

report22

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5/19/2021

data

```
vote <- read.csv("./codes/vote_data.csv")
str(vote)

## 'data.frame': 19775 obs. of 10 variables:
## $ from_requirement_threshold: num 0.4789 0.3838 0.0979 0.4568 0.4089 ...
## $ major.requirement : int 1 1 1 1 1 1 1 1 1 ...
## $ ISS.against.recommendation: int 0 0 1 0 0 0 0 1 0 0 ...
## $ shares.outstanding.base : int 0 1 0 0 0 0 0 1 0 0 ...
## $ special.meeting : int 0 0 0 0 0 0 0 0 0 0 ...
## $ analyst.coverage : num 0.693 0.693 1.386 1.792 1.946 ...
## $ institutional.ownership : num 0.563 0.563 1 1 0.968 ...
## $ past.stock.return : num 0.506 0.506 0.38 0.388 -0.149 ...
## $ q : num 5.68 5.68 1.18 1.46 1.11 ...
## $ firm.size : num 5.37 5.37 6.6 6.89 7.31 ...

vote <- subset(vote, abs(from_requirement_threshold) < 0.5)
bunch <- FALSE
pos.est <- TRUE
N_para <- 6
p <- 6

get.trim.data <- function(trim){
  vote <- subset(vote, abs(from_requirement_threshold) < trim/2)
  preds <- model.matrix(~ #major.requirement
                        + ISS.against.recommendation
                        #+ shares.outstanding.base
                        #+ special.meeting
                        + analyst.coverage
                        #+ institutional.ownership
                        + past.stock.return
                        + q
                        + firm.size,
                        data = vote) [, -1]
  preds.all <- scale(preds)
  x <- cbind(1, preds.all)
  dimnames(x)[[2]][1] <- "Intercept"
```

```

x.names <- dimnames(x)[[2]]
y <- 2*vote[, "from_requirement_threshold"]
return(list(x=x, y=y))
}

get.result.CI <- function(result_trim07_order2, N_para = 6, p = 6){
  result_CI_t7o2 <- data.frame()
  for(i in 1:N_para){
    one_set_r <- apply(result_trim07_order2[[i]]$a, 1, function(x) quantile(x, c(0.025, 0.975)))
    for(j in 1:p){
      result_CI_t7o2 <- rbind(result_CI_t7o2,
                                  data.frame(lower = one_set_r[1,j],
                                             upper = one_set_r[2,j],
                                             variable = paste0("a", j),
                                             setting = as.character(i)))
    }
  }
  rownames(result_CI_t7o2) <- NULL
  return(result_CI_t7o2)
}

```

order = 2

trimming = 0.5

```

set.seed(123)
order <- 2
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))
a_init <- replicate(N_para, rnorm(n = p, sd = 1.5))

data_trim05 <- get.trim.data(0.5)

result_trim05_order2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim_alphaPG(y=data_trim05$y, x=data_trim05$x, b=b_init[,i],
                                      burn=15000, nsamp=25000, thin=1, trim = 0.5, order = 2,
                                      jump=list(a=a_init[,i], prec = 1, positive=pos.est,
                                                 persistence=0.8, update.jbw=TRUE))

load("./report/report22/result_trim05_order2.RData")
result_CI_t5o2 <- get.result.CI(result_trim05_order2)

result_trim05_order2_coda <- multi_chain_coda(result_trim05_order2,
                                                burn = 15000, N_para, p, order = 2)
plot(result_trim05_order2_coda)
gelman.diag(result_trim05_order2_coda)
summary(result_trim05_order2_coda)

ggplot(result_CI_t5o2, aes(x = variable, colour = setting)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)

