SPSC

This Github repository contains SPSC R package. This package is currently in beta.

Installation

To install SPSC package in R, run the commands below:

```
{r} library(devtools) install_github("qkrcks0218/SPSC")
```

Example Usage

Here are some examples:

“‘{r} ##
Toy Example from Interactive Fixed Effect Models

Parameters

T0 <- T1 <- 50 # length of pre- and post-treatment period Tt <- T1+T0 # length of total time series N.Inv <- N.Val <- N.Donor <- 8 # number of W=valid donors and V=invalid donors rho.lambda <- 0.5 # AR coefficient of lantent factor corr.Y0.W <- 0.5 # corr(error of Y, error of W) W.coef <- rbind(8:1/4, rep(c(0.8,0.6,0.4,0.2),each=2)) # factor loadings of valid donors V.coef <- rbind(rep(1,8), rep(0.5,8)) # factor loadings of invalid donors Y0.coef <- c(W.coef[,1:N.Donor]%*%rep(1/N.Donor,N.Donor)) # factor loadings of Y SD <- 0.1 # sd of errors BT <- 1+c(0,0,(1:Tt/T0)) # baseline trend True.ATT <- 3 # true effect

Latent factor of W

lambda.eps.series <- matrix(0,2+Tt,2) lambda.eps.series[1:2,] <- rnorm(4)*SD for(time.index in 1:Tt){ lambda.eps.series[time.index+2,] <- rho.lambda*lambda.eps.series[time.index+1,] + rho.lambda*lambda.eps.series[time.index,]/ + rnorm(2)*SD } lambda.series <- lambda.eps.series + matrix(BT,2+Tt,2)

Latent factor of V

zeta.eps.series <- matrix(0,2+Tt,2) zeta.eps.series[1:2,] <- rnorm(4)*SD for(time.index in 1:Tt){ zeta.eps.series[time.index+2,] <- rho.lambda*zeta.eps.series[time.index+1,] + rho.lambda*zeta.eps.series[time.index,]/2 + rnorm(2)*SD } zeta.series <- zeta.eps.series + matrix(BT,2+Tt,2)

Generate Y,W,V

common.eps <- rnorm(2+Tt) Y0.idio.eps <- rnorm(2+Tt) W.idio.eps <- matrix(rnorm(N.Val*(2+Tt)),2+Tt,N.Val) V.idio.eps <- matrix(rnorm(N.Inv*(2+Tt)),2+Tt,N.Inv) Y0.eps <- SD*(corr.Y0.W*common.eps + sqrt(1-corr.Y0.W^2)*Y0.idio.eps) W.eps <- SD*(corr.Y0.W*matrix(common.eps,2+Tt,N.Val) + sqrt(1-corr.Y0.W^2)*W.idio.eps) V.eps <- SD*(V.idio.eps)

Y0.series <- c(lambda.series%%Y0.coef) + Y0.eps W.series <- lambda.series%%W.coef[,1:N.Val] + W.eps V.series <- zeta.series%*%V.coef[,1:N.Inv] + V.eps

Generate error-prone treatment effect

beta.eps <- c(rep(0,T0+2),rnorm(T1)) beta <- c(rep(0,T0+2),rep(True.ATT,T1)) beta.with.noise <- beta + beta.eps*SD

Post-treatment Y

Y1.series <- Y0.series + beta.with.noise

Observed Y

Yobs.series <- rep(0,T0+T1+2) Yobs.series[1:(2+T0)] <- Y0.series[1:(2+T0)] Yobs.series[(2+T0)+1:T1] <- Y1.series[(2+T0)+1:T1]

Pre-treatment series

Dmat.Pre <- cbind(W.series,V.series)[2+(1:T0),] Y1.Pre <- Y0.series[2+(1:T0)]

Post-treatment series

Dmat.Post <- cbind(W.series,V.series)[2+T0+(1:T1),] Y1.Post <- Y1.series[2+T0+(1:T1)] True.TT.Vec <- beta.with.noise[2+T0+1:T1]

SPSC

SPSC.Detrend <- SPSC(Y.Pre = Y1.Pre, Y.Post = Y1.Post, W.Pre = Dmat.Pre, W.Post = Dmat.Post, detrend = TRUE, detrend.ft = function(t){matrix(c(1,t),1,2)}, Y.basis = function(y){matrix(c(y),1,1)}, att.ft = function(t){matrix(c(1),1,1)}, lambda.type = "cv", lambda.value = NULL, lambda.grid = seq(-6,2,by=0.5), bootstrap.num = 100, conformal.period = 1:T1, conformal.cover = TRUE, true.effect = True.TT.Vec, conformal.interval = TRUE, conformal.pvalue = 0.05)

Average treatment effect and 95% confidence interval

cbind(SPSC.Detrend$ATT - 1.96 * SPSC.Detrend$ASE.ATT, SPSC.Detrend$ATT + 1.96 * SPSC.Detrend$ASE.ATT) True.ATT

Graphical summary

plot.SPSC(SPSC.Detrend)

```
```{figure} Simulation.png
---
height: 200px
---
```

```{r} ##################################################################
# Toy Example of California Smoking Example ######################################

## install.packages(tidysynth)

library(tidysynth) data("smoking") State <- unique(smoking$state)$N <- -length(unique(smoking$state))-1 Y <- smoking$cigsale[smoking$state=="California"] Tt <- length(Y) T0 <- 18 T1 <- Tt-T0 D <- matrix(0,Tt,N+1) for(jj in 1:(N+1)){ D[,jj] <- smoking$cigsale[smoking$state==State[jj]] } D <- D[,-which(State=="California")]

Y.Pre <- Y[1:T0] Y.Post <- Y[T0+1:T1] D.Pre <- D[1:T0,] D.Post <- D[T0+1:T1,]

### SPSC

### smaller regularization parameters return numeric error due to small sample size

SPSC.Smoking <- SPSC(Y.Pre = Y.Pre, Y.Post = Y.Post, W.Pre = D.Pre, W.Post = D.Post, detrend = TRUE, detrend.ft = function(t){matrix(c(1,t),1,2)}, Y.basis = function(y){matrix(c(y),1,1)}, att.ft = function(t){matrix(c(1,t),1,2)}, lambda.type = "cv", lambda.value = NULL, lambda.grid = seq(-1,2,by=0.5), bootstrap.num = 100, conformal.period = NULL, conformal.cover = FALSE, true.effect = NULL, conformal.interval = FALSE, conformal.pvalue = 0.05)

cbind(SPSC.Smoking$ATT-1.96*SPSC.Smoking$ASE.ATT, SPSC.Smoking$ATT+1.96*SPSC.Smoking$ASE.ATT)

cbind(SPSC.Smoking$ATT-1.96*SPSC.Smoking$BSE.ATT, SPSC.Smoking$ATT+1.96*SPSC.Smoking$BSE.ATT)

### Graphical summary

plot.SPSC(SPSC.Smoking) "'