

# 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

## Warning: package 'mnormt' was built under R version 4.3.0
library(boot) #Inverse logit transformation

## Warning: package 'boot' was built under R version 4.2.3
library(spdep) #Creating a grid

## Warning: package 'spdep' was built under R version 4.3.1
## Loading required package: spData
## Warning: package 'spData' was built under R version 4.3.1
## The legacy packages mapproj, rgdal, and rgeos, underpinning the sp package,
## which was just loaded, will retire in October 2023.
## Please refer to R-spatial evolution reports for details, especially
## https://r-spatial.org/r/2023/05/15/evolution4.html.
## It may be desirable to make the sf package available;
## package maintainers should consider adding sf to Suggests:.
## The sp package is now running under evolution status 2
## (status 2 uses the sf package in place of rgdal)

## 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
## Warning: package 'sf' was built under R version 4.3.1
## Linking to GEOS 3.11.2, GDAL 3.6.2, PROJ 9.2.0; sf_use_s2() is TRUE
```

- 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)
}

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

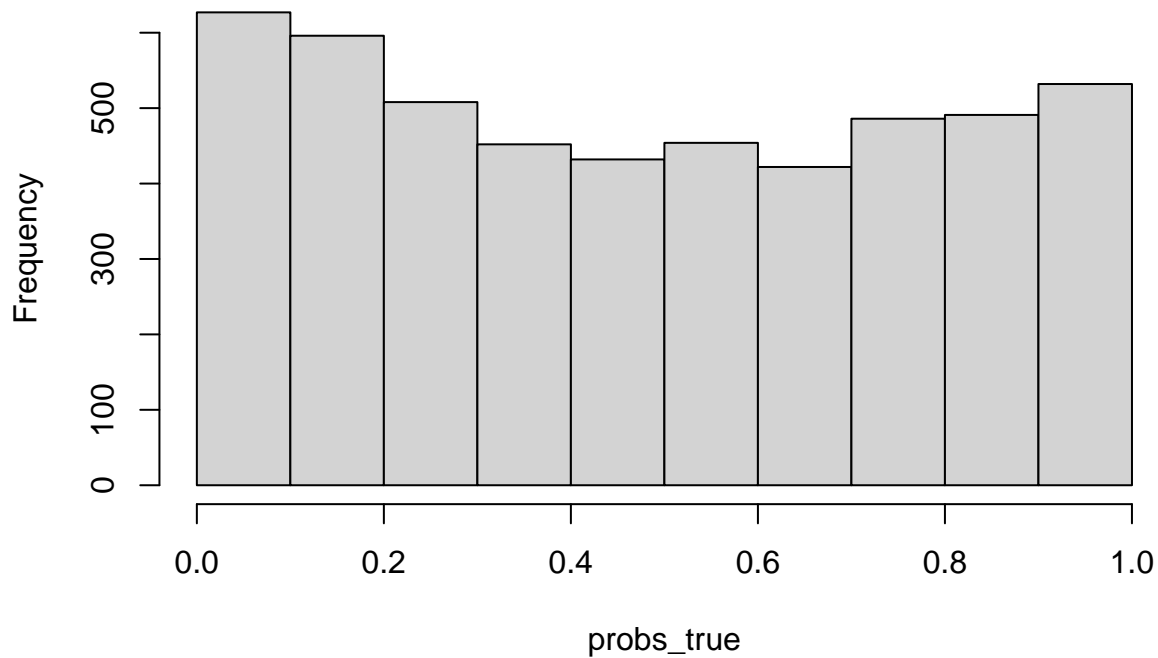
beta_true<- c(-0.10, 0.20)
sigma2_theta_true<-0.25
sigma2_eta_true<-0.05
phi_true<-0.20
Sigma_true<-sigma2_theta_true*chol2inv(chol(temporal_corr_fun(m, phi_true)[[1]]))
eta_true<-rmnorm(n=1,
                mean=rep(0, times=m),
                varcov=Sigma_true)
eta_true<-eta_true -
  mean(eta_true)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

```

**Histogram of probs\_true**



```
trials<-rep(1, times=n)
```

- Simulating the analysis dataset:

```
y<-rbinom(n=n,  
          size=trials,  
          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,  
                trials = trials,  
                likelihood_indicator = 0)
```

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```

```

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```

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## *****
## Progress: 100%
## 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)
```