```

trimming = 0.6

```
set.seed(123)
order <- 2
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))
a_init <- replicate(N_para, rnorm(n = p, sd = 1.5))

data_trim06 <- get.trim.data(0.6)

result_trim06_order2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim_alphanoPG(y=data_trim06$y, x=data_trim06$x, b=b_init[, , i],
                                         burn=15000, nsamp=25000, thin=1, trim = 0.6, order = 2,
                                         jump=list(a=a_init[, i], prec = 1, positive=pos.est,
                                                    persistence=0.8, update.jbw=TRUE))

load("./report/report22/result_trim06_order2.RData")
result_CI_t6o2 <- get.result.CI(result_trim06_order2)

result_trim06_order2_coda <- multi_chain_coda(result_trim06_order2,
                                                burn = 15000, N_para, p, order = 2)
plot(result_trim06_order2_coda)
gelman.diag(result_trim06_order2_coda)
summary(result_trim06_order2_coda)

ggplot(result_CI_t6o2, aes(x = variable, colour = setting)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)
```

trimming = 0.7

```
set.seed(123)
order <- 2
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))
a_init <- replicate(N_para, rnorm(n = p, sd = 1.5))

data_trim07 <- get.trim.data(0.7)

result_trim07_order2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim_alphanoPG(y=data_trim07$y, x=data_trim07$x, b=b_init[, , i],
                                         burn=15000, nsamp=25000, thin=1, trim = 0.7, order = 2,
                                         jump=list(a=a_init[, i], prec = 1, positive=pos.est,
                                                    persistence=0.8, update.jbw=TRUE))

load("./report/report22/result_trim07_order2.RData")
result_CI_t7o2 <- get.result.CI(result_trim07_order2)

result_trim07_order2_coda <- multi_chain_coda(result_trim07_order2,
                                                burn = 15000, N_para, p, order = 2)
plot(result_trim07_order2_coda)
gelman.diag(result_trim07_order2_coda)
summary(result_trim07_order2_coda)
```

```
ggplot(result_CI_t7o2, aes(x = variable, colour = setting)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)
```

order = 3

trimming = 0.5

```
set.seed(123)
order <- 2
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))
a_init <- replicate(N_para, rnorm(n = p, sd = 1.5))

data_trim05 <- get.trim.data(0.5)

result_trim05_order3 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim_alphanoPG(y=data_trim05$y, x=data_trim05$x, b=b_init[,i],
                                         burn=15000, nsamp=25000, thin=1, trim = 0.5, order = 3,
                                         jump=list(a=a_init[,i], prec = 1, positive=pos.est,
                                                    persistence=0.8, update.jbw=TRUE))

load("./report/report22/result_trim05_order3.RData")
result_CI_t5o3 <- get.result.CI(result_trim05_order3)

result_trim05_order3_coda <- multi_chain_coda(result_trim05_order3,
                                                burn = 15000, N_para, p, order = 3)
plot(result_trim05_order3_coda)
gelman.diag(result_trim05_order3_coda)
summary(result_trim05_order3_coda)

ggplot(result_CI_t5o3, aes(x = variable, colour = setting)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)
```

