

report18

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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))
}

```

trim, no alpha

trim = 0.5

```

set.seed(123)
order <- 3
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))

data_trim05 <- get.trim.data(0.5)

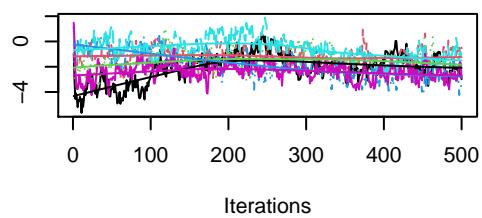
noa_multi_poly_trim05 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_poly_trim(y=data_trim05$y, x=data_trim05$x, b=b_init[, , i], burn=0, nsamp=500,
                           thin=1, trim = 0.5)

load("./report/report18/noa_multi_poly_trim05.RData")
noa_multi_poly_trim05_coda <- multi_chain_coda_noa(noa_multi_poly_trim05, burn = 0, N_para, p, order = 3)

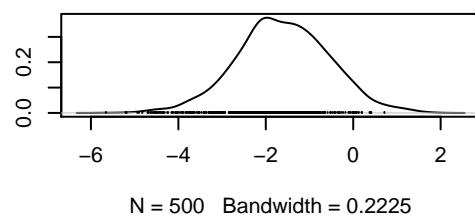
plot(noa_multi_poly_trim05_coda)

```

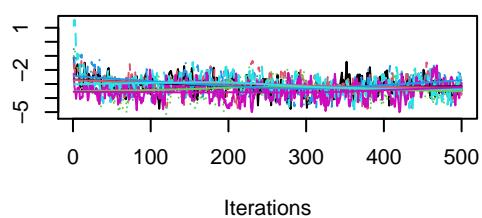
Trace of b_{11}



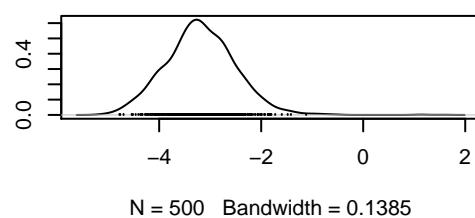
Density of b_{11}



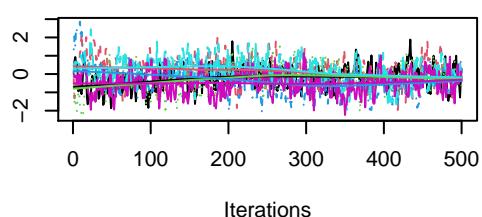
Trace of b_{12}



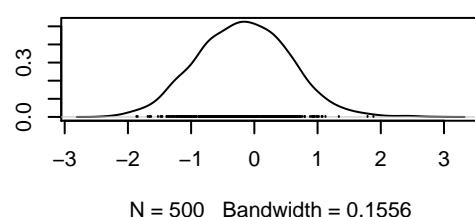
Density of b_{12}



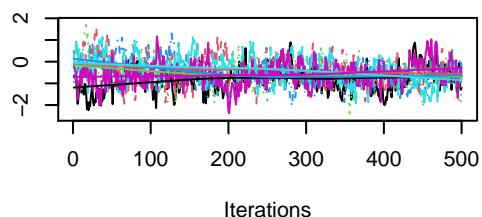
Trace of b_{13}



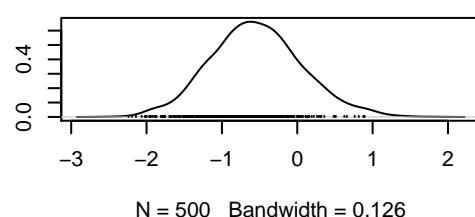
Density of b_{13}



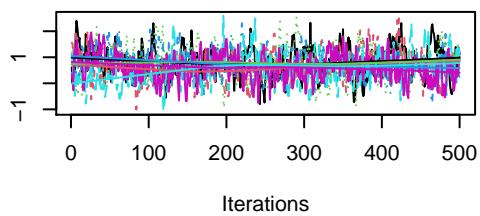
Trace of b_{14}



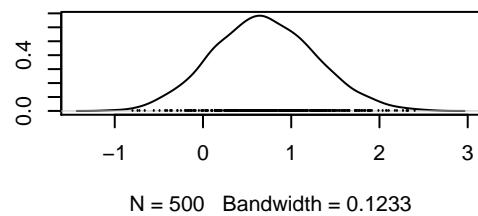
Density of b_{14}



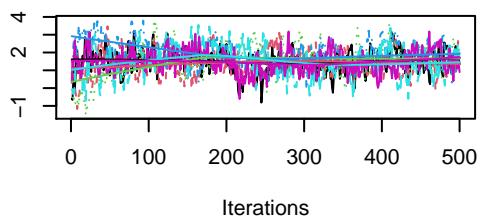
Trace of b15



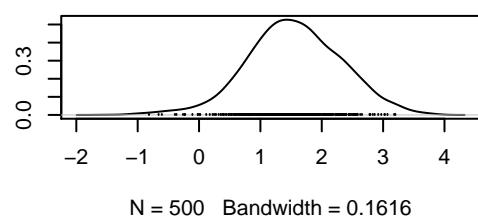
Density of b15



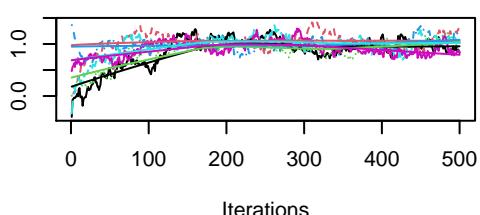
Trace of b16



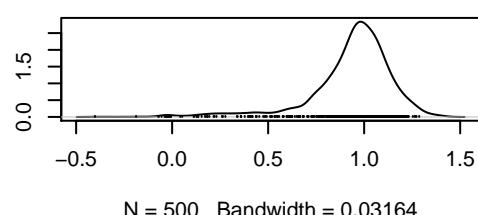
Density of b16



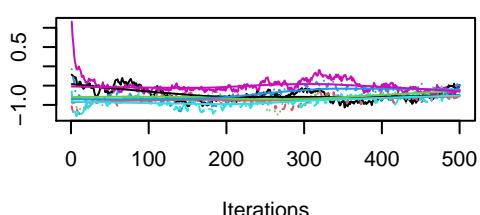
Trace of b21



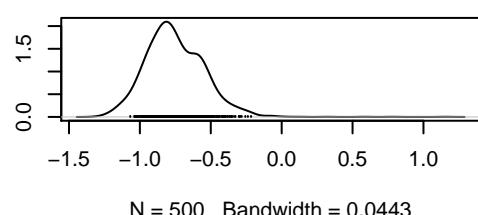
Density of b21



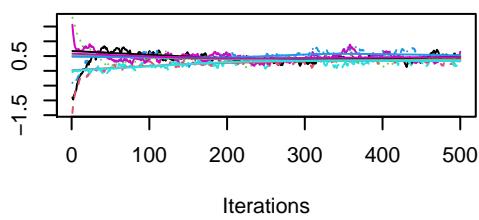
Trace of b22



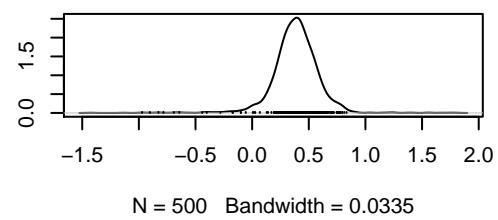
Density of b22



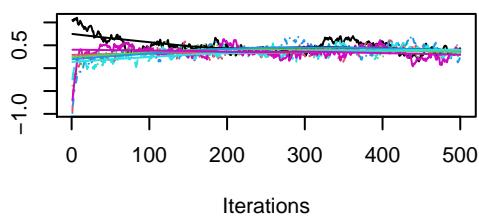
Trace of b23



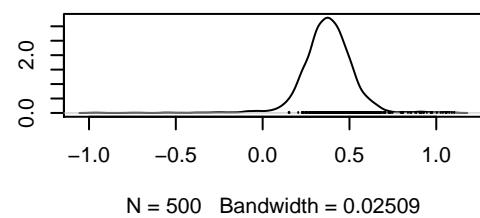
Density of b23



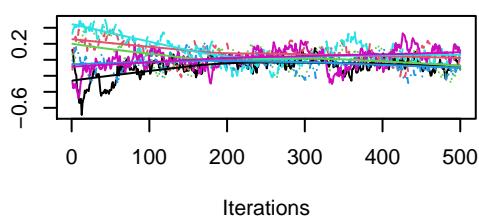
Trace of b24



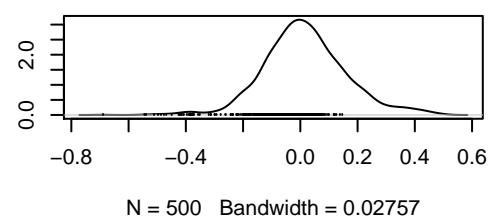
Density of b24



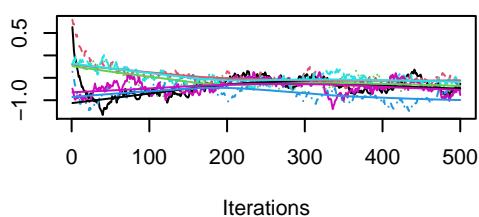
Trace of b25



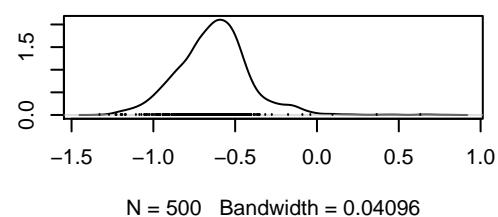
Density of b25



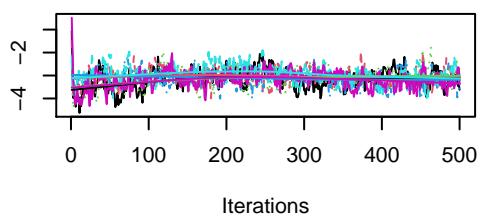
Trace of b26



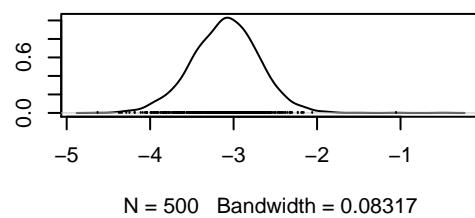
Density of b26



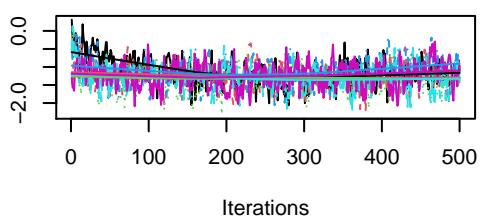
Trace of b31



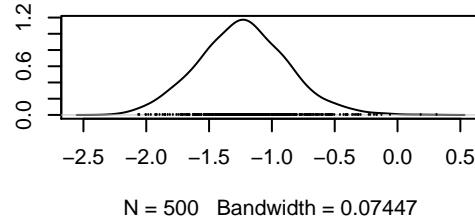
Density of b31



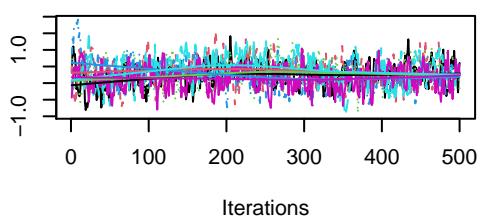
Trace of b32



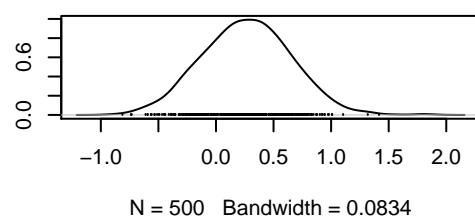
Density of b32



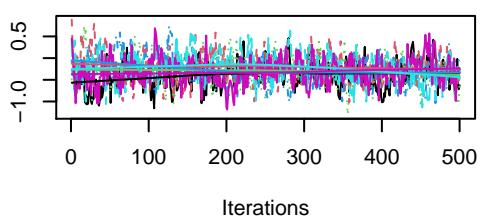
Trace of b33



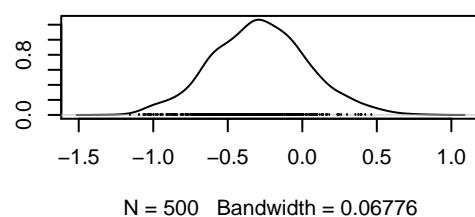
Density of b33

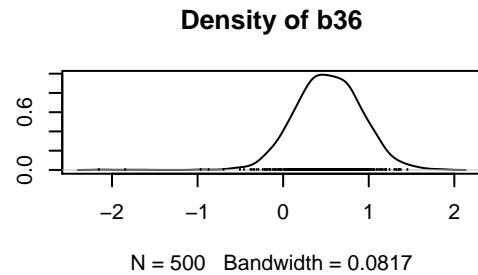
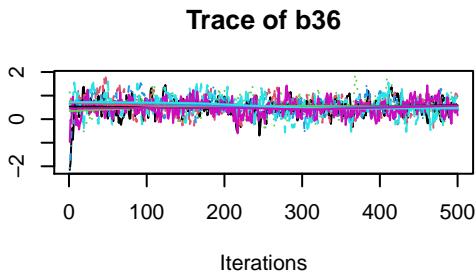
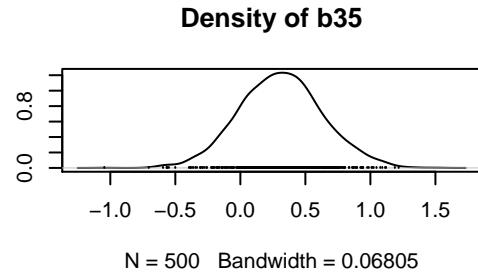
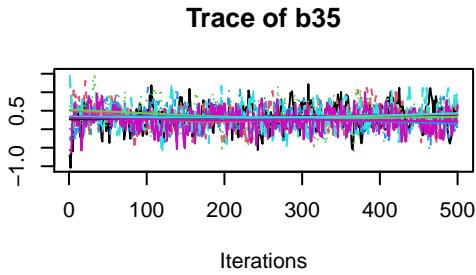


Trace of b34



Density of b34





`trim = 1, order = 3`

