

report19

Haoliang Zheng

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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))
}

```

adapt alpha, only alpha no PG, others not change

trim = 0.5, order = 2

```

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)

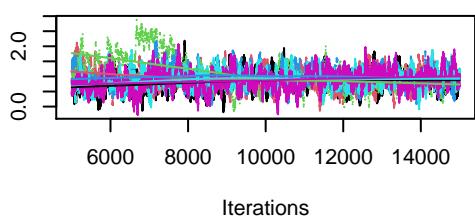
multi_adapt_poly_trim05_o2_alphaPG2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim_alphaPG(y=data_trim05$y, x=data_trim05$x, b=b_init[, , i],
                                      burn=5000, nsamp=10000, thin=1, trim = 0.5, order = 2,
                                      jump=list(a=a_init[, i], prec = 1, positive=pos.est,
                                                 persistence=0.8, update.jbw=FALSE))

load("./report/report19/multi_adapt_poly_trim05_o2_alphaPG2.RData")

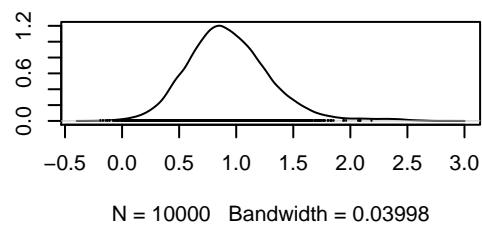
multi_adapt_poly_trim05_o2_alphaPG_coda2 <- multi_chain_coda(multi_adapt_poly_trim05_o2_alphaPG2,
                                                               burn = 5000, N_para, p, order = 2)
plot(multi_adapt_poly_trim05_o2_alphaPG_coda2)

```

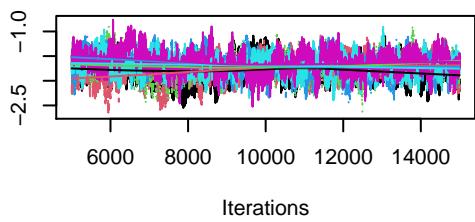
Trace of b_{11}



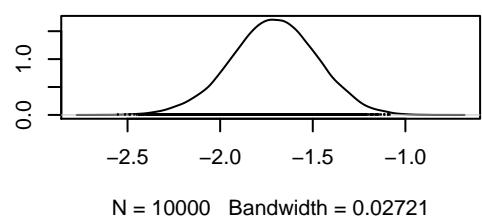
Density of b_{11}



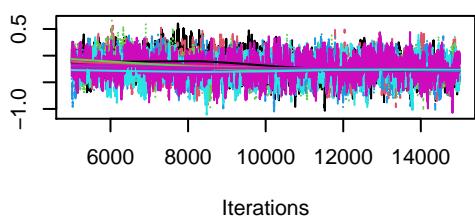
Trace of b_{12}



