SpGPCW: Spatially Varying Gaussian Process Model for Critical Window Estimation

SpGPCW_Example

[1] Simulate data from the proposed model:

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

```
set.seed(2365)

library(SpGPCW)
library(mnormt)  #Multivariate normal distribution
library(boot)  #Inverse logit transformation
library(spdep)  #Creating a grid
```

```
## Loading required package: sp

## Loading required package: spData

## To access larger datasets in this package, install the spDataLarge
## package with: `install.packages('spDataLarge',
## repos='https://nowosad.github.io/drat/', type='source')`

## Loading required package: sf

## Linking to GEOS 3.9.0, GDAL 3.2.1, PROJ 7.2.1
```

- Setting the global data values:

```
n<-5000  #Sample size
m<-25  #Number of exposure time periods
g<-4  #Size of square spatial grid
s<-g^2  #Number of spatial locations

grid<-cell2nb(nrow=g,
              ncol=g,
              type="rook",
              torus=FALSE)  #Evenly spaced grid
neighbors<-nb2mat(grid,
                  zero.policy=TRUE,
                  style="B")  #Adjacency matrix
MCAR<-diag(rowSums(neighbors)) -
      neighbors
site_id<-rep(s, times=n)
for(j in 1:s){
   site_id[(1 + floor(n/s)*(j-1)):(floor(n/s)*j)]<-j
   }

z<-matrix(0, nrow=n, ncol=m)
for(j in 1:s){
   z[(site_id == j),]<-matrix(rnorm(n=sum(site_id == j)),
                              nrow=sum(site_id == j),
                              ncol=m,
                              byrow=TRUE)  #Exposure design matrices
   }
for(j in 1:m){
   z[,j]<-z[,j]/IQR(z[,j])  #Data standardization (interquartile range)
```

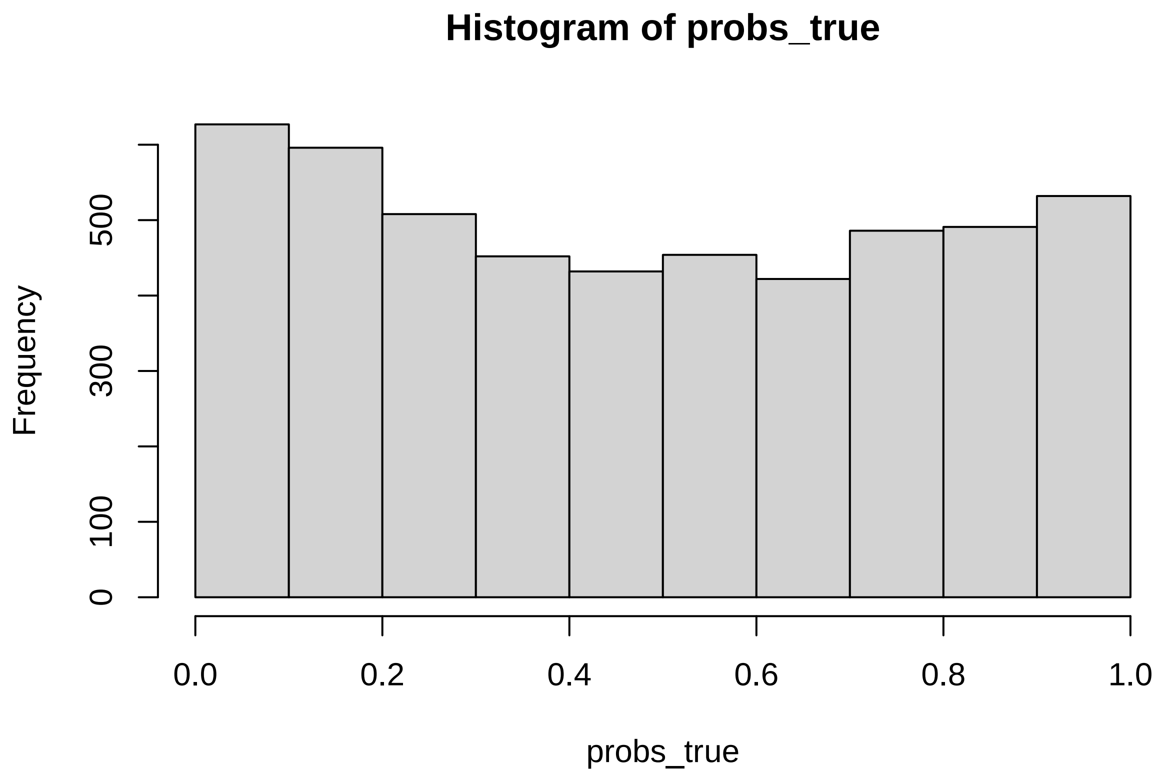
```r
   }

x<-matrix(1,
          nrow=n,
          ncol=2)  #Covariate design matrix
x[,2]<-rnorm(n)

beta_true<- c(-0.10, 0.20)
sigma2_theta_true<-0.25
sigma2_eta_true<-0.05
phi_true<-0.20
Sigma_true<-sigma2_theta_true*chol2inv(chol(temporal_corr_fun(m, phi_true)[[1]]))
eta_true<-rmnorm(n=1,
                 mean=rep(0, times=m),
                 varcov=Sigma_true)
eta_true<-eta_true -
          mean(eta_true)
rho_true<-0.45
theta_true<-rmnorm(n=1,
                   mean=rep(eta_true, times=s),
                   varcov=chol2inv(chol(kronecker((rho_true*MCAR + (1 - rho_true)*diag(s)),
                                                  chol2inv(chol(Sigma_true))))))

for(j in 1:s){
   theta_true[(1 + (j-1)*m):(m*j)]<-theta_true[(1 + (j-1)*m):(m*j)] -
                                    mean(theta_true[(1 + (j-1)*m):(m*j)])
   }

logit_p_true<-rep(0, times=n)
for(j in 1:s){
   logit_p_true[site_id == j]<-x[(site_id == j),]%*%beta_true +
                               z[(site_id == j),]%*%theta_true[(1 + (j-1)*m):(j*m)]
   }
probs_true<-inv.logit(logit_p_true)
hist(probs_true)
```