```

set.seed(123)
order <- 3
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))

data_trim1 <- get.trim.data(1)

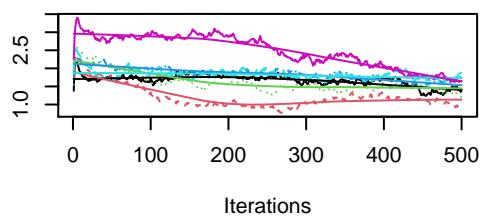
noa_multi_poly_trim1 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_poly_trim(y=data_trim1$y, x=data_trim1$x, b=b_init[,,i], burn=0, nsamp=500,
                           thin=1, trim = 1)

load("./report/report18/noa_multi_poly_trim1.RData")
noa_multi_poly_trim1_coda <- multi_chain_coda_noa(noa_multi_poly_trim1, burn = 0, N_para, p, order = 3)

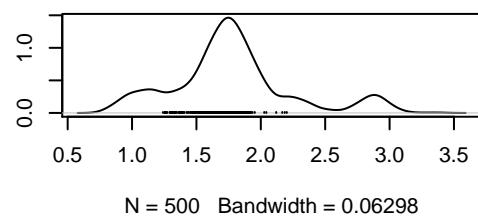
plot(noa_multi_poly_trim1_coda)

```

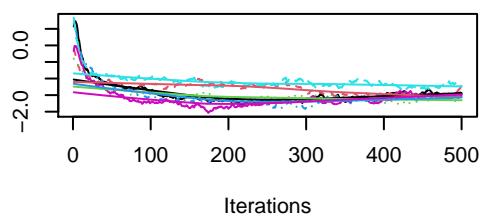
Trace of b_{11}



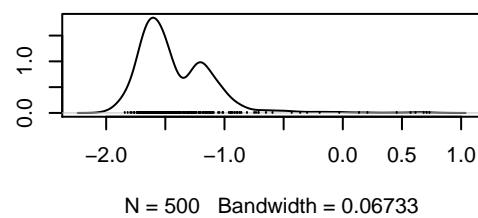
Density of b_{11}



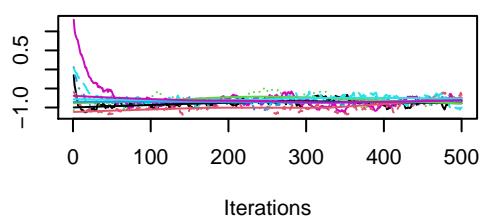
Trace of b_{12}



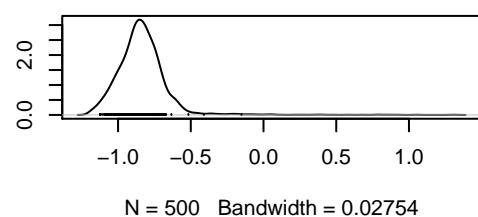
Density of b_{12}



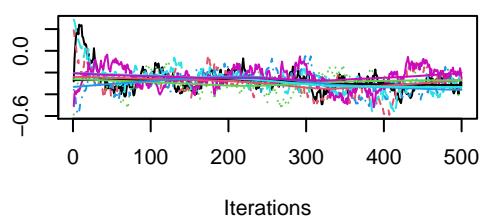
Trace of b_{13}



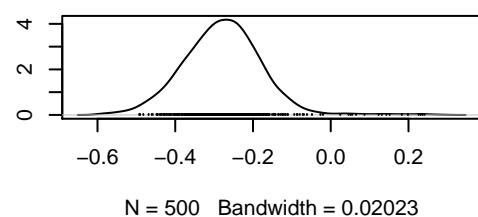
Density of b_{13}



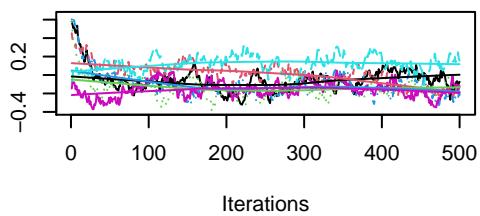
Trace of b_{14}



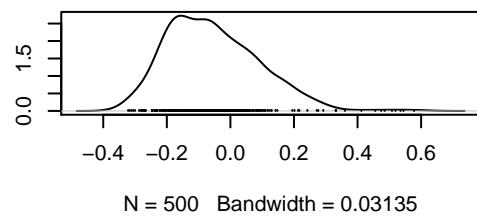
Density of b_{14}



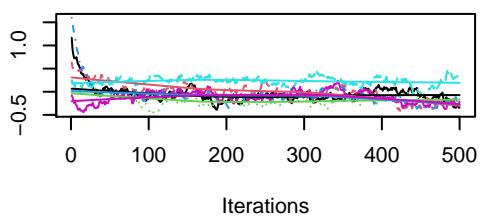
Trace of b15



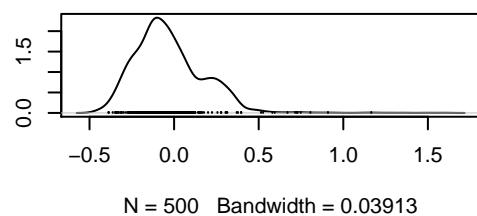
Density of b15



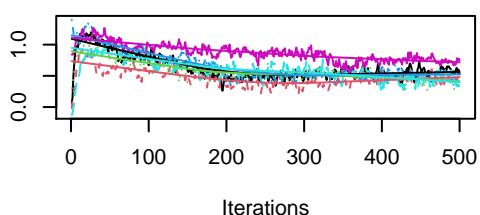
Trace of b16



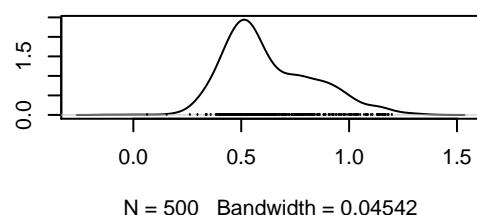
Density of b16



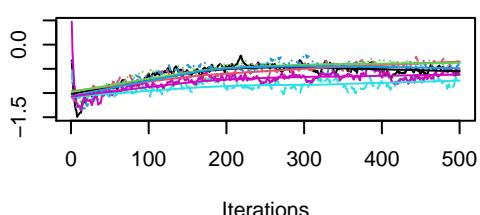
Trace of b21



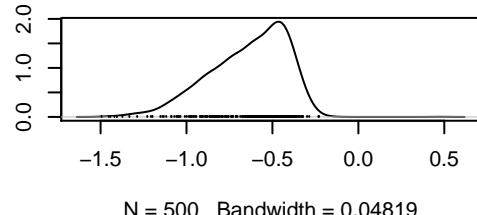
Density of b21



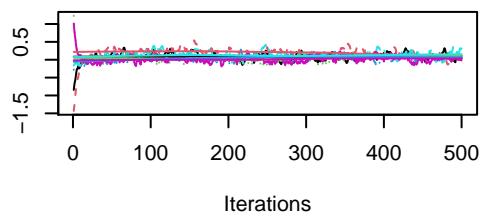
Trace of b22



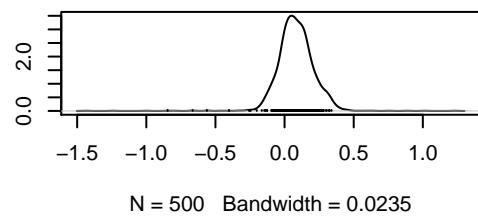
Density of b22