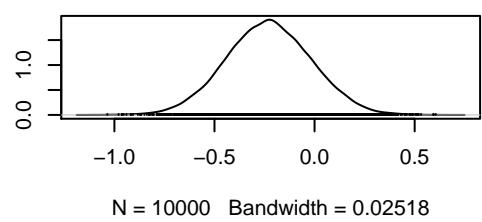
Density of b_{12}



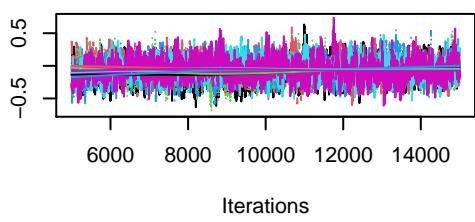
Trace of b_{13}



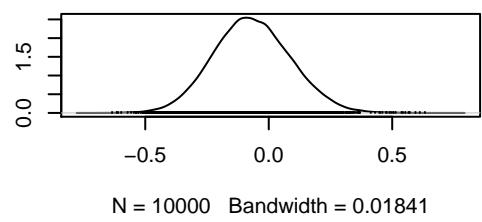
Density of b_{13}



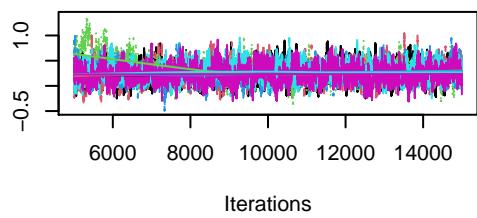
Trace of b_{14}



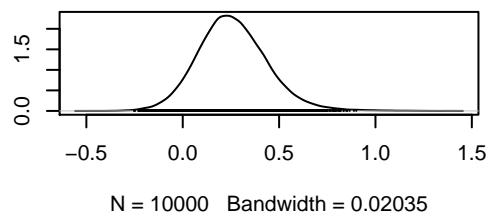
Density of b_{14}



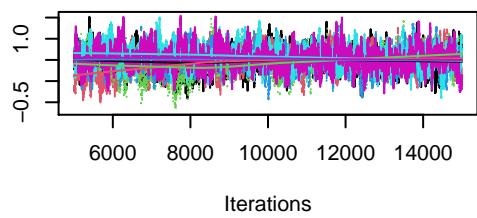
Trace of b15



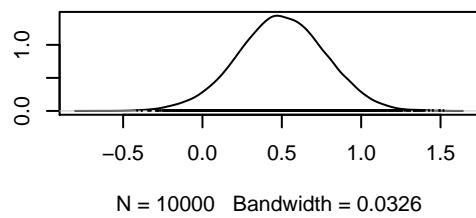
Density of b15



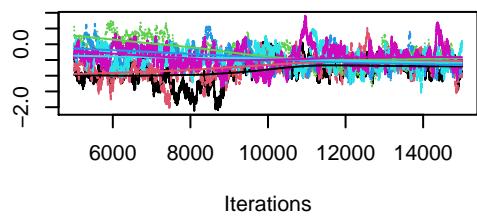
Trace of b16



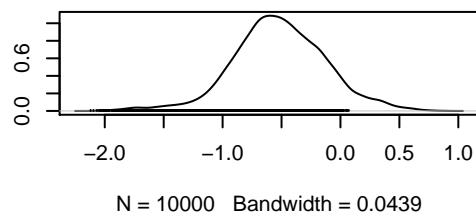
Density of b16



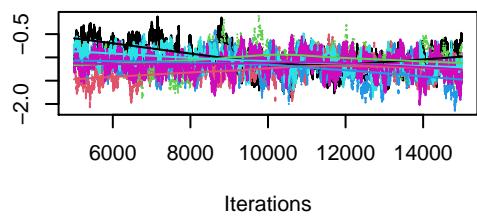
Trace of b21



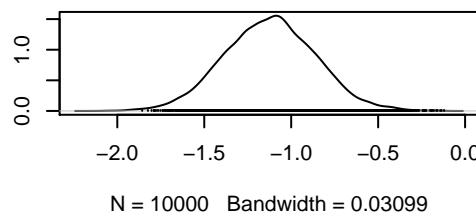
