

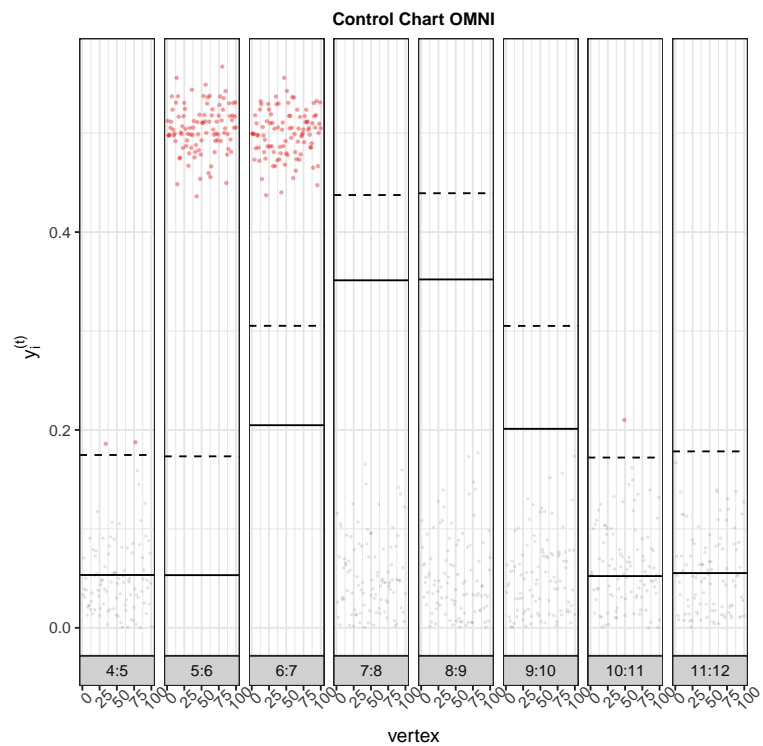
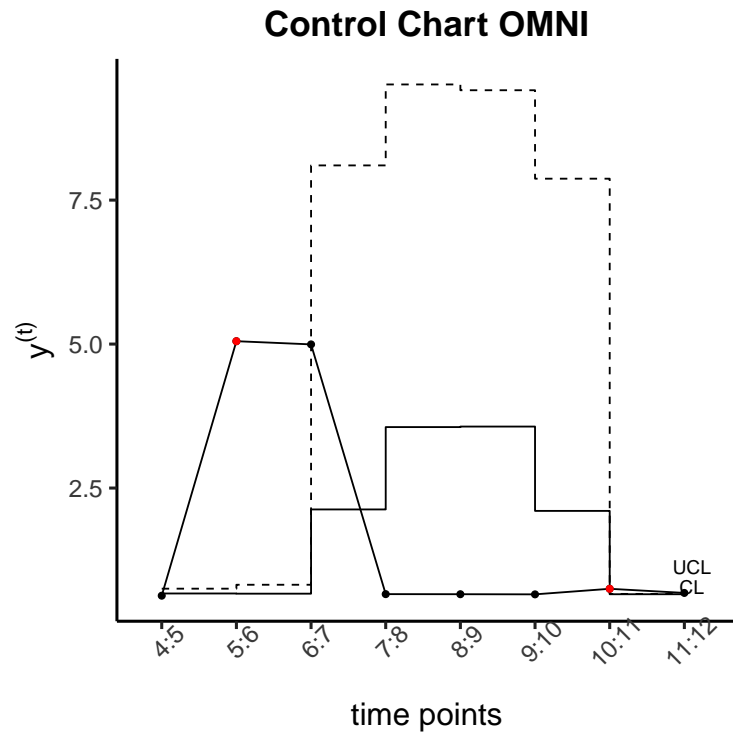
A Report Generated by knitr

August 14, 2020

The results below are generated from an R script.

```
#source("utilAD.R")
#source("simulation.R")
#Example 1
#Generate a time series of ER graphs of length 12,
#create graph anomaly at time point 6
n <- 100
glist <- list()
for (i in 1:5) {
  glist[[i]] <- sample_gnp(n,.1)
}
glist[[6]] <- sample_gnp(n,.9)
glist[[7]] <- sample_gnp(n,.1)
for (i in 8:12) {
  glist[[i]] <- sample_gnp(n,.1)
}
# Do anomaly detection with OMNI, provide the quantitative control chart for GraphAD and VertexAD
result.OMNI<- qccAD(glist, l=4,d=1,dsvd=NULL,method="OMNI",
  diag.augment = TRUE, approx=FALSE, par=FALSE, numpar=2)

## Warning: 'switch' is deprecated.
## Use 'strip.position' instead.
## See help("Deprecated")
```