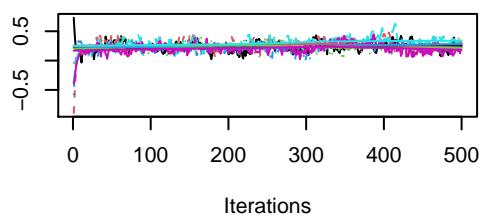
Trace of b23



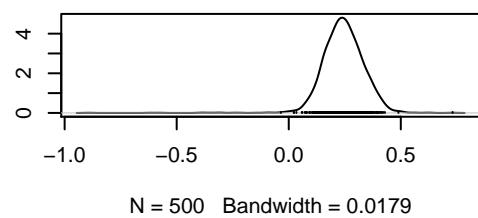
Density of b23



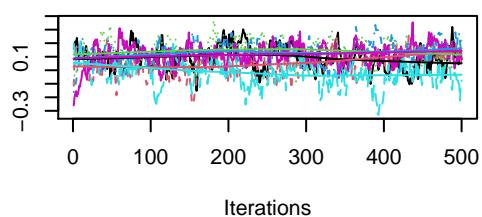
Trace of b24



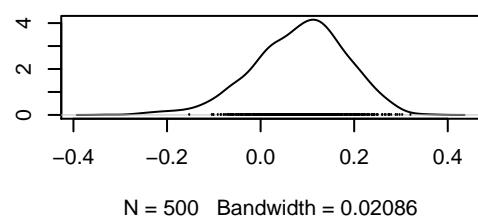
Density of b24



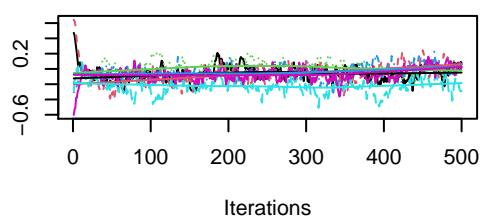
Trace of b25



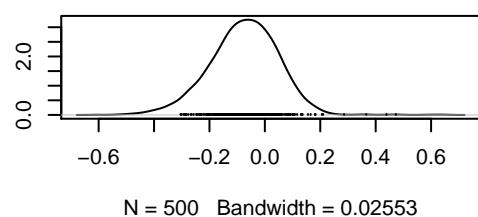
Density of b25



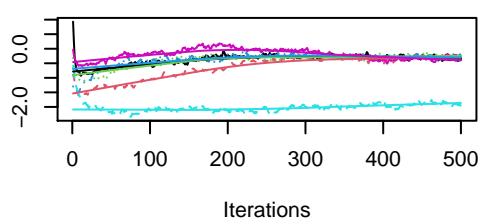
Trace of b26



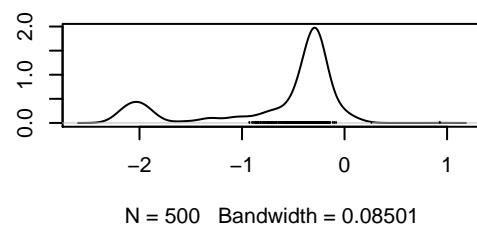
Density of b26



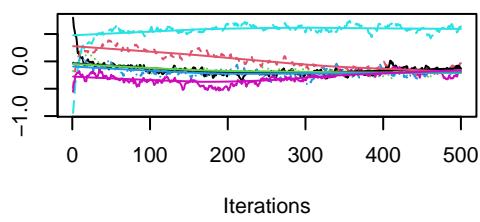
Trace of b31



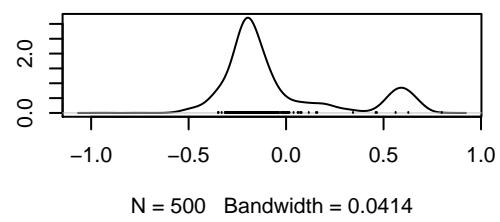
Density of b31



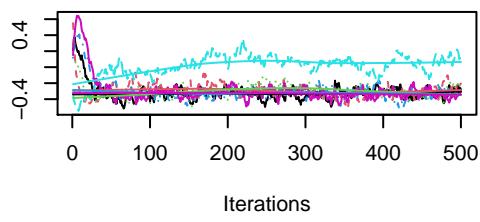
Trace of b32



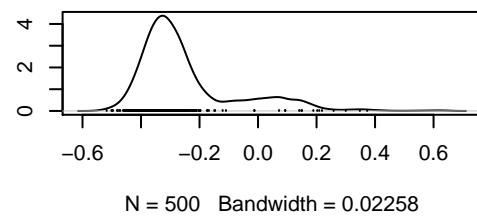
Density of b32



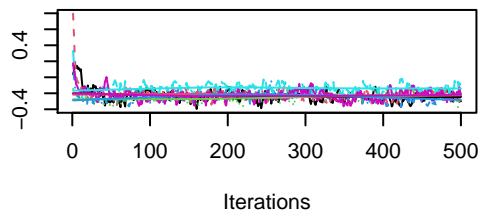
Trace of b33



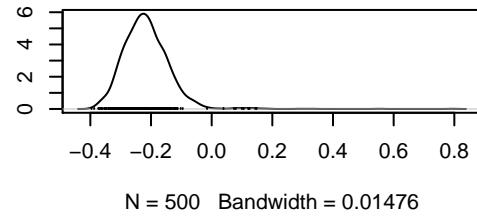
Density of b33

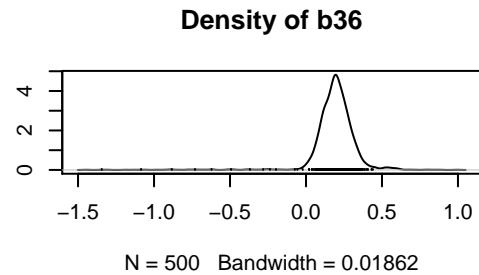
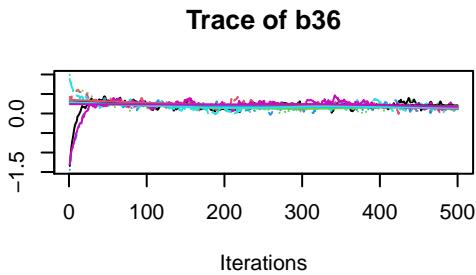
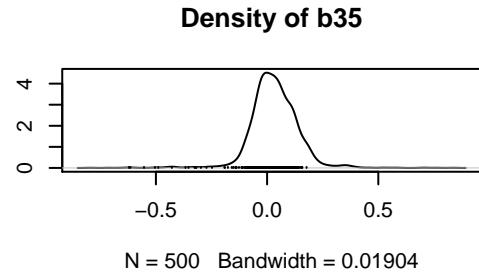
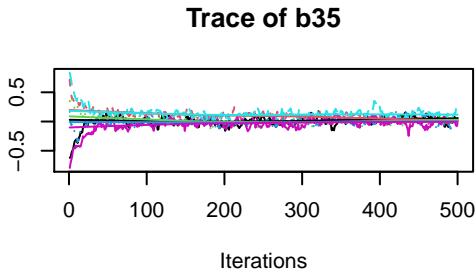


Trace of b34



Density of b34





trim = 1, order = 2

```

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

data_trim1 <- get.trim.data(1)

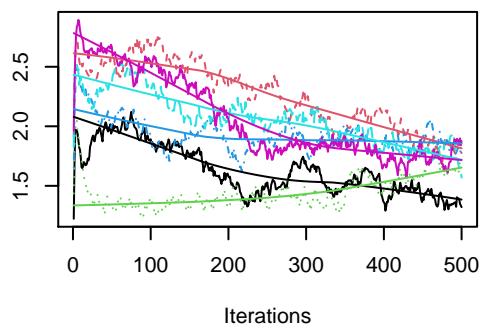
noa_multi_poly_trim1_o2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_poly_trim(y=data_trim1$y, x=data_trim1$x, b=b_init[,,i], burn=0, nsamp=500,
                           thin=1, trim = 1, order = 2)

load("./report/report18/noa_multi_poly_trim1_o2.RData")
noa_multi_poly_trim1_o2_coda <- multi_chain_coda_noa(noa_multi_poly_trim1_o2, burn = 0, N_para, p, order = 2)