trimming = 0.6

```
set.seed(123)
order <- 2
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))
a_init <- replicate(N_para, rnorm(n = p, sd = 1.5))

data_trim06 <- get.trim.data(0.6)

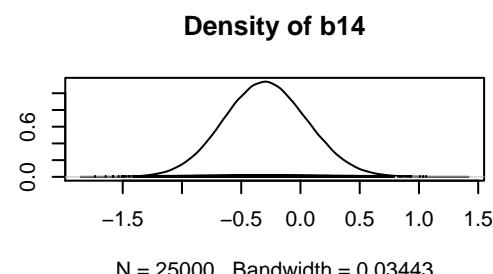
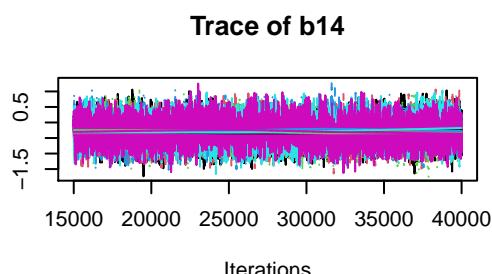
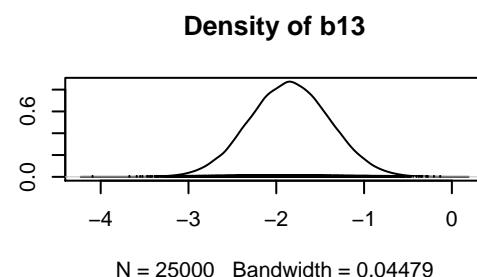
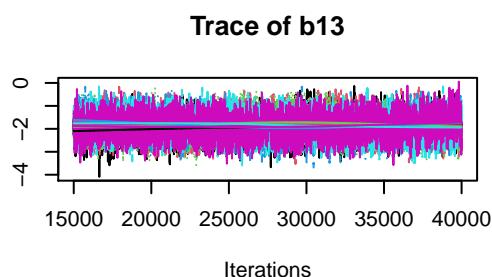
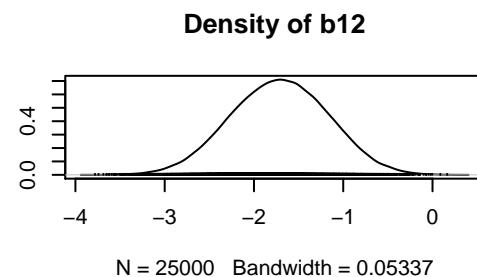
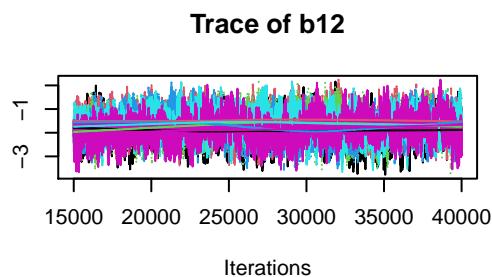
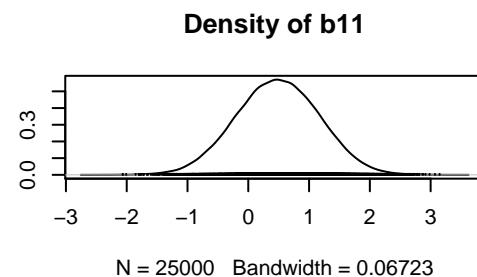
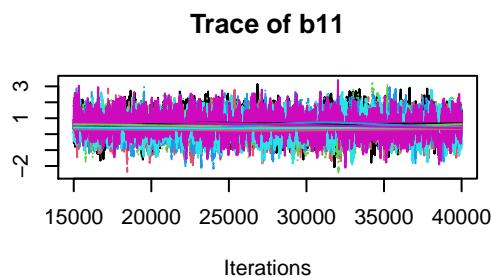
result_trim06_order3 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim_alphanoPG(y=data_trim06$y, x=data_trim06$x, b=b_init[,i],
                                         burn=15000, nsamp=25000, thin=1, trim = 0.6, order = 3,
                                         jump=list(a=a_init[,i], prec = 1, positive=pos.est,
                                                    persistence=0.8, update.jbw=TRUE))
```

```

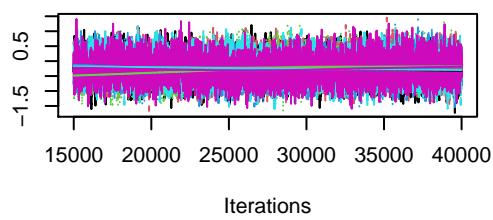
load("./report/report22/result_trim06_order3.RData")
result_CI_t6o3 <- get.result.CI(result_trim06_order3)

result_trim06_order3_coda <- multi_chain_coda(result_trim06_order3,
                                                burn = 15000, N_para, p, order = 3)
plot(result_trim06_order3_coda)

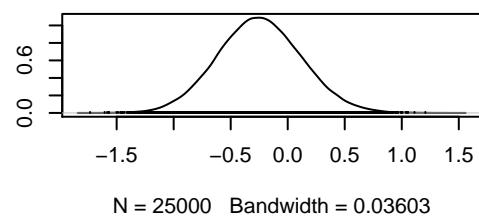
```



