README

01/31/2025

```
################# set working directory #################
# please specify the path
path="/Users/rakheon_kim/Desktop/Research/SparseCovReg/"
```

Numbers for tables: MA(1) model under Setting 1 with n=200, p=50, q=30

Numbers for other settings can be obtained by loading the R data for each setting.

```
load(file=paste0(path,"data/main/fit_n200p50q30_MA_set1.RData"))
# Table 1
mean(S_diff); mean(ST_diff); mean(covreg_diff); mean(lse_diff); mean(covlpd_diff)
```

```
## [1] 3.219506
```

```
## [1] 2.014333
```

```
## [1] 7.810432
```

```
## [1] 15.08602
```

```
## [1] 1.874898
```

```
sd(S_diff); sd(ST_diff); sd(covreg_diff); sd(lse_diff); sd(covlpd_diff)
```

```
## [1] 0.07939699
```

```
## [1] 0.06482416
```

```
## [1] 0.3448368
```

```
## [1] 0.3379816
```

```
## [1] 0.06224962
```

```
# Table 2
mean(sqrt(covl_err_est)); sd(sqrt(covl_err_est)); mean(lasso_TPR); mean(lasso_FPR)
```

```
## [1] 4.581958
```

```
## [1] 0.1651217

## [1] 0.7662121

## [1] 0.007572249
```

```
# Table 3
colMeans(tb_COV)
```

```
## [1] 0.9380469 0.9269388 0.9380612 0.9502101 0.9475510 0.9502136
```

Figure 1

```
load(file=paste0(path,"data/main/fit_n500p50q30_MA_set1.RData"))
# Code for creating the picture can be found in simul.R
```
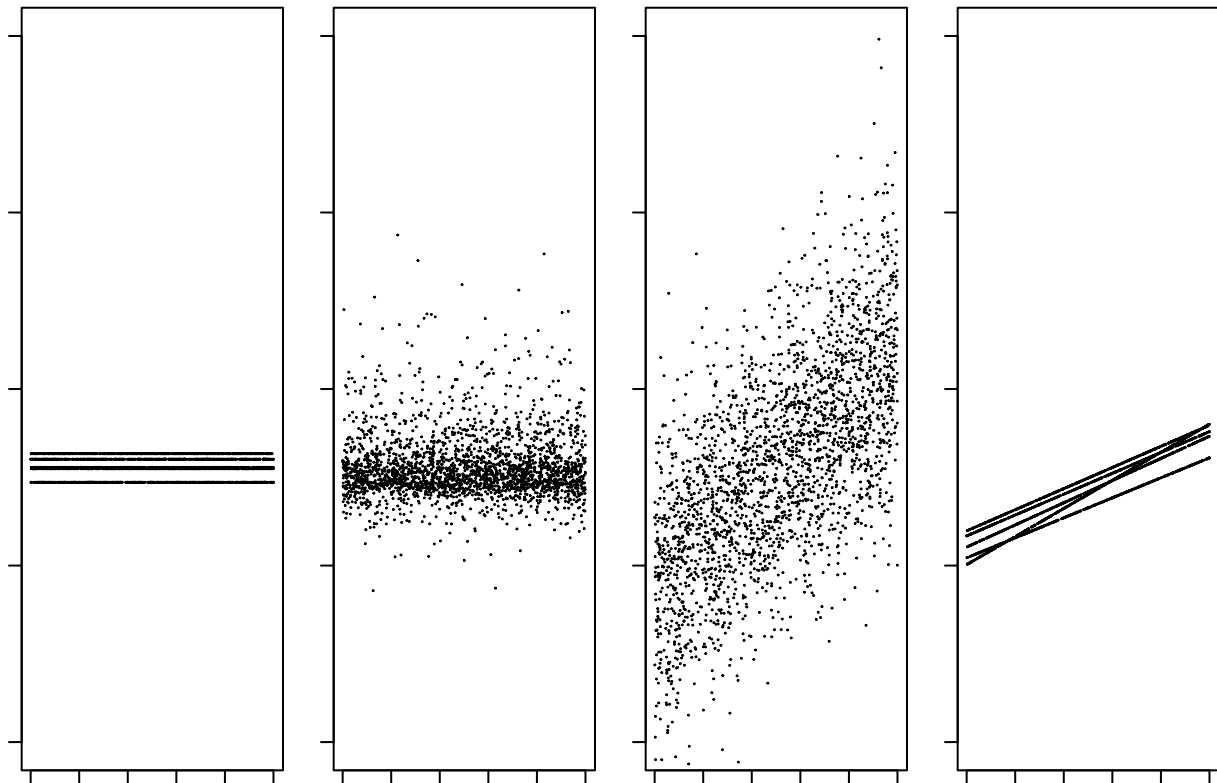