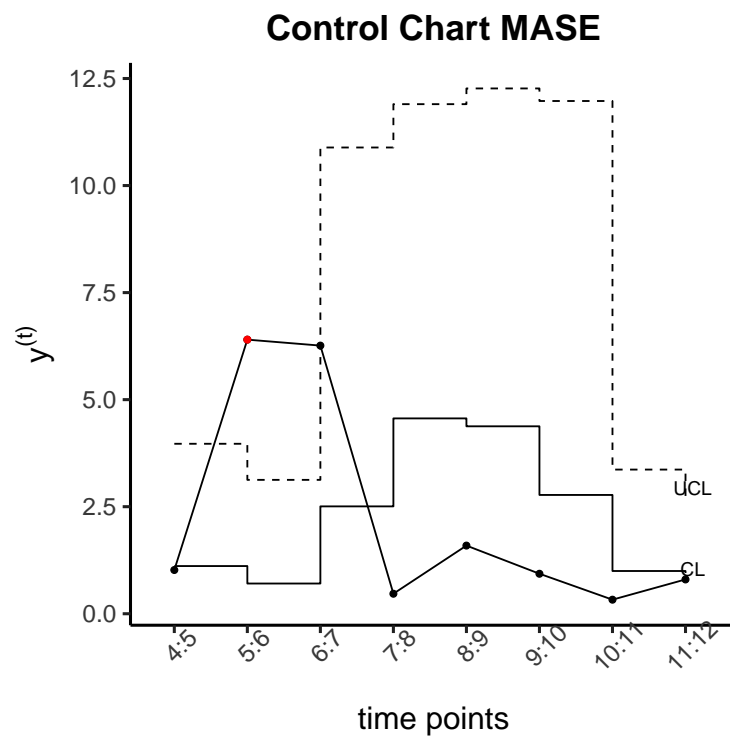
```
#print the number of deviation for GraphAD, only positive ones are meaningful
print(result.OMNI$GraphAD)
```

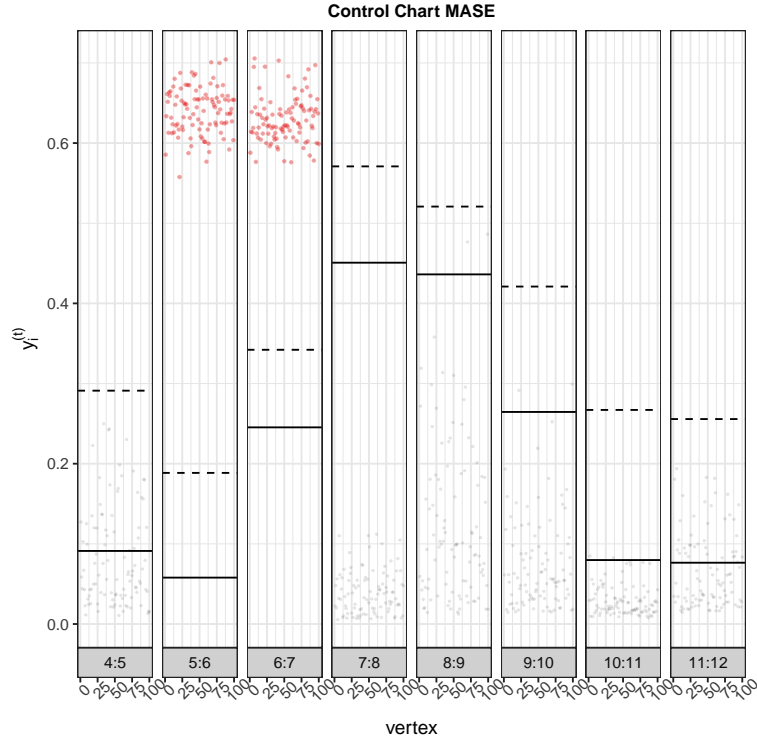
```
##      Samples
## Group      [,1]
##      1 -1.3733018
```

```
##      2 84.7970026
##      3  1.4393122
##      4 -1.4625044
##      5 -1.4953193
##      6 -0.7535285
##      7 53.6121408
##      8 -0.1885784

# Do anomaly detection with MASE
result.MASE<- qccAD(glist, l=4,d=2,dsvd=2,method="MASE",
                    diag.augment = TRUE, approx=FALSE, par=FALSE, numpar=2)

## Warning: 'switch' is deprecated.
## Use 'strip.position' instead.
## See help("Deprecated")
```





```
#print the number of deviation for GraphAD, only positive ones are meaningful
print(result.MASE$GraphAD)
```

```
##      Samples
## Group      [,1]
##      1 -0.09656679
##      2  7.05849907
##      3  1.34410088
##      4 -1.67362160
##      5 -1.05903744
##      6 -0.59989383
##      7 -0.84758103
##      8 -0.26854924
```

```
#Example 2
```

```
# Sample a time series of RDPG graph (length tmax > 17) with same 1-1 matched vertices unweighted
# hollow symmetric undirected graphs, the latent positions i.i.d uniform.
# Some vertices in 16-th and 17-th graphs are given perturbations so there exists anomalies at 16:17.
```

```
n <- 100 #number of vertices
```

```
nperturb <- 20 #number of perturbed vertices
```

```
cperturb <- .12 #number of perturbation, larger cperturb means more obvious anomalies.
```

```
rmin <- .2 # parameter for uniform[rmin, rmax].
```

```
rmax <- .8 # parameter for uniform[rmin, rmax].
```

```
tmax <- 22 # number of graphs must be greater than 17.
```

```
#Generate data or load the data you want
```