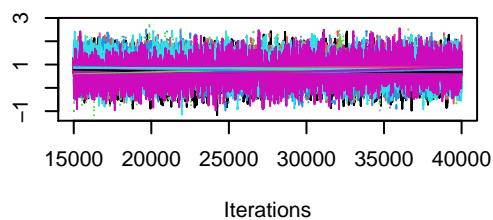
Trace of b15



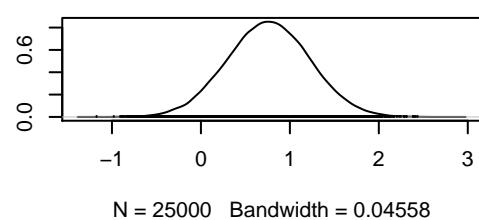
Density of b15



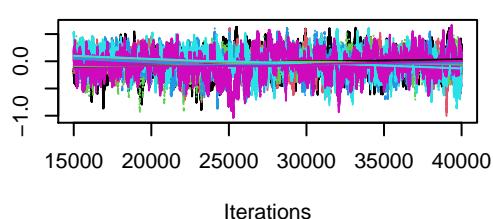
Trace of b16



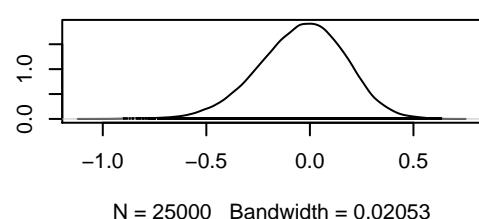
Density of b16



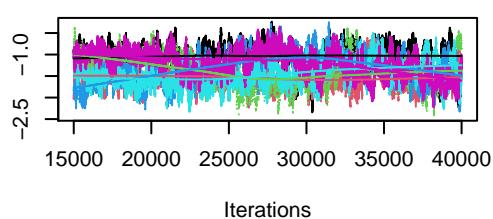
Trace of b21



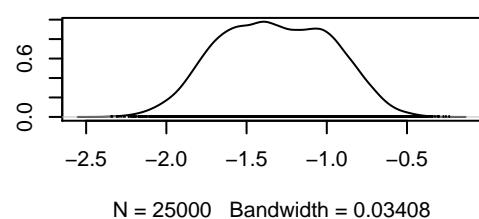
Density of b21



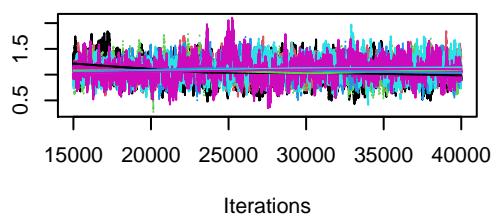
Trace of b22



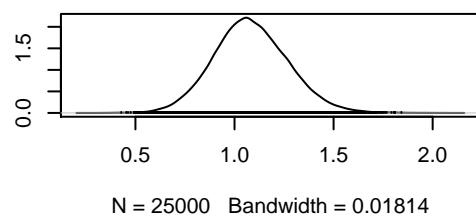
Density of b22



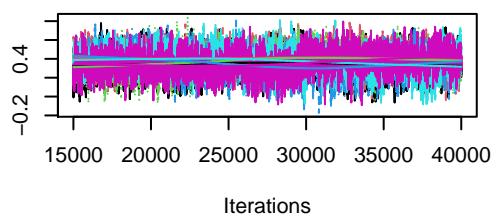
Trace of b23