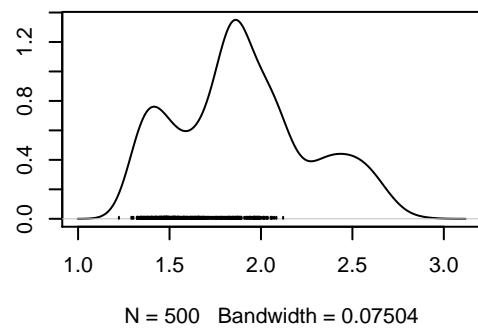
plot(noa_multi_poly_trim1_o2_coda)

```

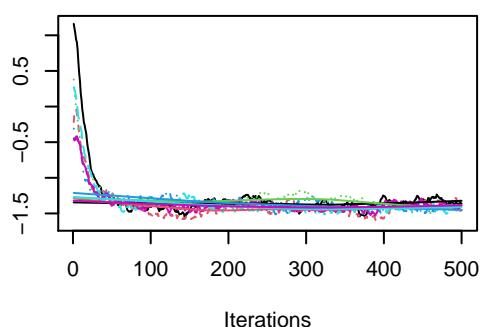
Trace of b_{11}



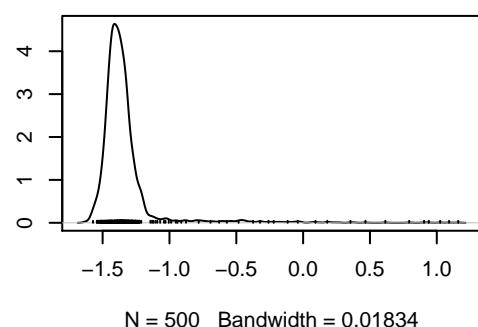
Density of b_{11}



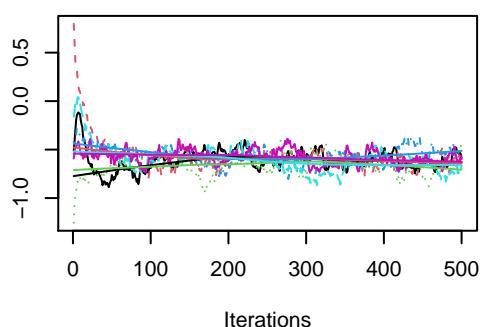
Trace of b_{12}



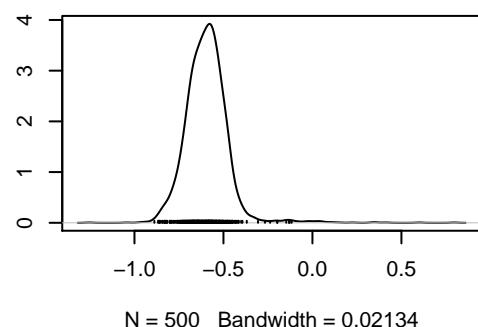
Density of b_{12}



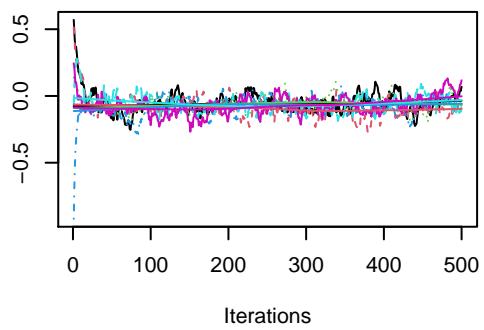
Trace of b_{13}



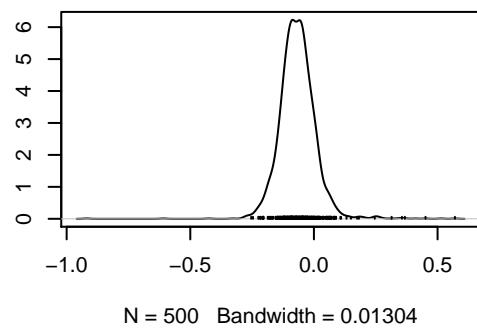
Density of b_{13}



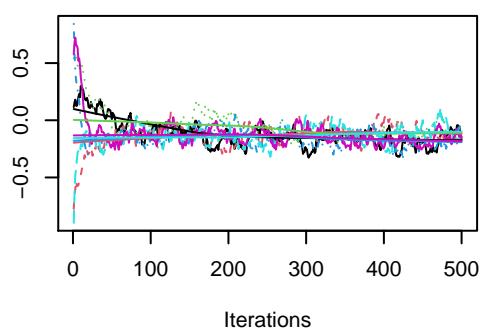
Trace of b14



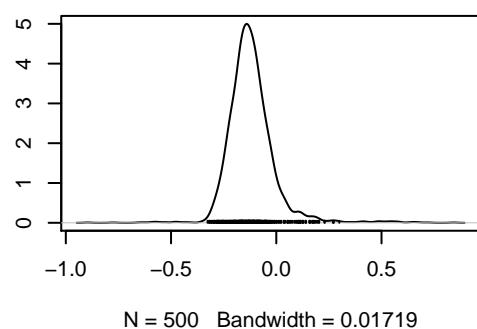
Density of b14



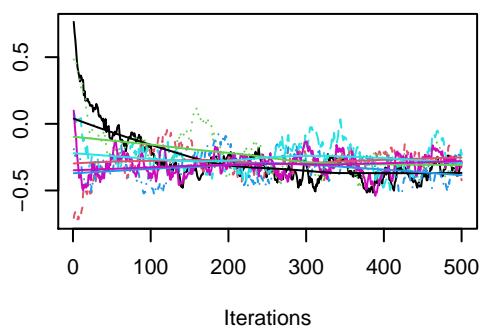
Trace of b15



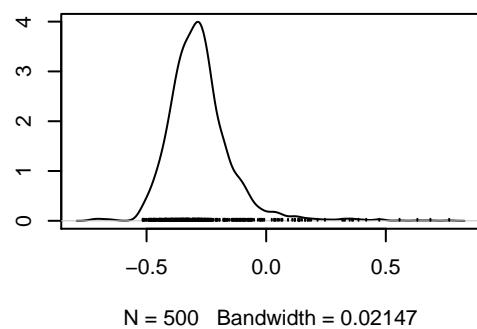
Density of b15



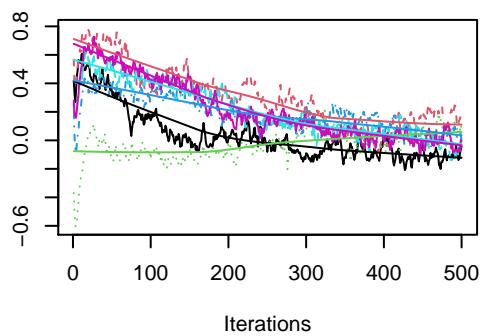
Trace of b16



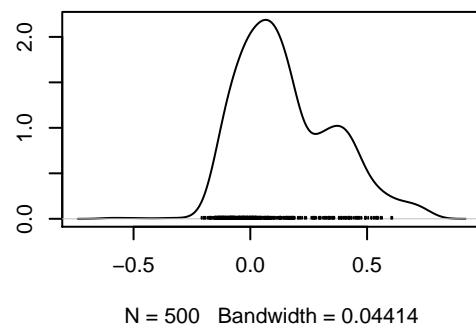
Density of b16



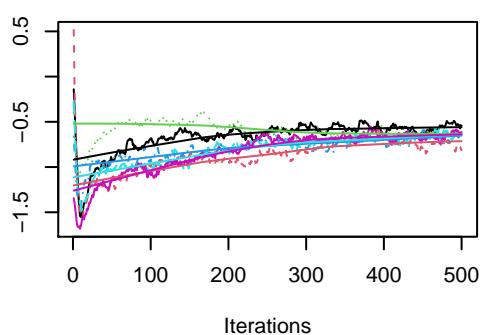
Trace of b21



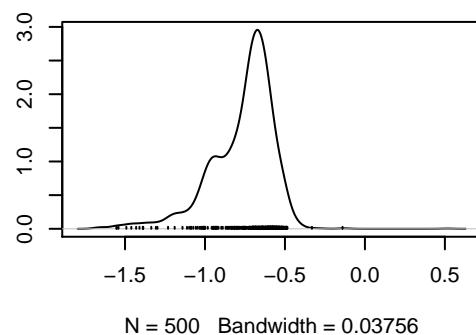
Density of b21



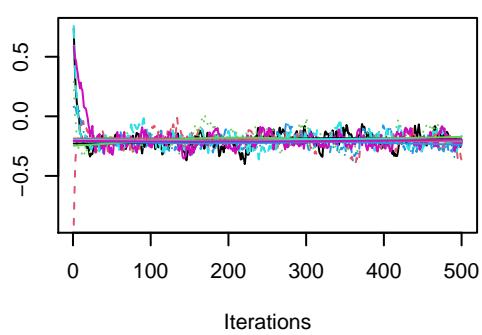
Trace of b22



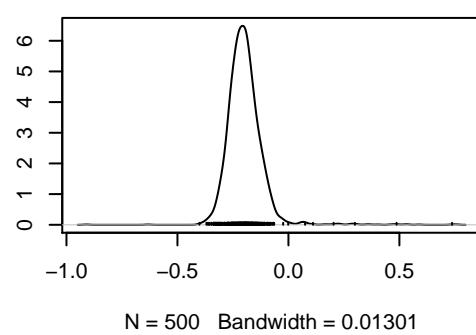
Density of b22



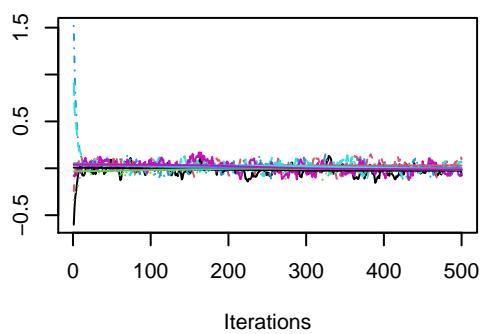