Figure 2

```
load(file=paste0(path,"data/main/fit_n500p50q100_MA_set2.RData"))
# Code for creating the picture can be found in simul.R
```
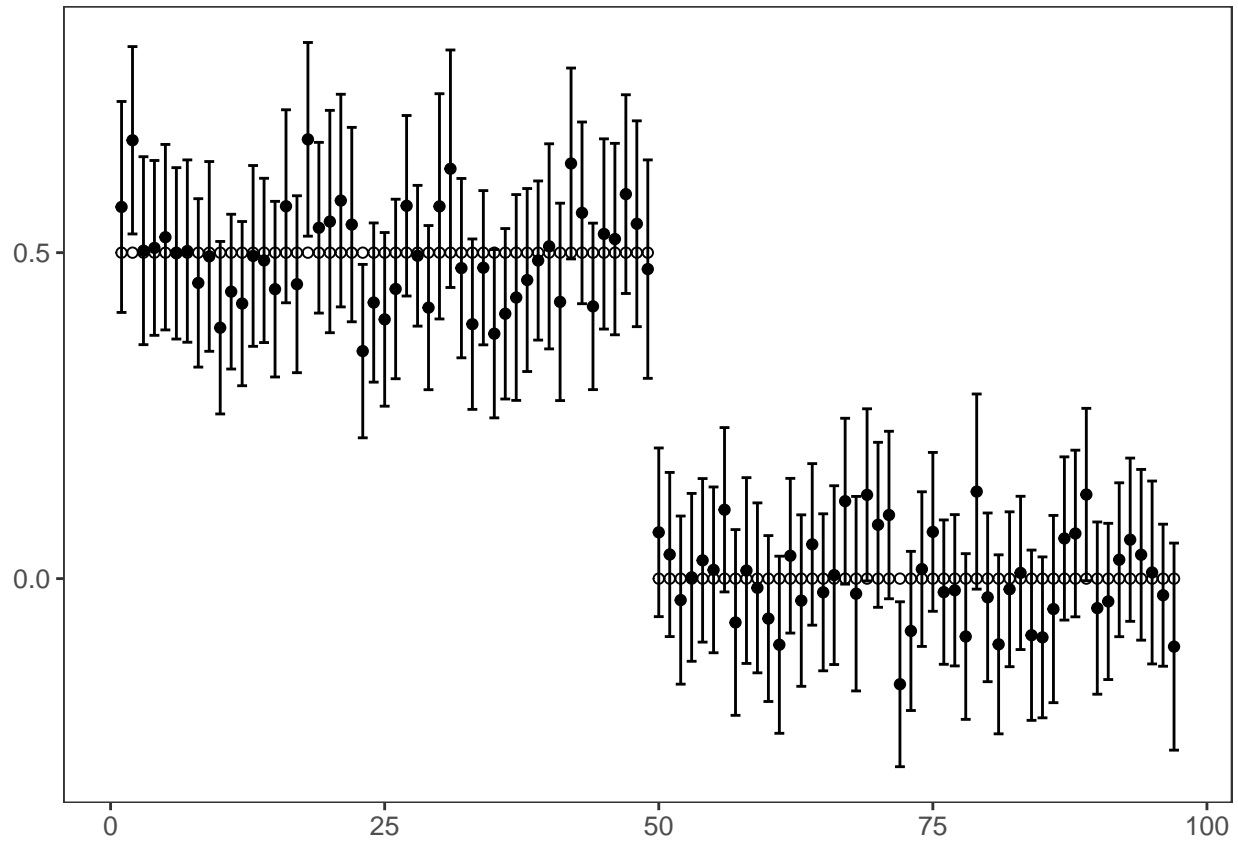
Figure S2

```r
library(mvtnorm)
n=200; p=2; q=3; ii=1
set.seed(10000*ii)
z = matrix(runif(n*q), ncol=q)
z = cbind(z, z[,1]*z, z[,2]*z[,2:3], z[,3]*z[,3])
B0 = matrix(c(1,-1,1,1), ncol=2)
C0 = B0 %*% diag(c(1,1/3)) %*% t(B0) # diag(2) # B0 %*% diag(c(1,1/3)) %*% t(B0)
z1 = cbind(matrix(1,nrow=n,ncol=1), z[,1])
Sigma_indiv = array(0, dim=c(p,p,n))
dat = matrix(0, nrow = n, ncol = p)
for (i in 1:n){
  Sigma_indiv[1:2,1:2,i] = (C0/2) + (B0/2)%*%z1[i,]%*%t(z1[i,])%*%t(B0/2)
  dat[i,] = rmvnorm(1,mean=rep(0,p),sigma=Sigma_indiv[,,i])
}
par(mfrow=c(1,2), mar = c(2, 2, 2, 1))
plot(z[,1], Sigma_indiv[1,2,], col="white", pch=16, ylim=c(-6,2), xlab=NA, ylab=NA)