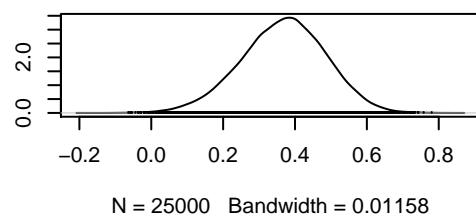
Density of b23



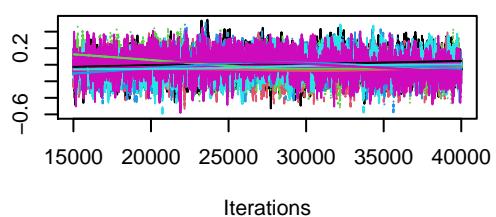
Trace of b24



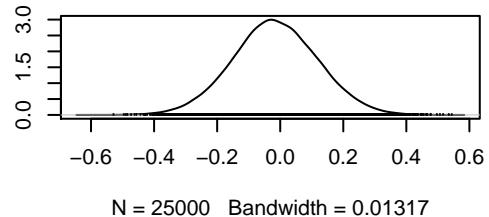
Density of b24



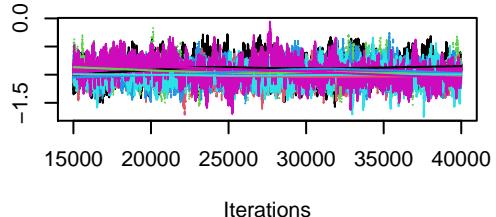
Trace of b25



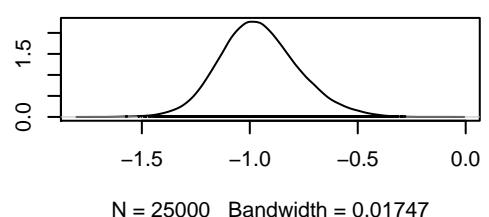
Density of b25



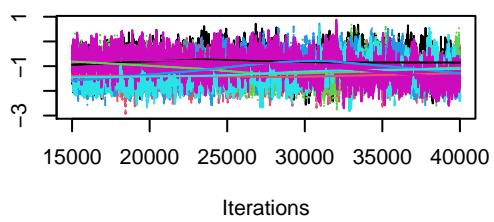
Trace of b26



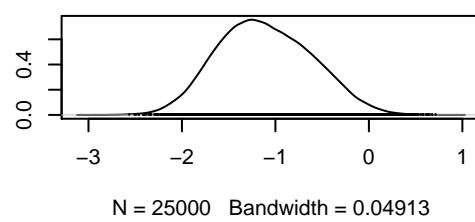
Density of b26



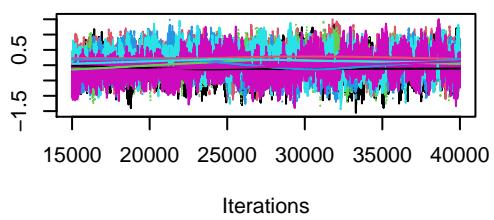
Trace of b31



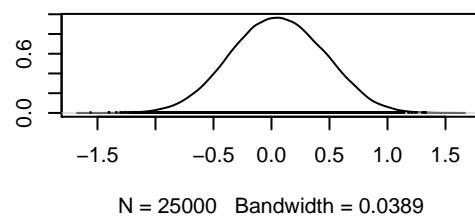
Density of b31



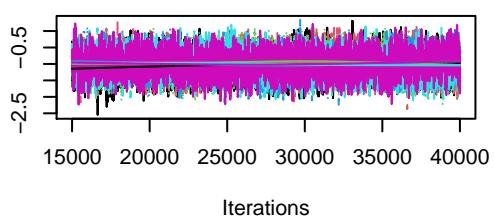