Density of b21



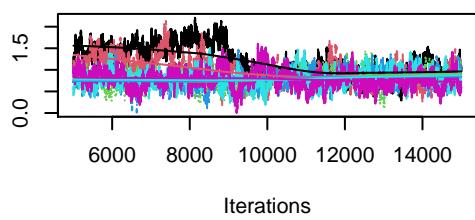
Trace of b22



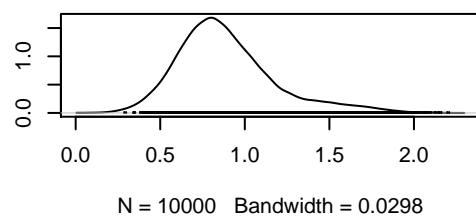
Density of b22



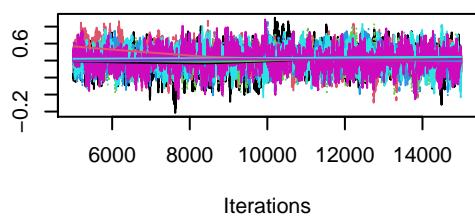
Trace of b23



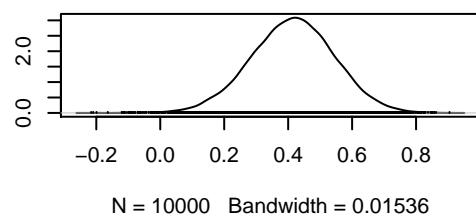
Density of b23



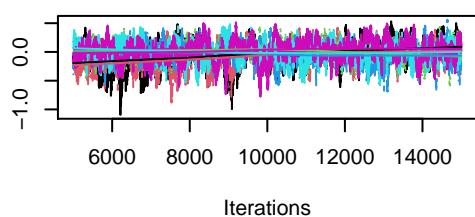
Trace of b24



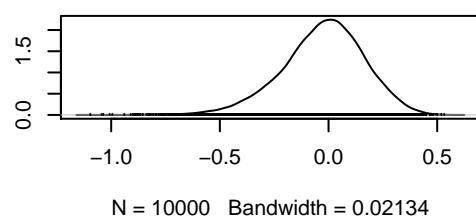
Density of b24



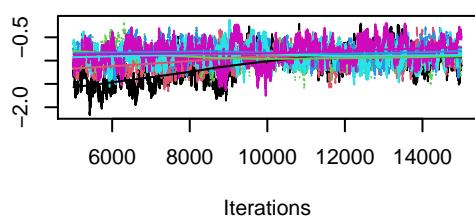
Trace of b25



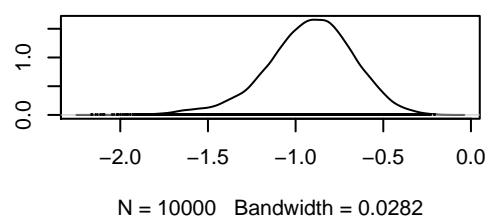
Density of b25

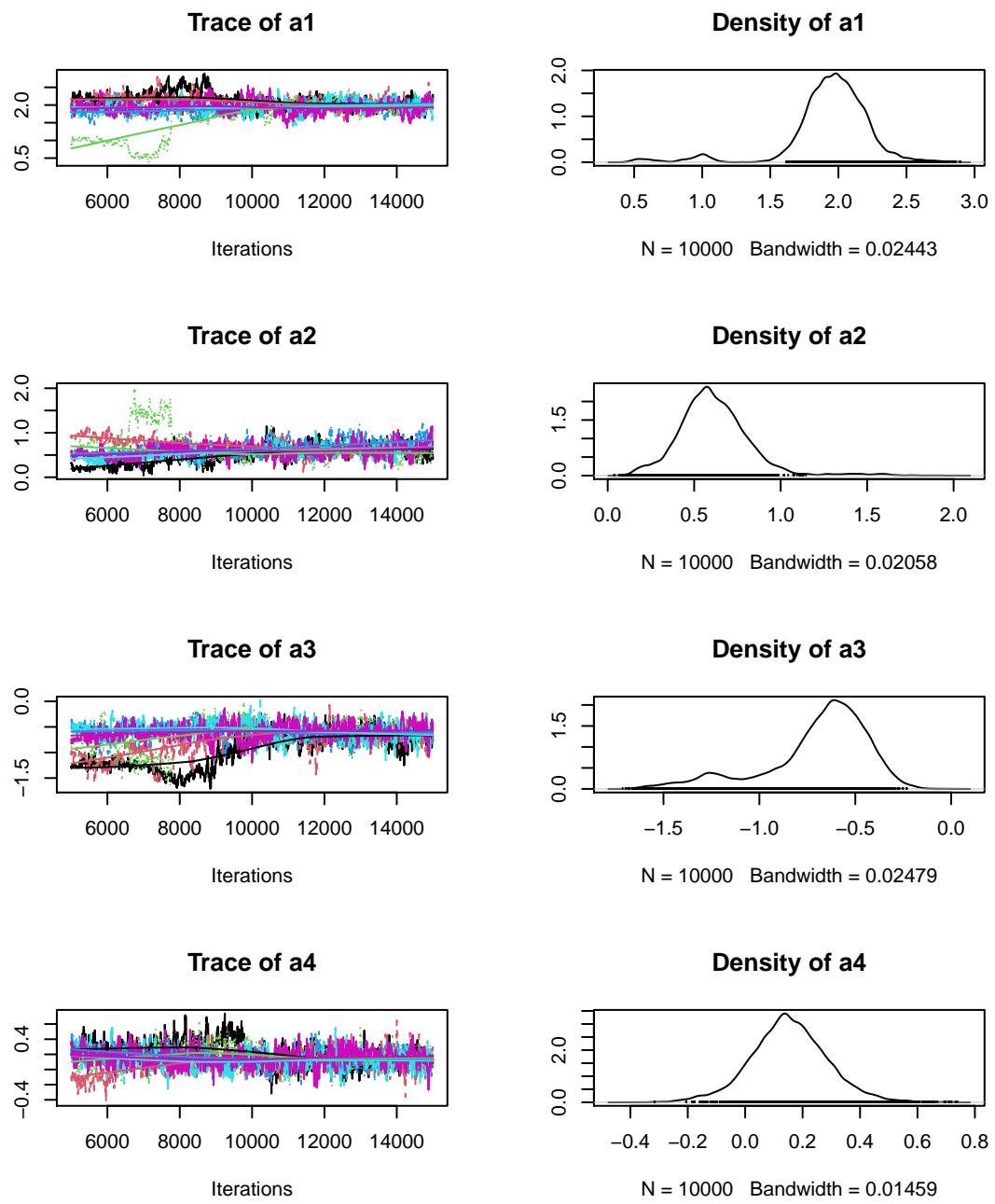


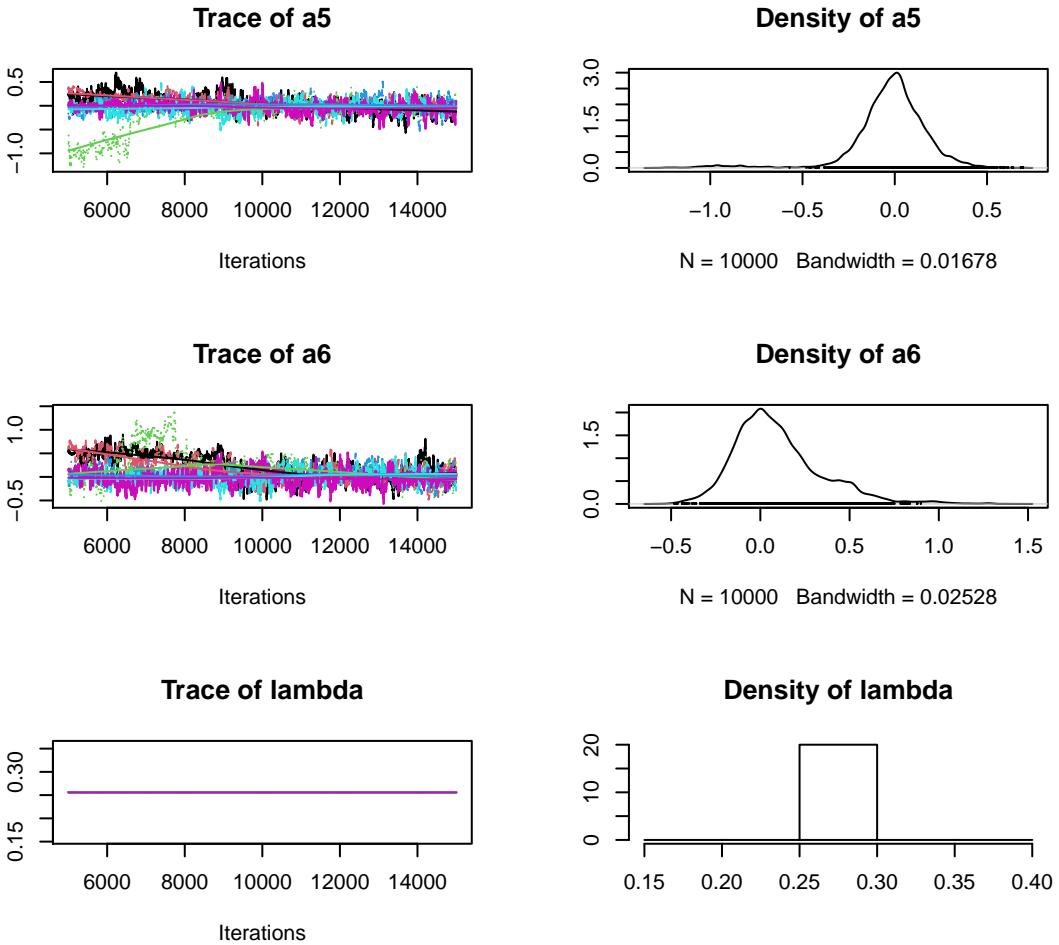
Trace of b26



Density of b26







adapt alpha, all PG, not change

