

GPCW_Example

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[1] Simulate data from the proposed model:

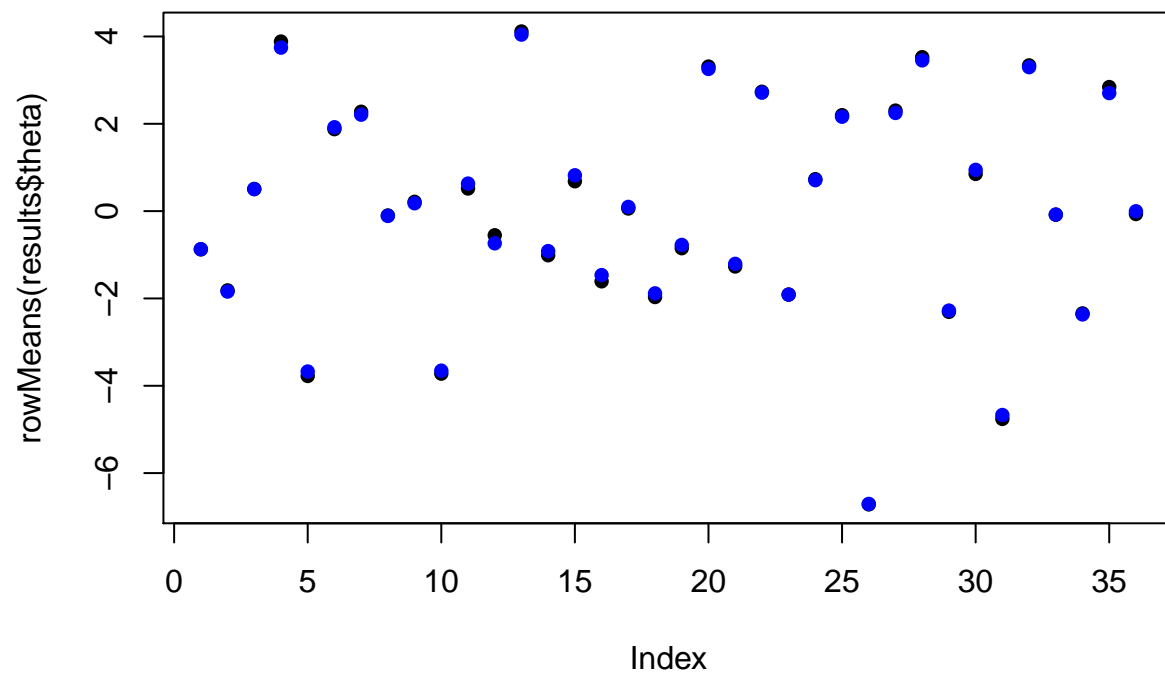
```
#####  
#Reproducibility Seed  
#####  
set.seed(78453)  
  
#####  
#Packages  
#####  
library(GPCW)  
library(mnormt)  
library(boot)  
  
#####  
#Data Settings  
#####  
n<-10000  
m<-36  
x<-matrix(1,  
          nrow=n,  
          ncol=1)  
z<-matrix(rnorm(n=(n*m)),  
          nrow=n,  
          ncol=m)  
  
#Standardizing the Exposures at Each Time Period  
for(j in 1:m){  
  z[,j]<-(z[,j] - median(z[,j]))/IQR(z[,j])  
}  
  
#####  
#True Parameter Values  
#####  
beta_true<- -0.30  
phi0_true<-0.50  
phi1_true<-0.10  
Sigma<-phi0_true*temporal_corr_fun(m,  
                                   phi1_true)[[1]]  
  
theta_true<-c(rmnorm(n=1,  
                    mean=rep(0, times=m),  
                    varcov=Sigma))  
  
logit_p<-x%*%beta_true +  
         z%*%theta_true  
probs<-inv.logit(logit_p)
```

```
#####
#Simulated Response
#####
y<-rbinom(n=n,
          size=1,
          prob=probs)
```

[2] Fit GPCW to Estimate Critical Windows of Susceptibility:

[3] Analyzing Output:

```
plot(rowMeans(results$theta), pch=16)
points(theta_true, pch=16, col="blue")
```



You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.