Trace of b32



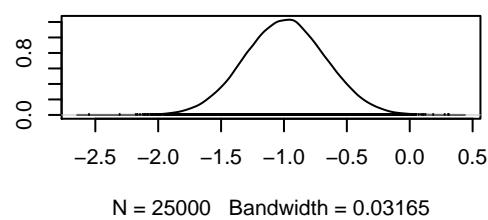
Density of b32



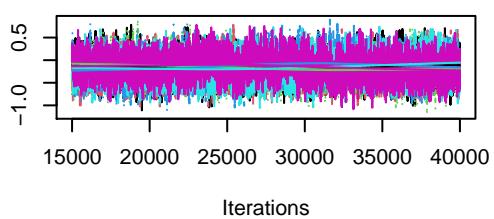
Trace of b33



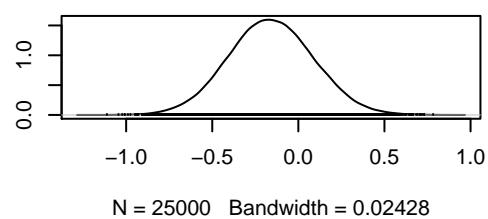
Density of b33



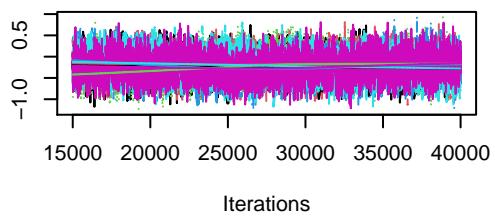
Trace of b34



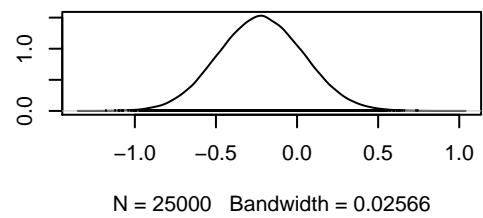
Density of b34



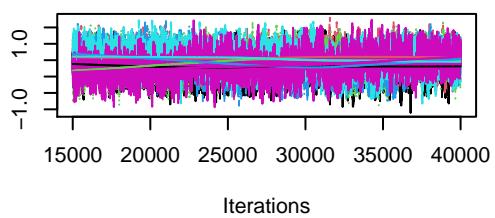
Trace of b35



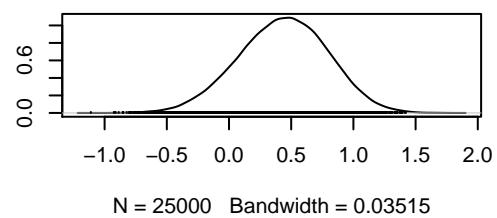
Density of b35



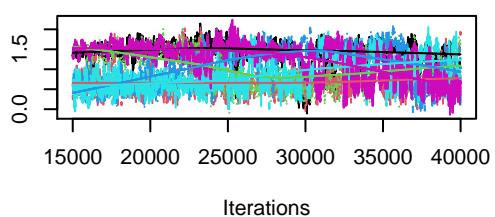
Trace of b36



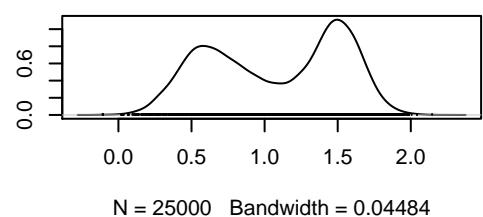