Trace of b23



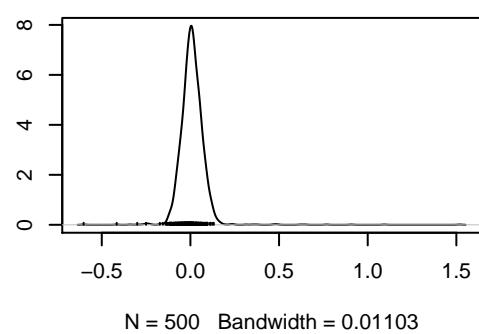
Density of b23



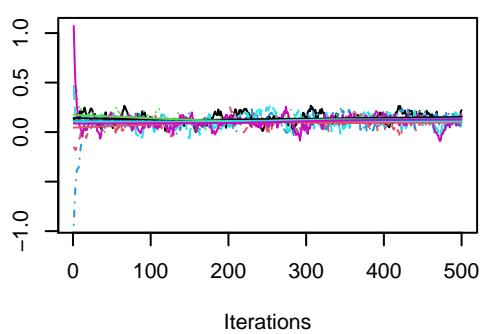
Trace of b24



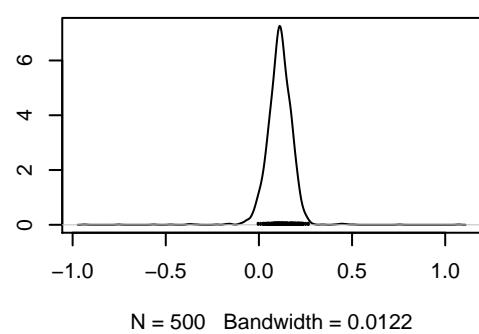
Density of b24



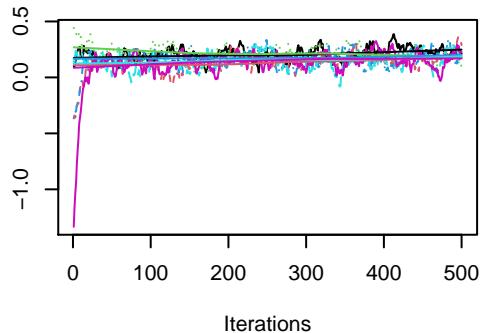
Trace of b25



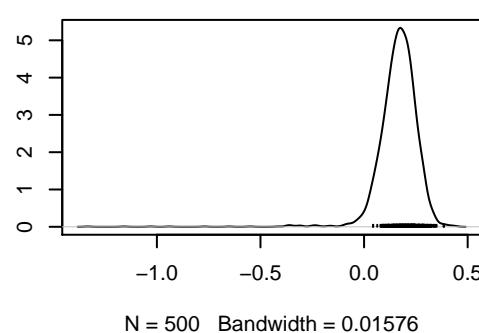
Density of b25



Trace of b26



Density of b26



adapt alpha

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)
```

```

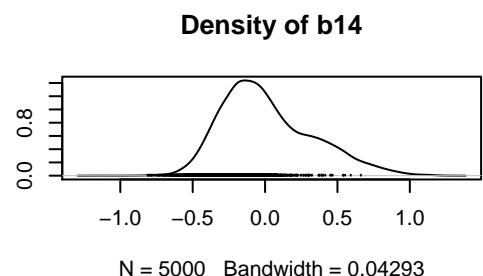
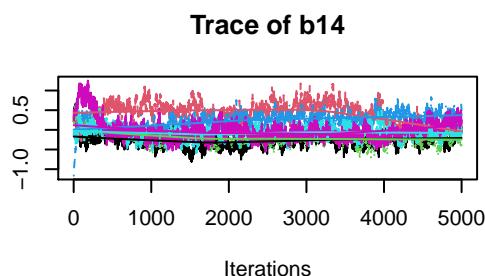
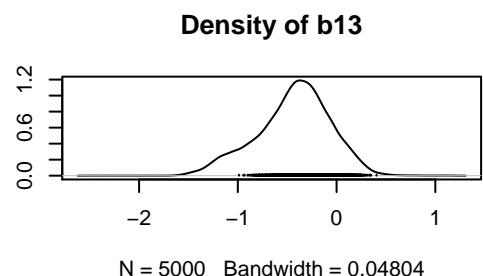
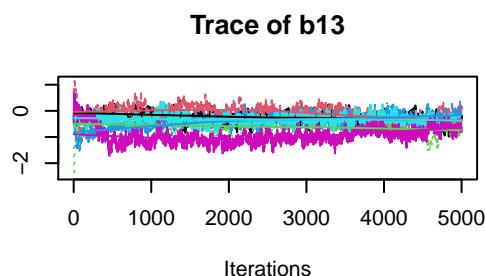
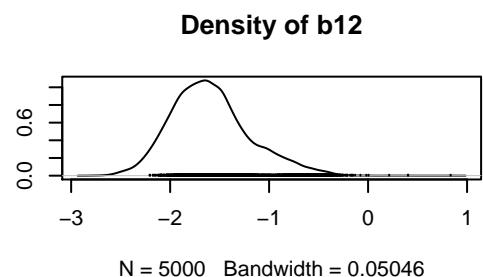
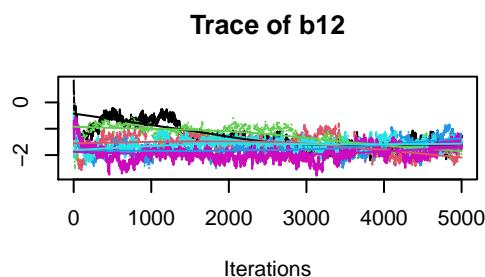
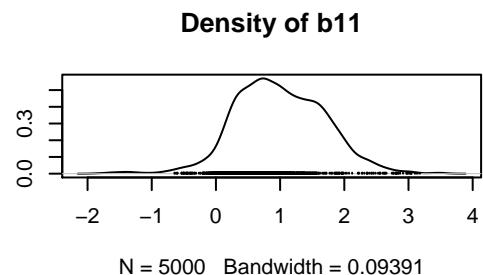
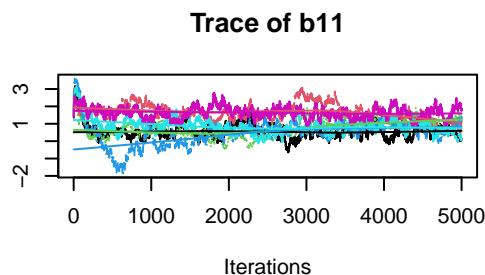
multi_adapt_poly_trim05_o2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim(y=data_trim05$y, x=data_trim05$x, b=b_init[, , i],
    burn=0, nsamp=5000, thin=1, trim = 0.5, order = 2,
    jump=list(a=a_init[, i], prec = 1, positive=pos.est,
      persistence=0.8, update.jbw=FALSE))