```

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)

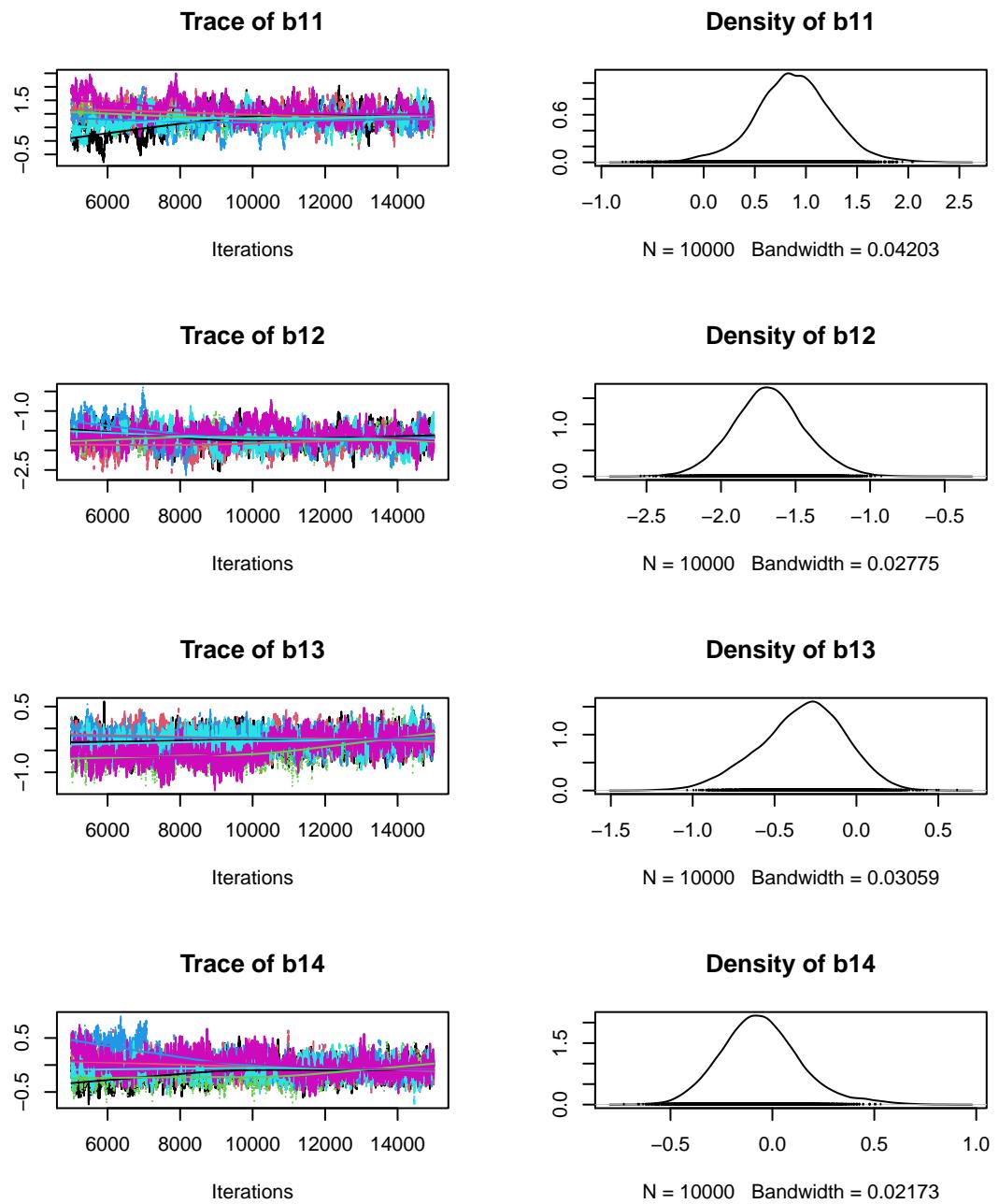
multi_adapt_poly_trim05_o2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim(y=data_trim05$y, x=data_trim05$x, b=b_init[,i],
    burn=5000, nsamp=10000, thin=1, trim = 0.5, order = 2,
    jump=list(a=a_init[,i], prec = 1, positive=pos.est,
      persistence=0.8, update.jbw=FALSE))