points(z[,1], (dat[,1]-mean(dat[,1]))*(dat[,2]-mean(dat[,2])), cex=0.5, pch=16)
plot(z[,2], Sigma_indiv[1,2,], col="white", pch=16, ylim=c(-6,2), xlab=NA, ylab=NA)
points(z[,2], (dat[,1]-mean(dat[,1]))*(dat[,2]-mean(dat[,2])), cex=0.5, pch=16)
```
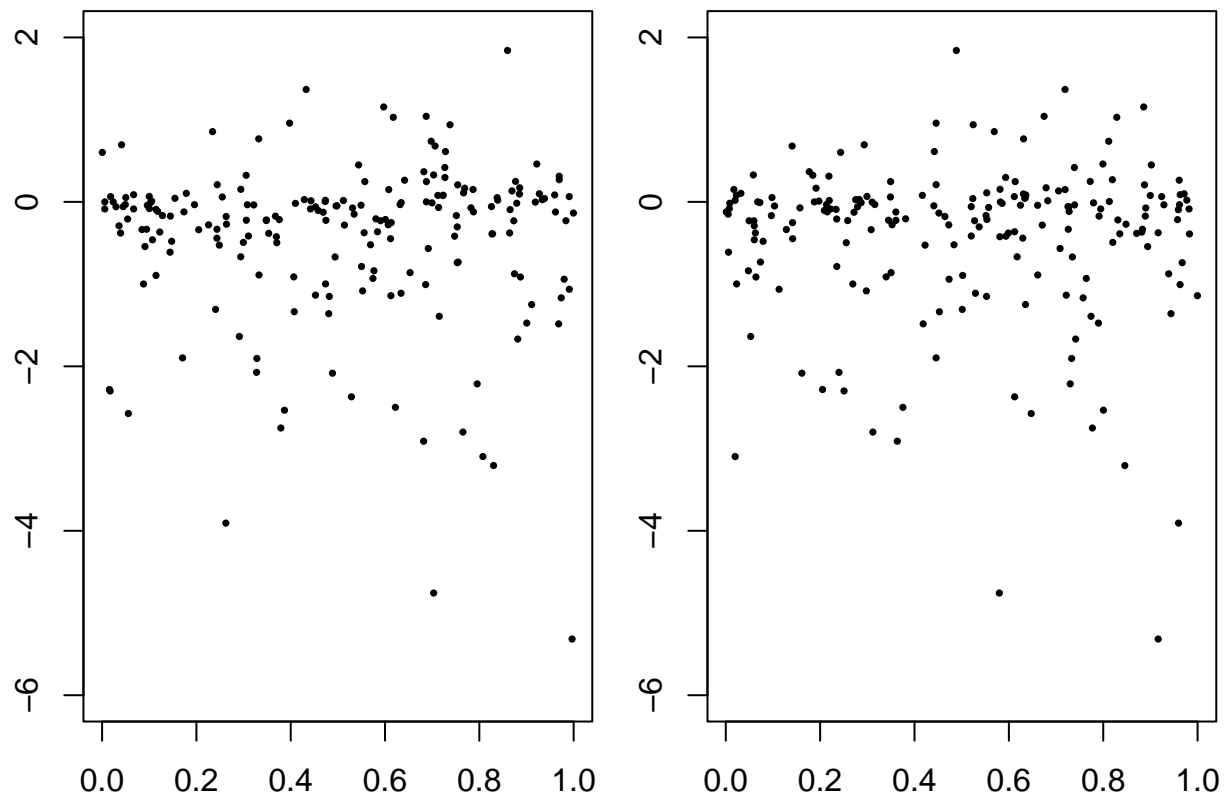
Numbers for Supplement S9 (when q=1)

Numbers for other settings can be obtained by loading the R data for each setting.

```
load(file=paste0(path,"data/supp/supp_q1.RData"))
# Table S1
mean(covreg_mcmc_diff); mean(covl_diff3); mean(covl_diff)
```

```
## [1] 0.2308865
```

```
## [1] 0.2518296
```

```
## [1] 0.2898408
```

```
sd(covreg_mcmc_diff); sd(covl_diff3); sd(covl_diff)
```

```
## [1] 0.09205443
```

```
## [1] 0.08425484
```

```
## [1] 0.0943065
```

All of these can be obtained https://github.com/rakheon/SparseCovReg.