

# SpGPCW: Spatially Varying Gaussian Process Modeling 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: Matrix
```

```
## 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')`
```

- 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] - median(z[,j]))/IQR(z[,j]) #Data standardization (interquartile range)
}
```

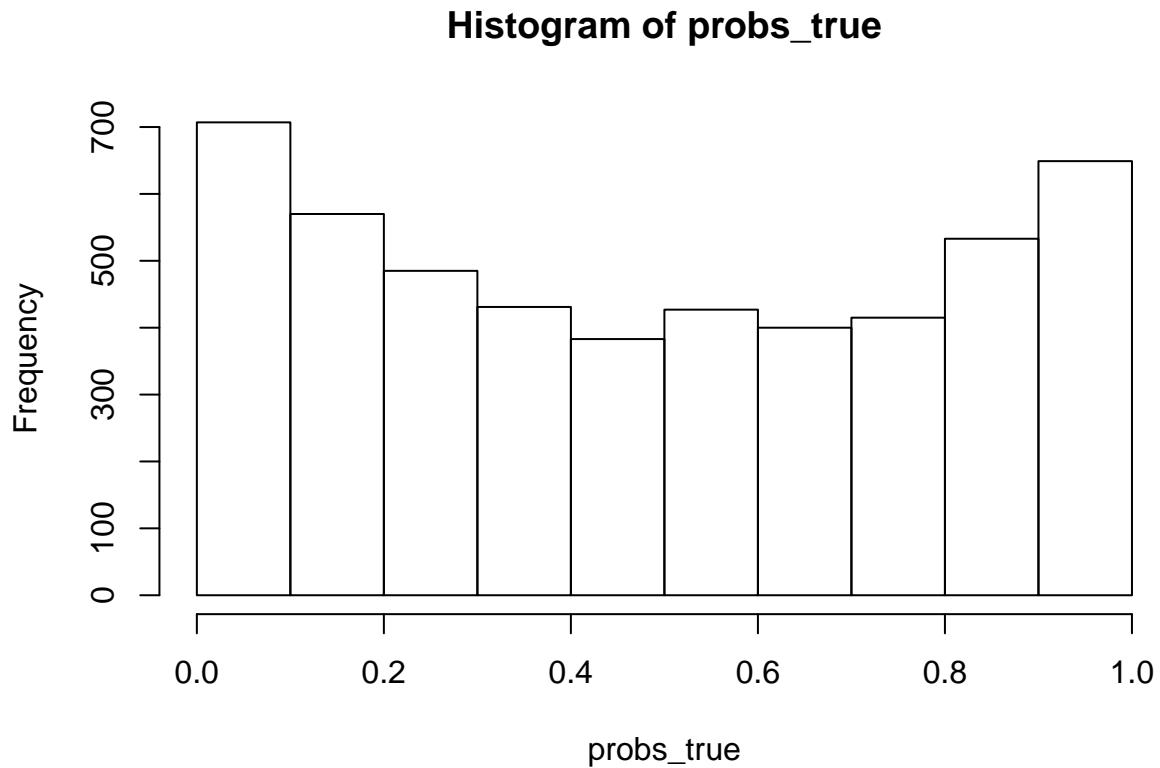
```

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]]))
theta_true<-rmnorm(n=1,
                  mean=rep(0, times=m),
                  varcov=Sigma_true)
theta_true<-theta_true -
              mean(theta_true)
rho_true<-0.45
eta_true<-rmnorm(n=1,
                mean=rep(0, times=(m*s)),
                varcov=chol2inv(chol(kronecker((rho_true*MCAR + (1 - rho_true)*diag(s)),
                                           chol2inv(chol(Sigma_true))))))
eta_true<-eta_true -
              mean(eta_true)

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 +
                             z[(site_id == j),]%*%eta_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)
```

```
## Progress: 5%
## rho Acceptance: 26%
## phi Acceptance: 24%
## *****
## Progress: 10%
## rho Acceptance: 27%
## phi Acceptance: 24%
## *****
## Progress: 15%
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## *****
## Progress: 20%
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## phi Acceptance: 25%
```

```

## *****
## Progress: 25%
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## *****
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## *****
## Progress: 90%

```

```
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## *****
## Progress: 95%
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## phi Acceptance: 24%
## *****
## Progress: 100%
## rho Acceptance: 29%
## phi Acceptance: 24%
## *****
```

[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$theta[,1001:10000]),
     theta_true)
abline(0, 1)

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