```

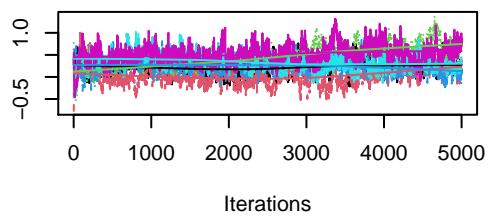
```
load("./report/report18/multi_adapt_poly_trim05_o2.RData")
```

```
multi_adapt_poly_trim05_o2_coda <- multi_chain_coda(multi_adapt_poly_trim05_o2, burn = 0, N_para, p, or
```

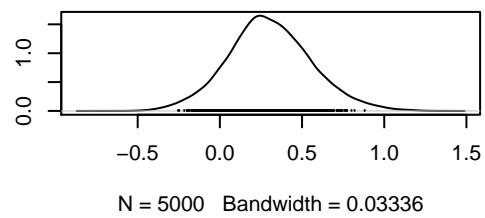
```
plot(multi_adapt_poly_trim05_o2_coda)
```



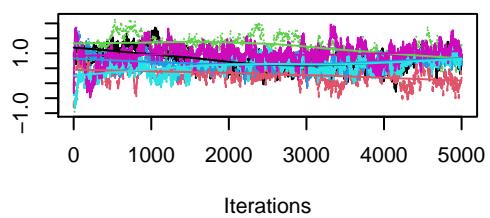
Trace of b15



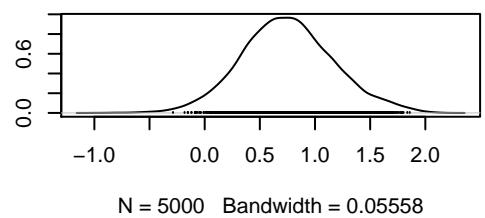
Density of b15



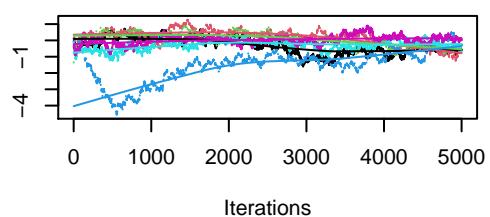
Trace of b16



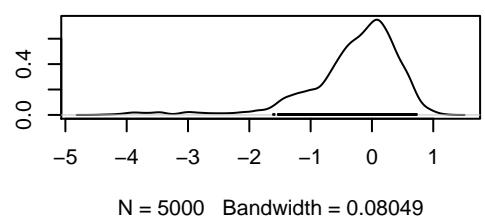
Density of b16



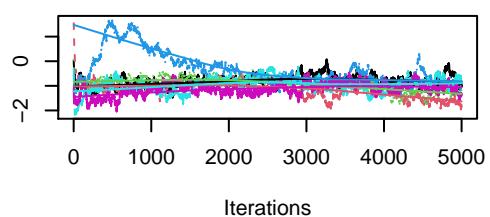
Trace of b21



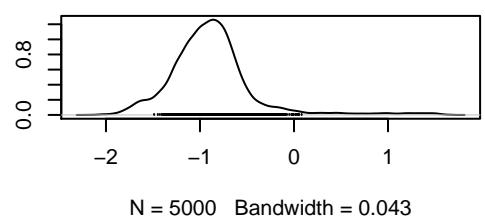
Density of b21



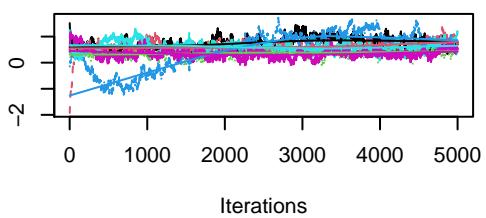
Trace of b22



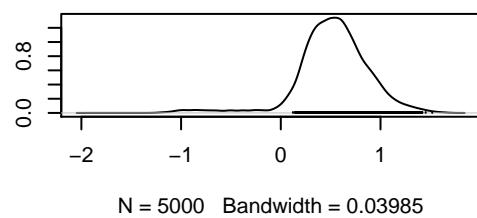
Density of b22



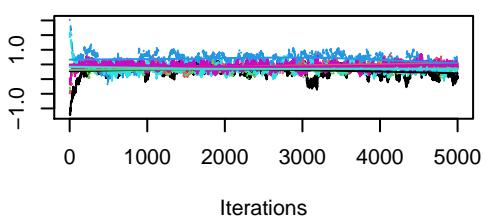
Trace of b23



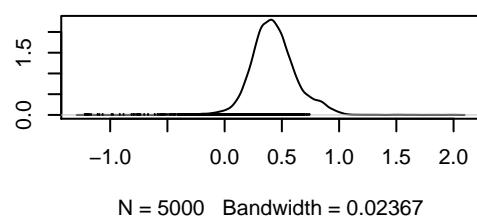
Density of b23



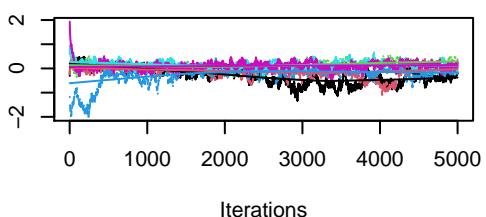
Trace of b24



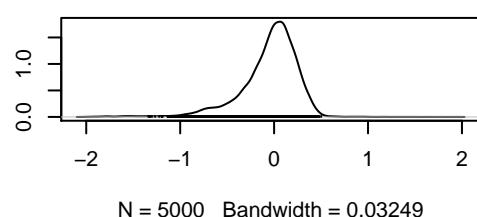
Density of b24



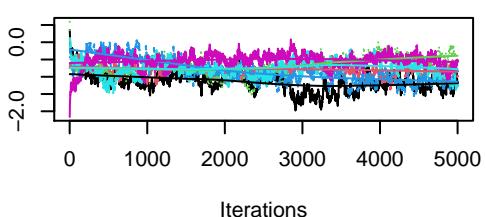
Trace of b25



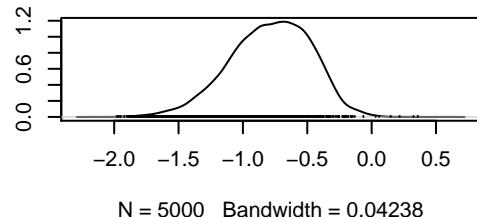
Density of b25

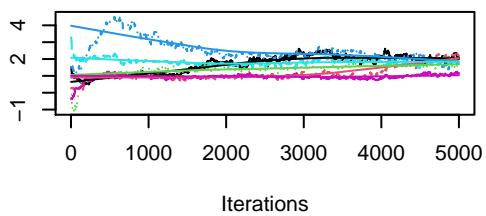
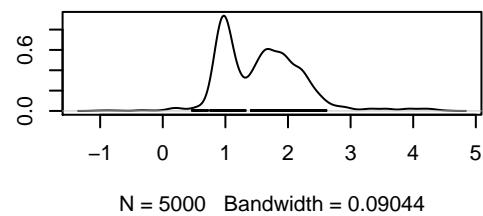
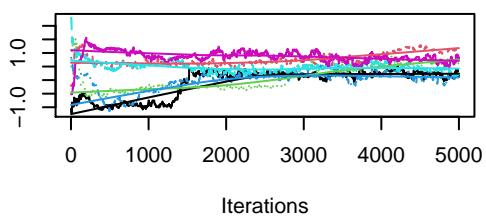
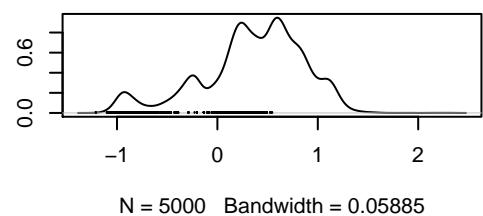
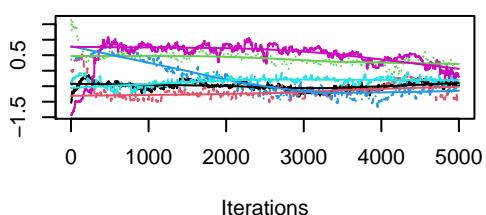
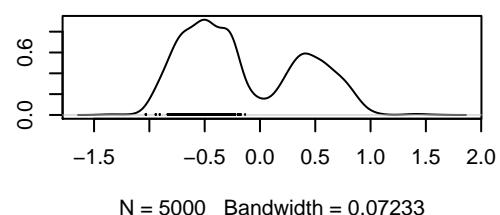
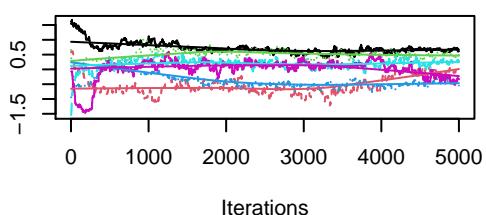
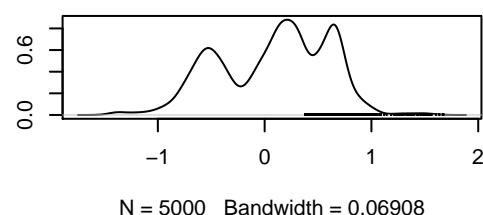


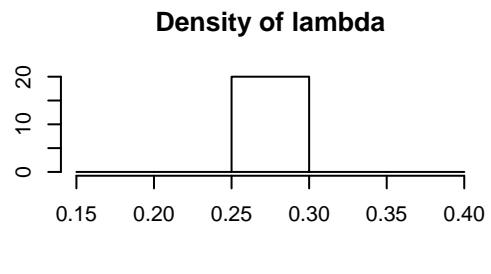
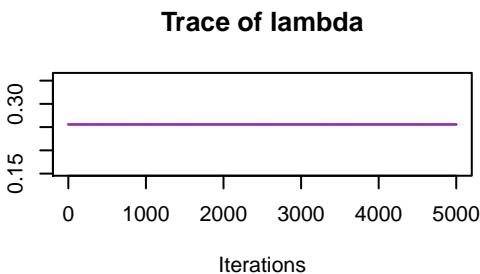
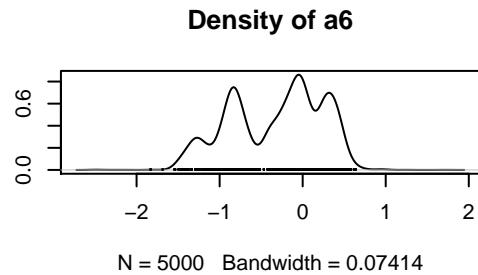
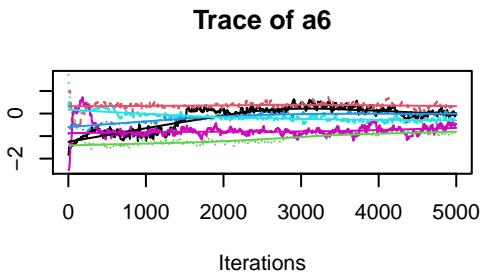
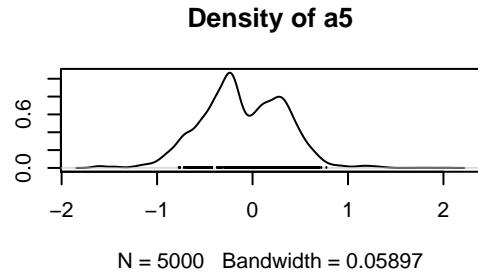
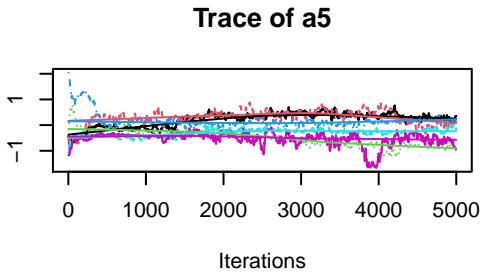
Trace of b26



Density of b26



Trace of a1**Density of a1****Trace of a2****Density of a2****Trace of a3****Density of a3****Trace of a4****Density of a4**



trim = 0.5, order = 3

```

set.seed(123)
order <- 3
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))

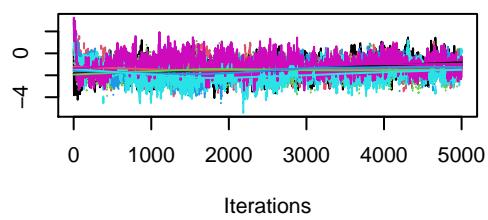
data_trim05 <- get.trim.data(0.5)

multi_adapt_poly_trim05_o3 <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim(y=data_trim05$y, x=data_trim05$x, b=b_init[,i],
    burn=0, nsamp=5000, thin=1, trim = 0.5, order = 3,
    jump=list(a=a_init[,i], prec = 1, positive=pos.est,
      persistence=0.8, update.jbw=FALSE))

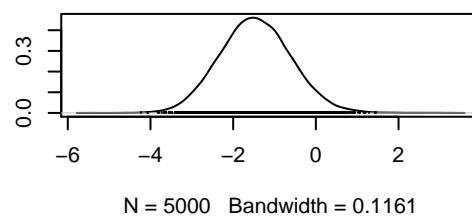
load("./report/report18/multi_adapt_poly_trim05_o3.RData")
multi_adapt_poly_trim05_o3_coda <- multi_chain_coda(multi_adapt_poly_trim05_o3, burn = 0, N_para, p, order = 3)
plot(multi_adapt_poly_trim05_o3_coda)