load("./report/report19/multi_adapt_poly_trim05_o2.RData")

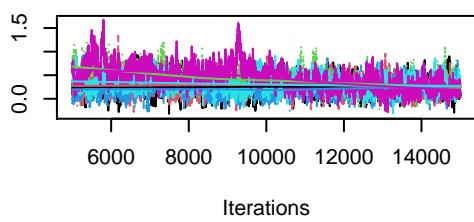
multi_adapt_poly_trim05_o2_coda <- multi_chain_coda(multi_adapt_poly_trim05_o2,
  burn = 5000, N_para, p, order = 2)

plot(multi_adapt_poly_trim05_o2_coda)

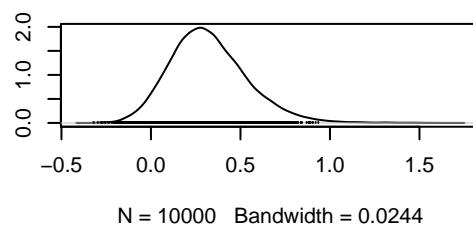
```



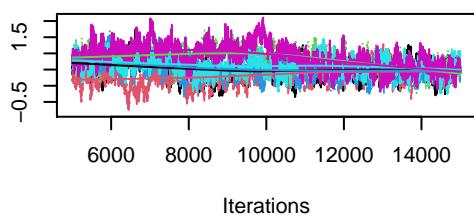
Trace of b15



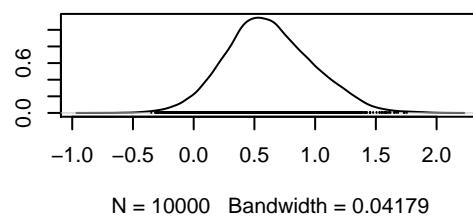
Density of b15



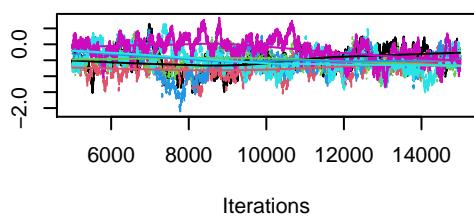
Trace of b16



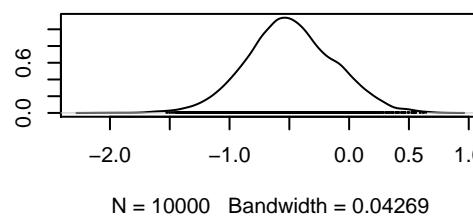
Density of b16