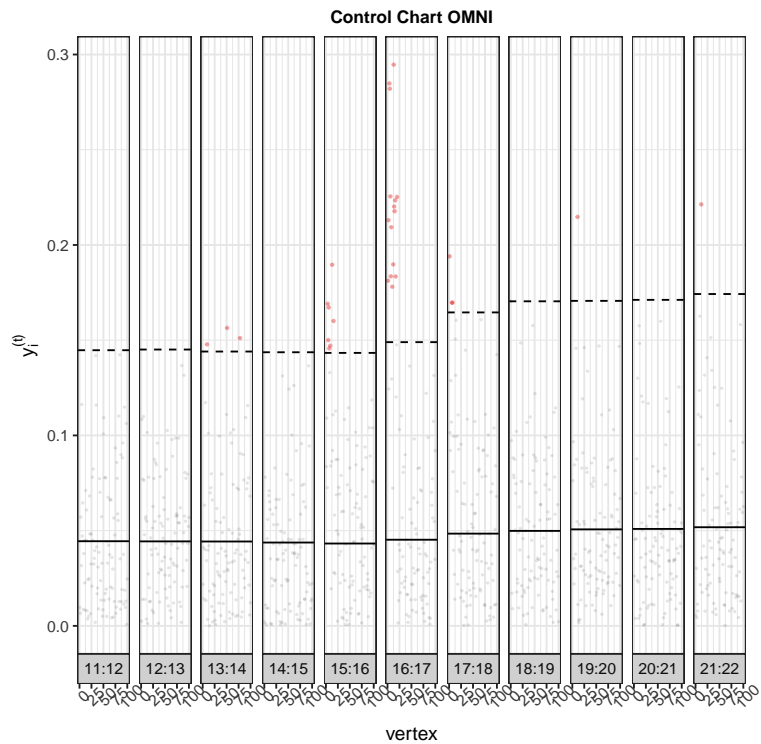
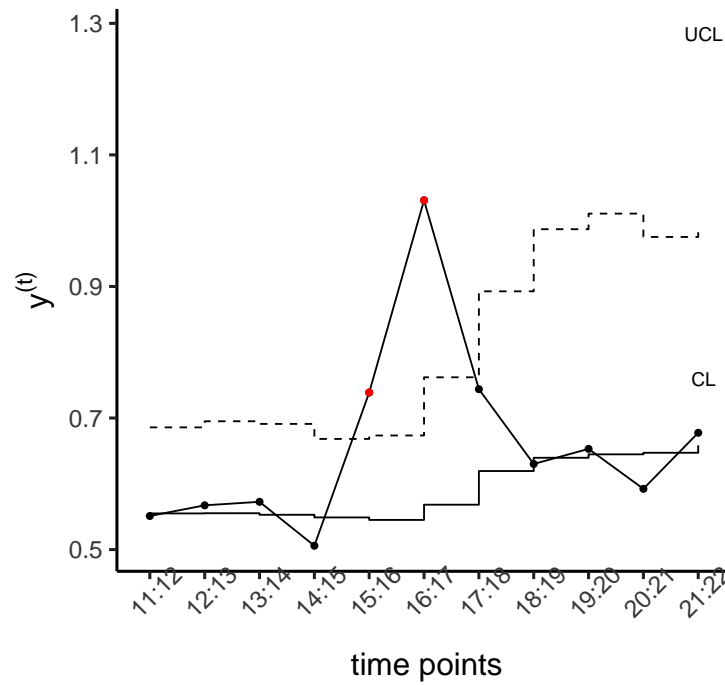
```
glist <- generate.tsg(n, nperturb, cperturb=NULL, rmin, rmax, tmax)$glist
```

```
#Do anomaly detection with OMNI in parallel
```

```
result.OMNI <- qccAD(glist, l=11,d=1,dsvd=NULL,method="OMNI",
  diag.augment = TRUE, approx=FALSE, par=TRUE, numpar=2)
```

```
## Warning: 'switch' is deprecated.
## Use 'strip.position' instead.
## See help("Deprecated")
```