- Simulating the analysis dataset:

```
y<-rbinom(n=n,
          size=1,
          prob=probs_true)
```

[2] Fit SpGPCW to estimate spatially varying critical windows of susceptibility:

```
results<-SpGPCW(mcmc_samples = 10000,
                y = y, x = x, z = z, site_id = site_id, neighbors = neighbors,
                metrop_var_rho_trans = 1.4,
                metrop_var_phi_trans = 0.15)
```

```
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```

```
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## Progress: 80%
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## Progress: 85%
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## Progress: 90%
```

```
## rho Acceptance: 27%
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## *******************
```

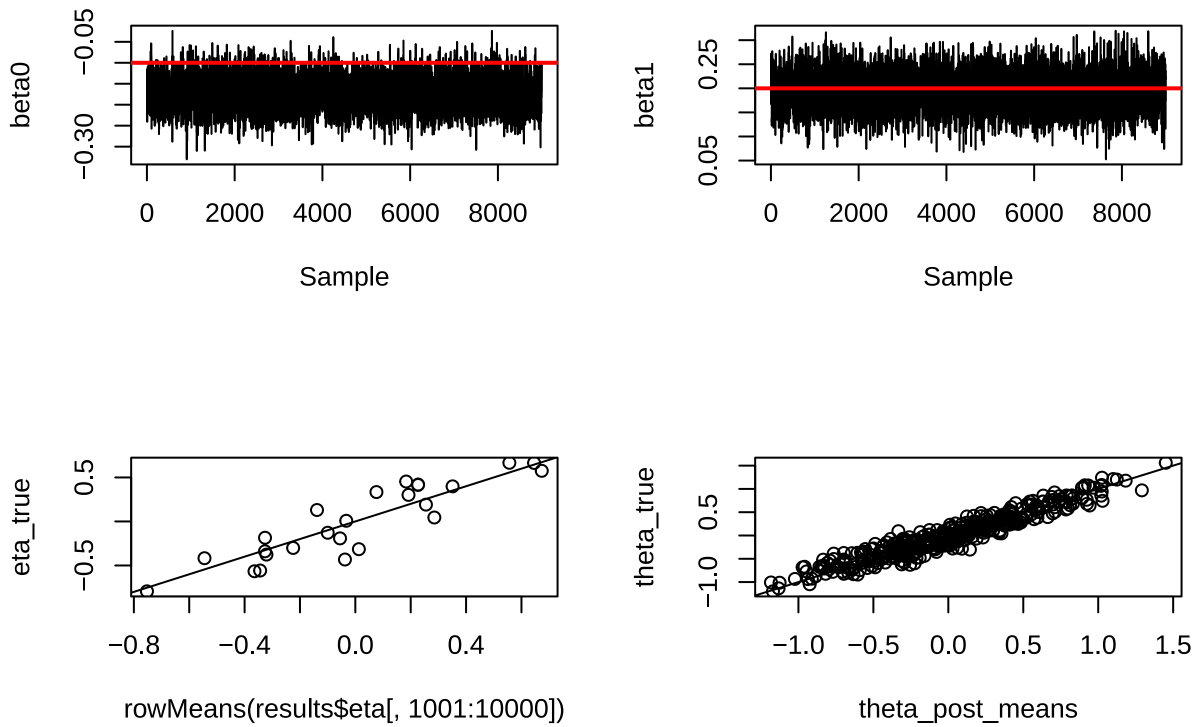
[3] Analyzing Output:

```
par(mfrow=c(2,2))
plot(results$beta[1, 1001:10000],
     type="l",
     ylab="beta0",
     xlab="Sample")
abline(h=beta_true[1],
       col="red",
       lwd=2)  #True value

plot(results$beta[2, 1001:10000],
     type="l",
     ylab="beta1",
     xlab="Sample")
abline(h=beta_true[2],
       col="red",
       lwd=2)  #True value

plot(rowMeans(results$eta[,1001:10000]),
     eta_true)
abline(0, 1)

theta<-simplify2array(results$theta)
theta_post_means<-rep(0, times=(s*m))
counter<-0
for(j in 1:s){
   for(k in 1:m){
      counter<-counter + 1
      theta_post_means[counter]<-mean(theta[j,k,1001:10000])
      }
    }
plot(theta_post_means,
     theta_true)
abline(0, 1)
```


beta0
−0.30
−0.05
0
2000
4000
6000
8000
Sample
beta1
0.05
0.25
0
2000
4000
6000
8000
Sample
eta_true
−0.5
0.5
−0.8
−0.4
0.0
0.4
rowMeans(results$eta[, 1001:10000])
theta_true
−1.0
0.5
−1.0
−0.5
0.0
0.5
1.0
1.5
theta_post_means