```

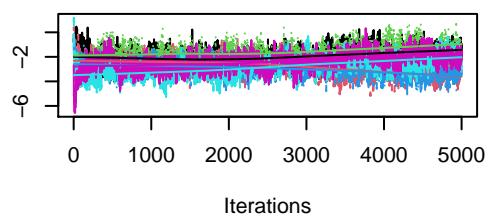
Trace of b_{11}



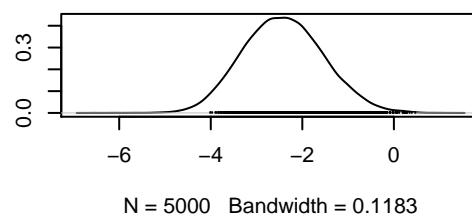
Density of b_{11}



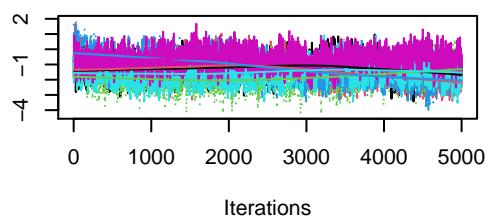
Trace of b_{12}



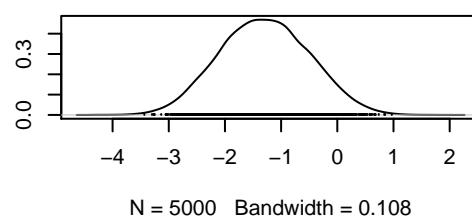
Density of b_{12}



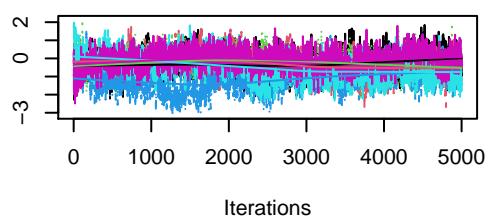
Trace of b_{13}



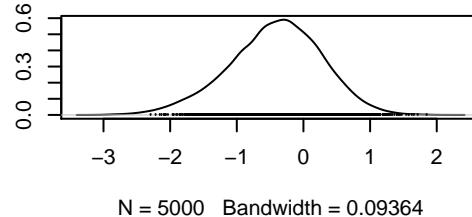
Density of b_{13}



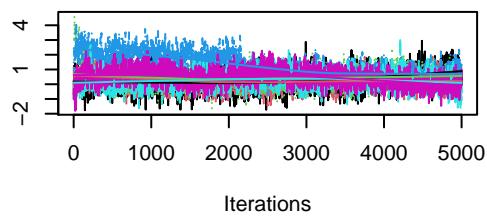
Trace of b_{14}



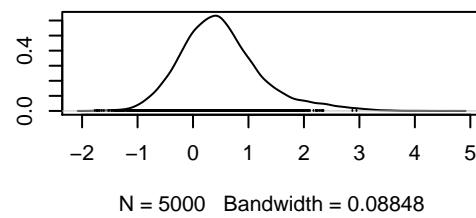
Density of b_{14}



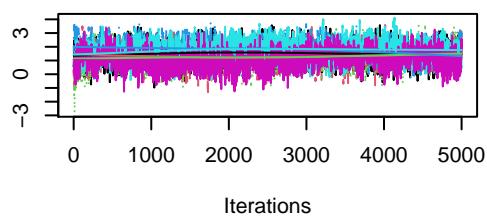
Trace of b15



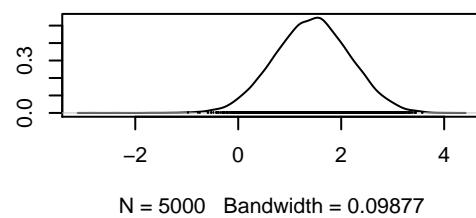
Density of b15



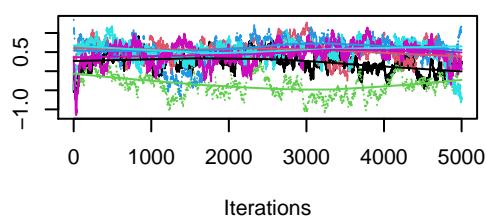
Trace of b16



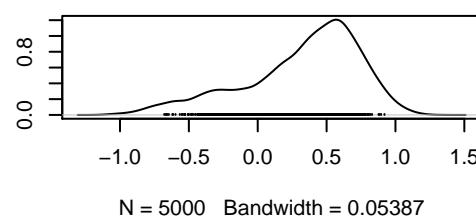
Density of b16



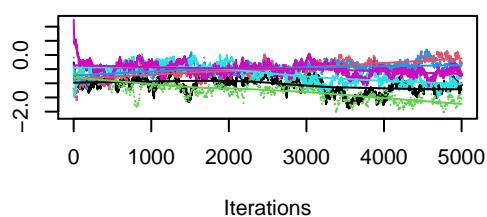
Trace of b21



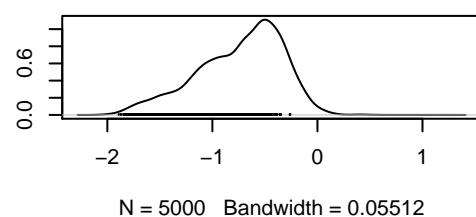
Density of b21

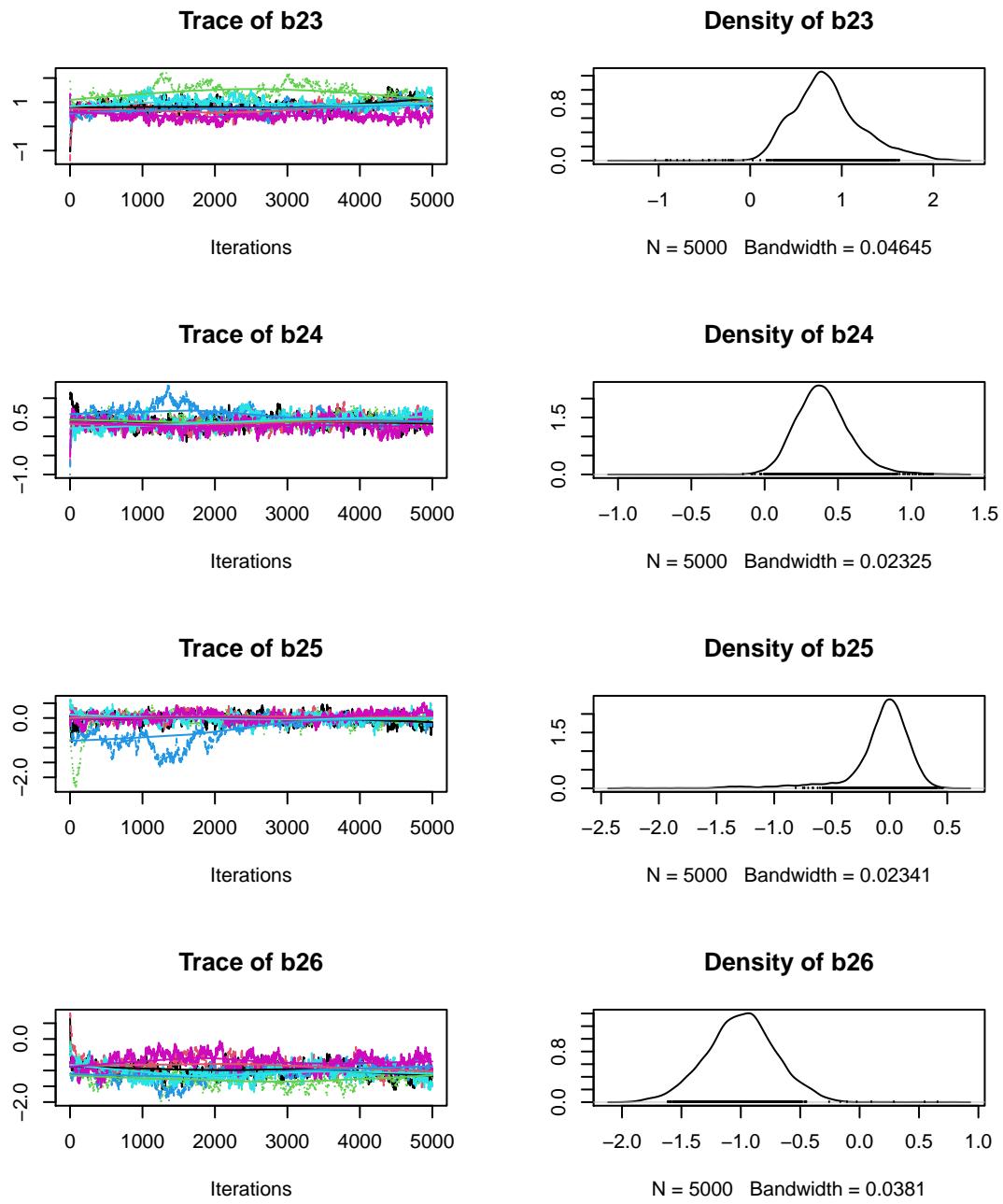


Trace of b22

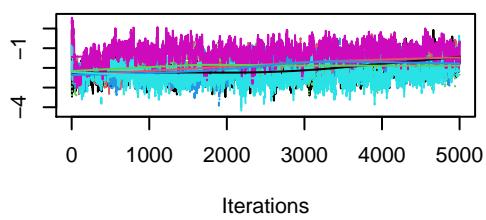


Density of b22

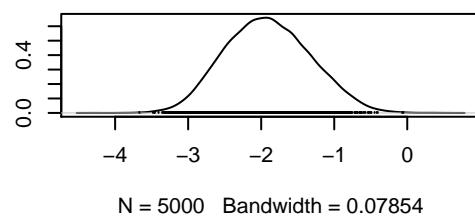




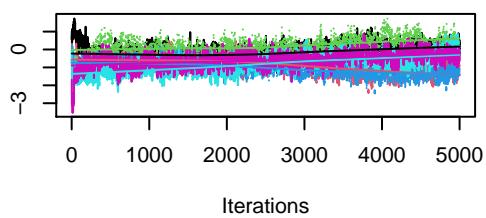
Trace of b31



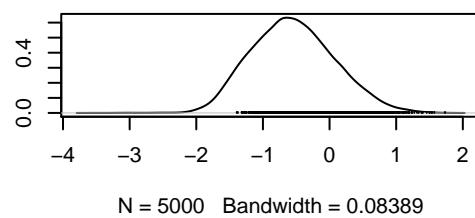
Density of b31



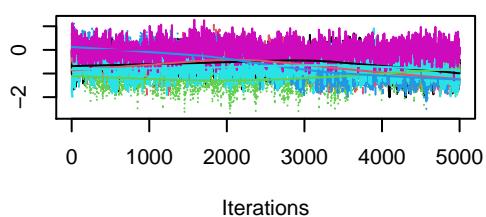
Trace of b32



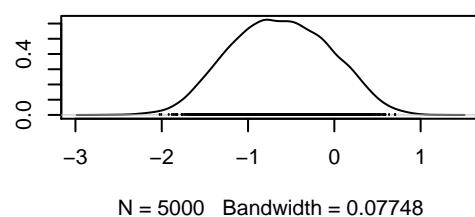
Density of b32



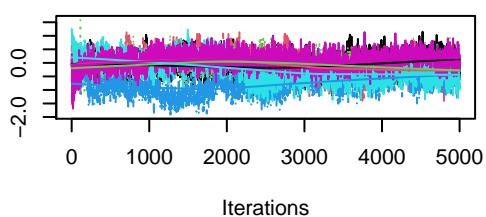
Trace of b33



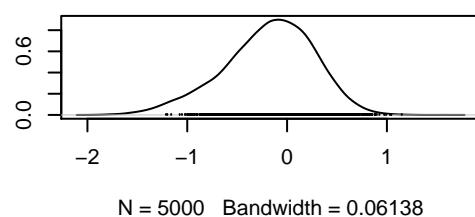
Density of b33



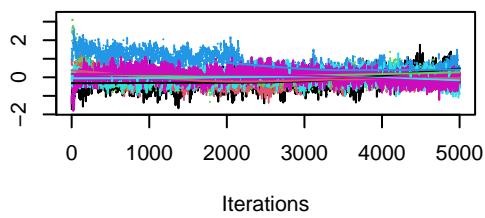
Trace of b34



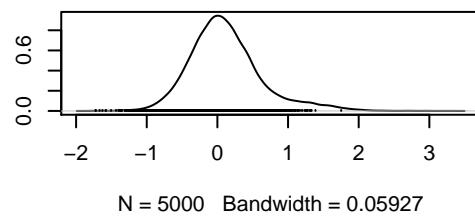
Density of b34



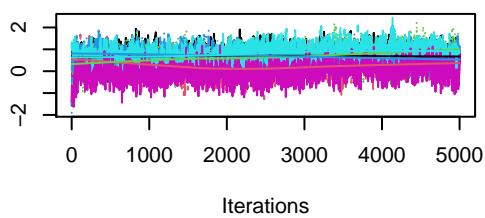
Trace of b35



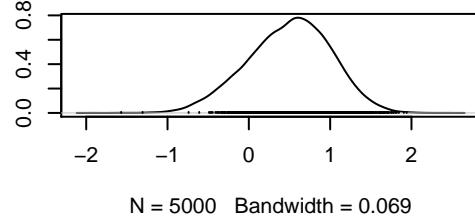
Density of b35



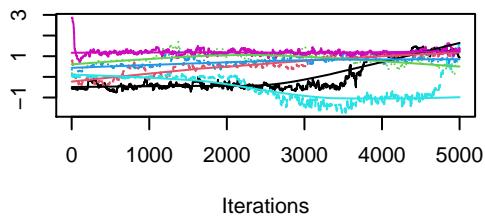
Trace of b36



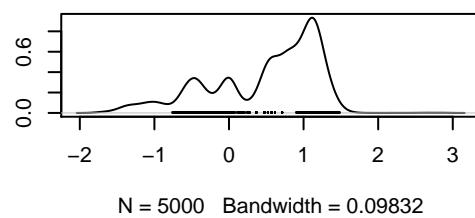
Density of b36



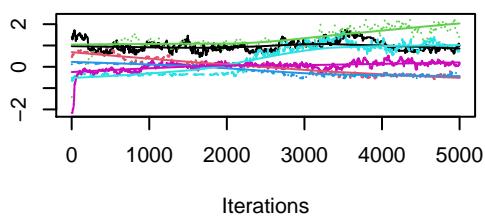
Trace of a1



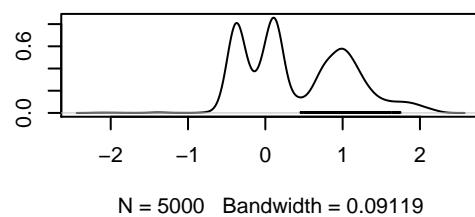
Density of a1

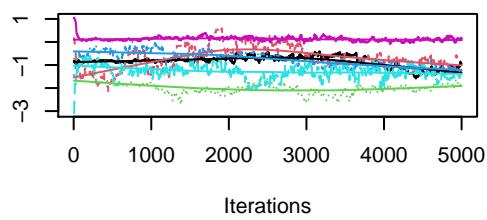
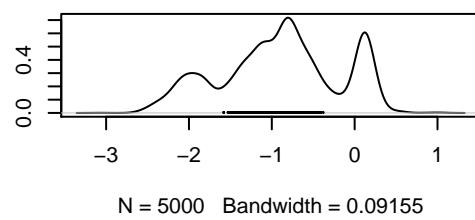
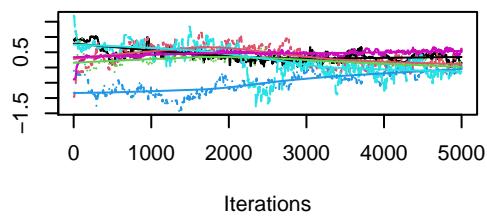
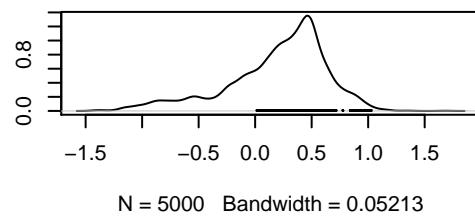
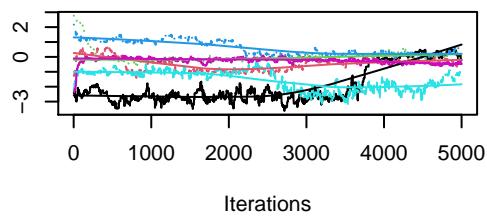