Control Chart OMNI



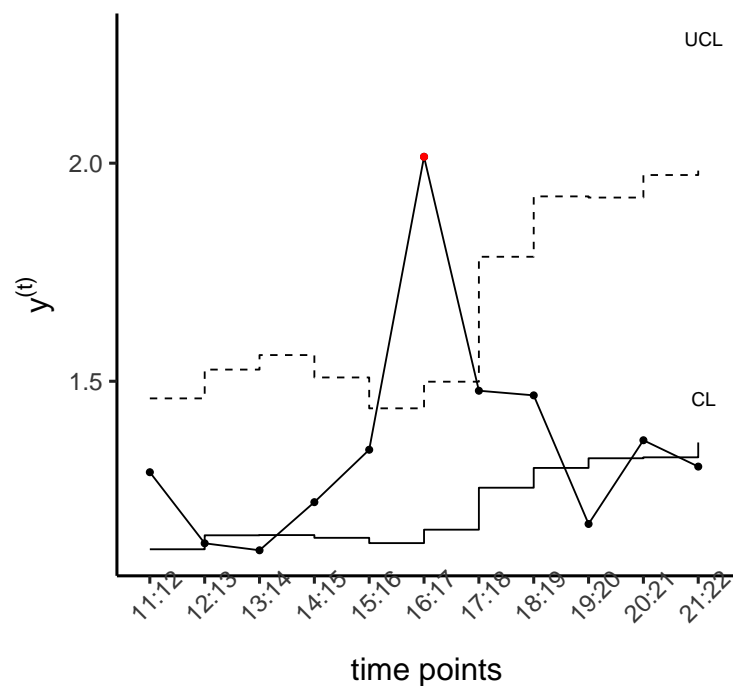
```
#print the number of deviation for GraphAD, only positive ones are meaningful
print(result.OMNI$GraphAD)
```

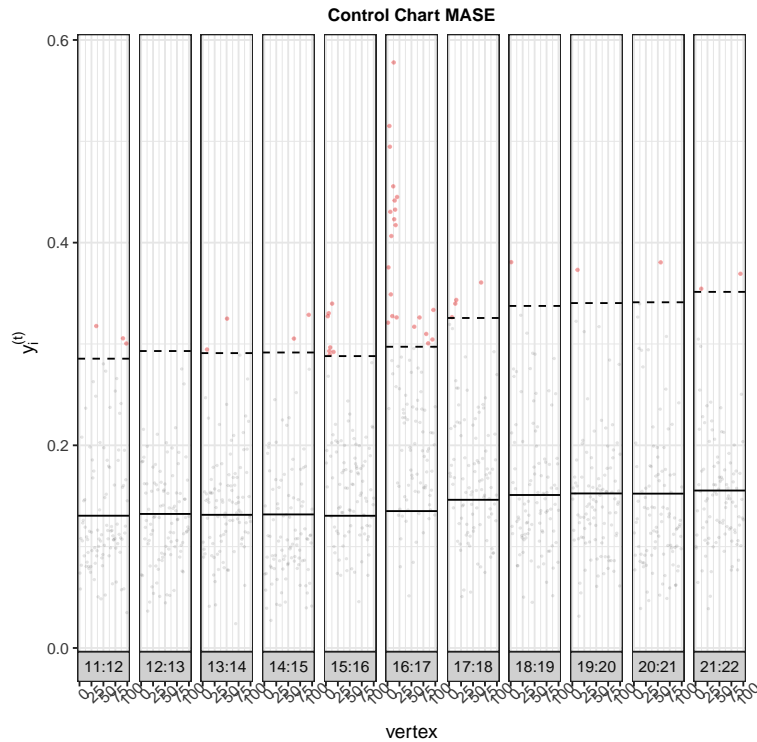
```
##      Samples
## Group      [,1]
##    1 -0.08934863
##    2  0.25822764
##    3  0.42770895
##    4 -1.08170542
##    5  4.52750339
##    6  7.16829467
##    7  1.36646321
##    8 -0.08146716
##    9  0.06800435
##   10 -0.50088884
##   11  0.17556834
```

```
# Do anomaly detection with MASE in parallel
result.MASE<- qccAD(glist, l=11,d=1,dsvd=2,method="MASE",
                    diag.augment = TRUE, approx=FALSE, par=TRUE, numpar=2)
```

```
## Warning: 'switch' is deprecated.
## Use 'strip.position' instead.
## See help("Deprecated")
```