Density of b36



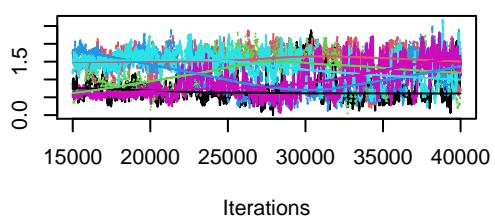
Trace of a1



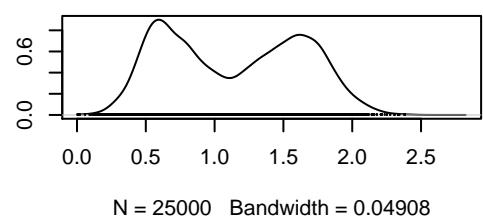
Density of a1

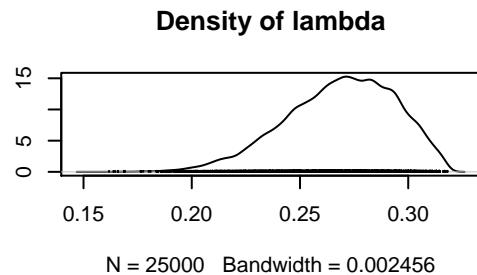
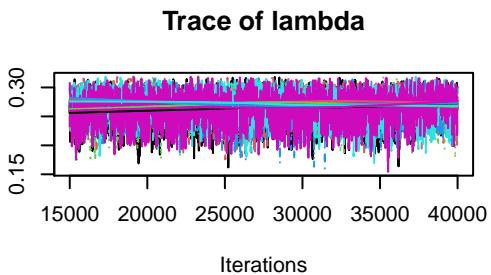
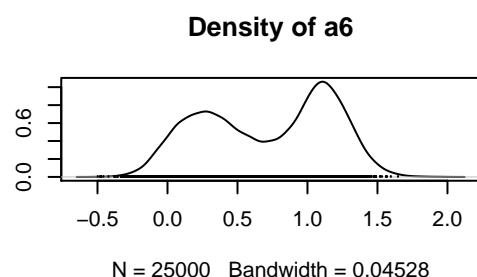
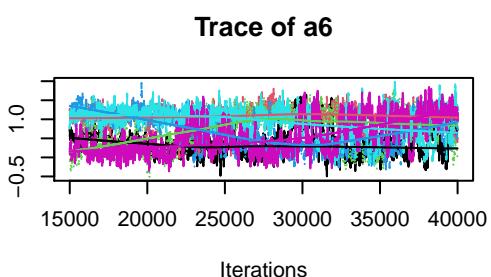
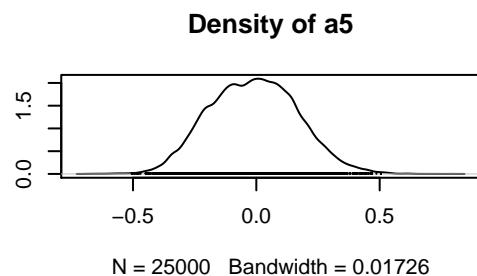
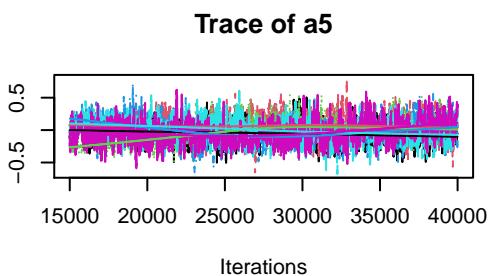
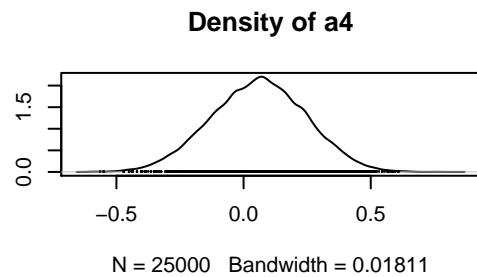
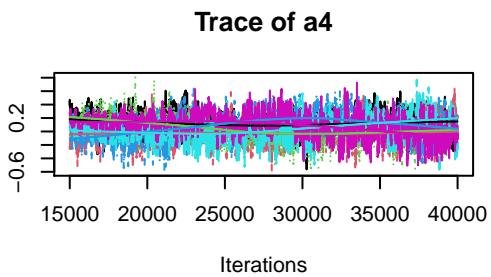
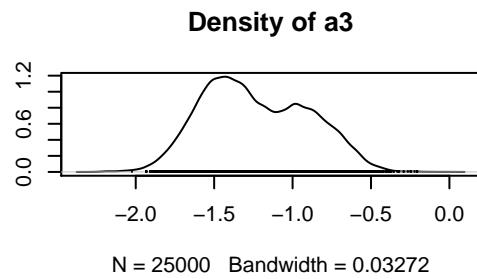
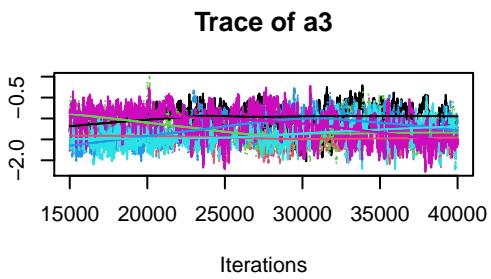