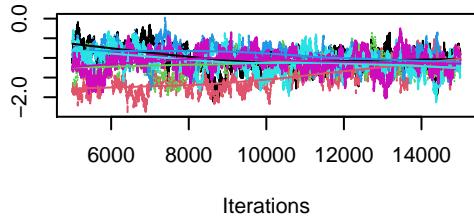
Trace of b21



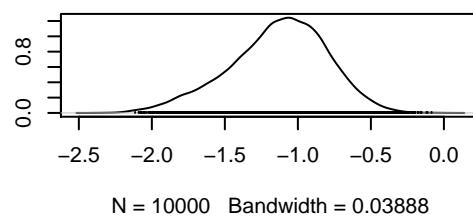
Density of b21



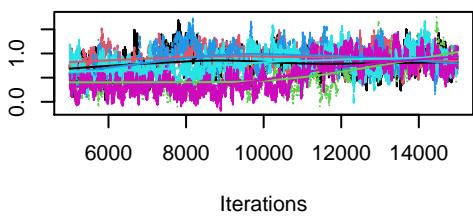
Trace of b22



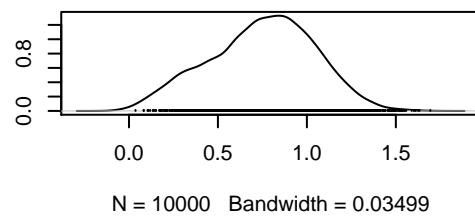
Density of b22



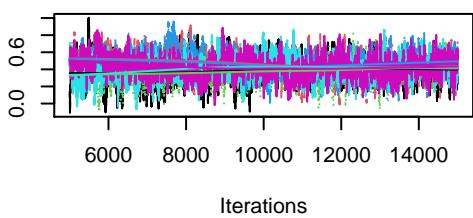
Trace of b23



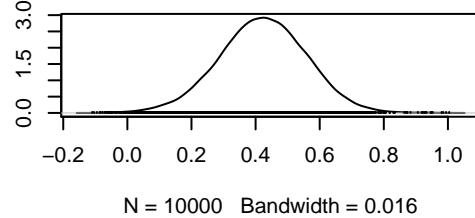
Density of b23



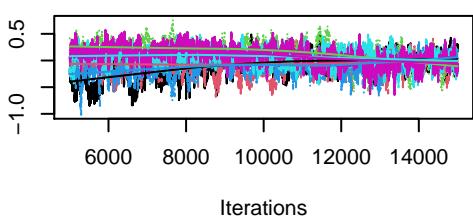
Trace of b24



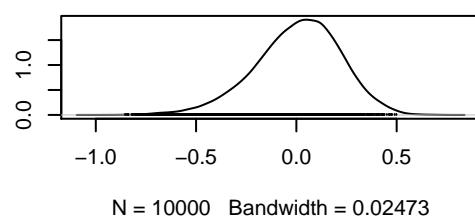
Density of b24



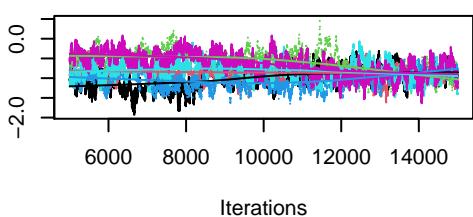
Trace of b25



Density of b25



Trace of b26



Density of b26

