phi[W[center,] == 1] +
    3.00
phi[center]<-phi[center] +
    3.00
neighbor_set<-c(1:nrow(W))[W[center,] == 1]

par(mfrow = c(1,2))
image.plot(matrix(c(phi),
                  nrow = n.space,
                  ncol = n.space,
                  byrow=TRUE))

logit_p<-x%*%beta_true +
    phi

hist(logit_p)

```



```
y<-rbinom(n = nrow(W),
          size = trials,
          prob = 1.00/(1.00 + exp(-logit_p)))
```

[2] Fit KSBound to estimate spatial boundaries:

```
results<-KSBound(mcmc_samples = 25000,
                 m_max = 2000,
                 spatial_neighbors = W,
                 y = y,
                 x = x,
                 likelihood_indicator = 1,
                 trials = trials,
                 alpha_a_prior = 10.00,
                 alpha_b_prior = 10.00,
                 keep_all_ind = 0.00)
```

```
## Progress: 10%
## Progress: 20%
## Progress: 30%
## Progress: 40%
## Progress: 50%
## Progress: 60%
## Progress: 70%
## Progress: 80%
## Progress: 90%
## Progress: 100%
```

[3] Analyzing Output:

```
par(mfrow=c(2,2))
plot(results$beta[1, 5001:25000],
     type="l",
     ylab="beta",
     xlab="Sample")
abline(h=beta_true[1],
      col="red",
      lwd=2) #True value
plot(results$beta[2, 5001:25000],
     type="l",
     ylab="beta",
     xlab="Sample")
abline(h=beta_true[2],
      col="red",
      lwd=2) #True value
plot(rowMeans(results$theta_g[,5001:25000]),
     pch=16,
     ylab="eta",
     xlab="Time",
     ylim = c(-1,7))
points(phi,
      pch=16,
      col="red") #True values
```