Trace of a2



Density of a2





```
gelman.diag(result_trim06_order3_coda)
```

```
## Potential scale reduction factors:
```

```

##          Point est. Upper C.I.
## b11           1.03    1.07
## b12           1.05    1.11
## b13           1.01    1.02
## b14           1.00    1.01
## b15           1.00    1.01
## b16           1.01    1.03
## b21           1.01    1.01
## b22           1.17    1.39
## b23           1.02    1.05
## b24           1.03    1.08
## b25           1.03    1.07
## b26           1.07    1.16
## b31           1.11    1.25
## b32           1.06    1.15
## b33           1.00    1.01
## b34           1.01    1.02
## b35           1.01    1.02
## b36           1.06    1.14
## a1            1.18    1.41
## a2            1.22    1.49
## a3            1.20    1.46
## a4            1.06    1.15
## a5            1.04    1.10
## a6            1.22    1.50
## lambda        1.01    1.02
##
## Multivariate psrf
##
## 1.2

ggplot(result_CI_t6o3, aes(x = variable, colour = setting)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)

```

trimming = 0.7

```

set.seed(123)
order <- 2
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))
a_init <- replicate(N_para, rnorm(n = p, sd = 1.5))

data_trim07 <- get.trim.data(0.7)

result_trim07_order3 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim_alphanoPG(y=data_trim07$y, x=data_trim07$x, b=b_init[,i],
                                         burn=15000, nsamp=25000, thin=1, trim = 0.7, order = 3,
                                         jump=list(a=a_init[,i], prec = 1, positive=pos.est,
                                                    persistence=0.8, update.jbw=TRUE))

```

```

load("./report/report22/result_trim07_order3.RData")
result_CI_t7o3 <- get.result.CI(result_trim07_order3)

result_trim07_order3_coda <- multi_chain_coda(result_trim07_order3,
                                                burn = 15000, N_para, p, order = 3)
plot(result_trim07_order3_coda)
gelman.diag(result_trim07_order3_coda)
summary(result_trim07_order3_coda)

ggplot(result_CI_t7o3, aes(x = variable, colour = setting)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)

```

alpha CI plot

```

result_CI_t5o2$type = "t5o2"
result_CI_t6o2$type = "t6o2"
result_CI_t7o2$type = "t7o2"
result_CI_t5o3$type = "t5o3"
result_CI_t6o3$type = "t6o3"
result_CI_t7o3$type = "t7o3"

result_CI <- rbind(result_CI_t5o2,
                     result_CI_t6o2,
                     result_CI_t7o2,
                     result_CI_t5o3,
                     result_CI_t6o3,
                     result_CI_t7o3)

result_CI %>%
  mutate(across(type, factor,
               levels=c("t5o2","t6o2","t7o2",
                       "t5o3","t6o3","t7o3"))) %>%
  ggplot(aes(x = variable, colour = setting)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2) +
  facet_wrap(vars(type))

```