Control Chart MASE





```
#print the number of deviation for GraphAD, only positive ones are meaningful
print(result.MASE$GraphAD)
```

```
##      Samples
## Group      [,1]
##    1  1.5323442
##    2 -0.1446884
##    3 -0.2533122
##    4  0.6673617
##    5  2.0787768
##    6  7.5591279
##    7  1.2601383
##    8  0.8019631
##    9 -0.7557727
##   10  0.1816826
##   11 -0.2652905
```

```
#Example 3
```

```
#five of ER tsg with change point at t=6 and five at t=8.
```

```
n <- 100
```

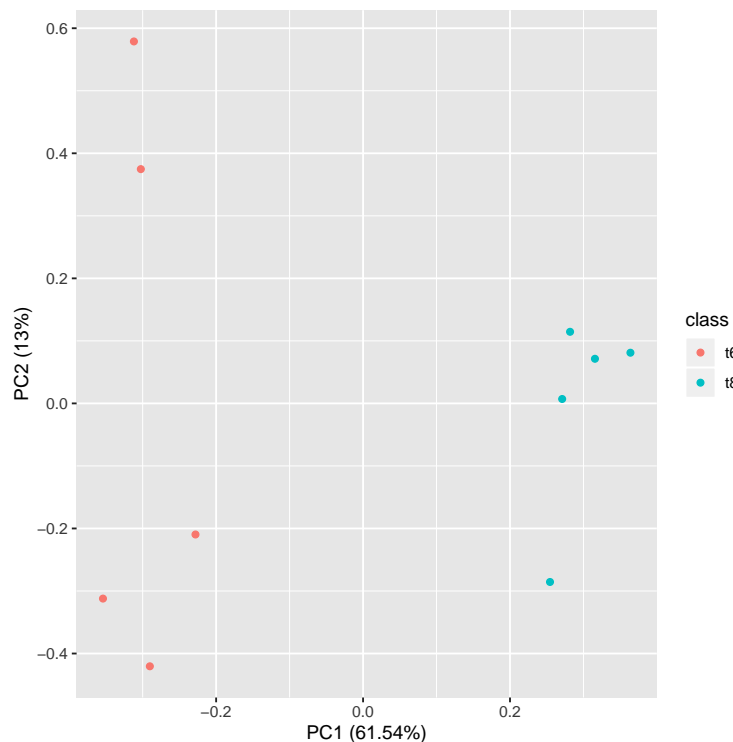
```
dat <- matrix(0, 10, 8)
```

```
for (j in 1:5) {
  glist <- list()
  for (i in 1:5) {
    glist[[i]] <- sample_gnp(n,.1)
  }
  glist[[6]] <- sample_gnp(n,.9)
  for (i in 7:12) {
    glist[[i]] <- sample_gnp(n,.1)
  }
}
```

```

# Do anomaly detection with OMNI, provide the quantitative control chart for GraphAD and VertexAD
result.OMNI<- qccAD(glist, l=4,d=1,dsvd=NULL,method="OMNI",
                    diag.augment = TRUE, approx=FALSE, par=FALSE, numpar=2, plot.figure = FALSE)
dat[j,] <- result.OMNI$GraphAD
}
for (j in 6:10) {
  glist <- list()
  for (i in 1:7) {
    glist[[i]] <- sample_gnp(n,.1)
  }
  glist[[8]] <- sample_gnp(n,.9)
  for (i in 9:12) {
    glist[[i]] <- sample_gnp(n,.1)
  }
  # Do anomaly detection with OMNI, provide the quantitative control chart for GraphAD and VertexAD
  result.OMNI<- qccAD(glist, l=4,d=1,dsvd=NULL,method="OMNI",
                      diag.augment = TRUE, approx=FALSE, par=FALSE, numpar=2, plot.figure = FALSE)
  dat[j,] <- result.OMNI$GraphAD
}
df <- data.frame(dat,class=factor(c(rep("t6",5),rep("t8",5))))
pca_res <- prcomp(dat, scale. = TRUE)
library(ggfortify)
autoplot(pca_res, data = df, colour="class")

```



The R session information (including the OS info, R version and all packages used):

```

sessionInfo()

## R version 3.6.1 (2019-07-05)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)

```