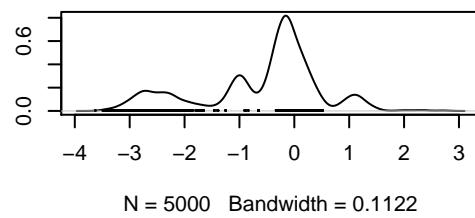
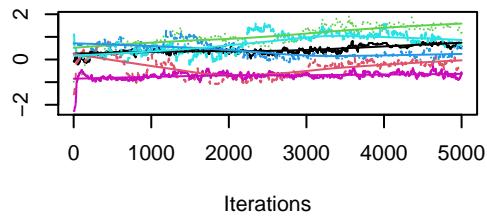
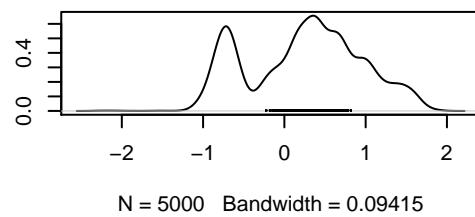
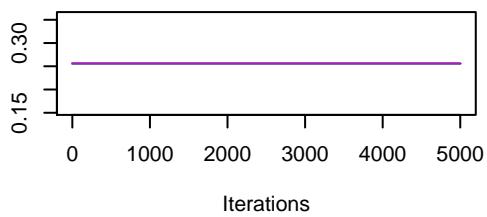
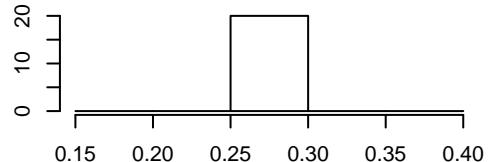


Trace of a2



Density of a2



Trace of a3**Density of a3****Trace of a4****Density of a4****Trace of a5****Density of a5****Trace of a6****Density of a6****Trace of lambda****Density of lambda**

trim = 0.5, order = 2, update.jbw

```
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))

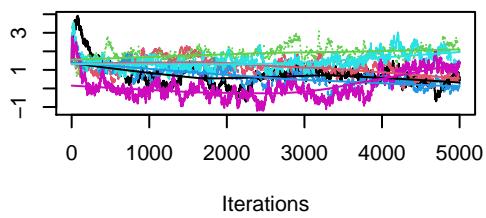
data_trim05 <- get.trim.data(0.5)

multi_adapt_poly_trim05_o2_jbw <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim(y=data_trim05$y, x=data_trim05$x, b=b_init[,i],
    burn=0, nsamp=5000, thin=1, trim = 0.5, order = 2,
    jump=list(a=a_init[,i], prec = 1, positive=pos.est,
      persistence=0.8, update.jbw=TRUE))

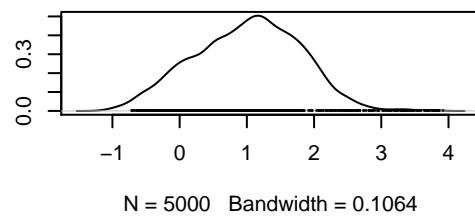
load("./report/report18/multi_adapt_poly_trim05_o2_jbw.RData")
multi_adapt_poly_trim05_o2_jbw_coda <- multi_chain_coda(multi_adapt_poly_trim05_o2_jbw, burn = 0, N_para)

plot(multi_adapt_poly_trim05_o2_jbw_coda)
```

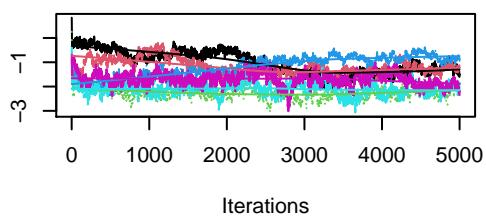
Trace of b_{11}



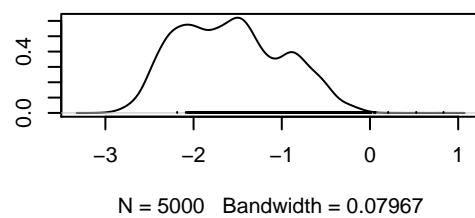
Density of b_{11}



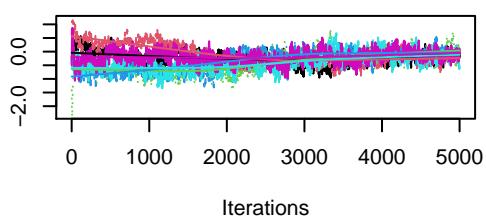
Trace of b_{12}



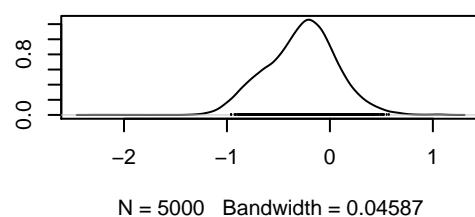
Density of b_{12}



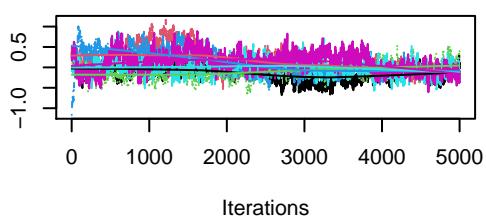
Trace of b_{13}



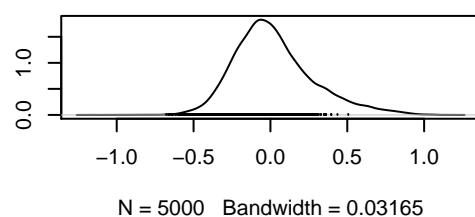
Density of b_{13}



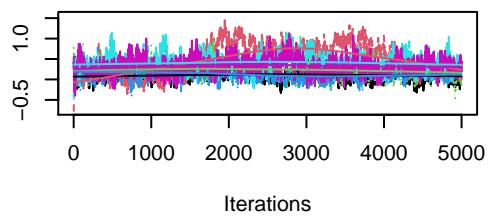
Trace of b_{14}



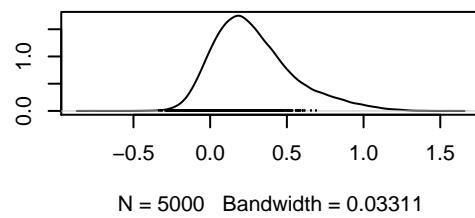
Density of b_{14}



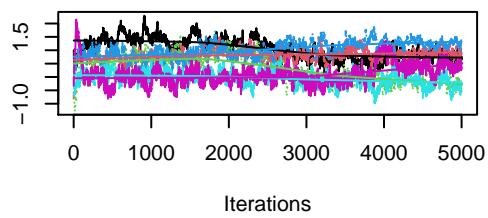
Trace of b15



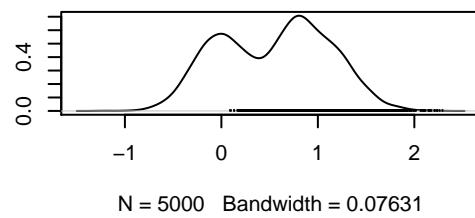
Density of b15



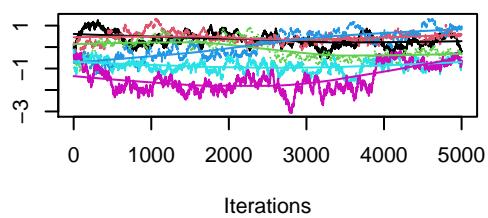
Trace of b16



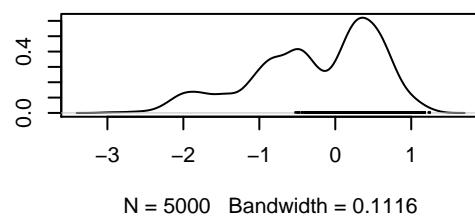
Density of b16



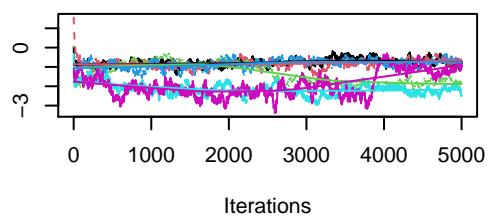
Trace of b21



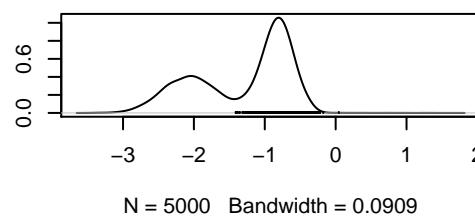
Density of b21



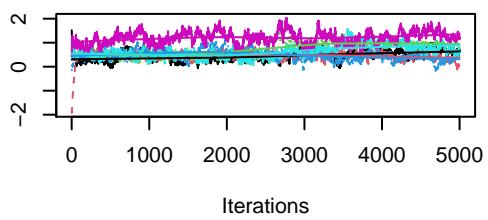
Trace of b22



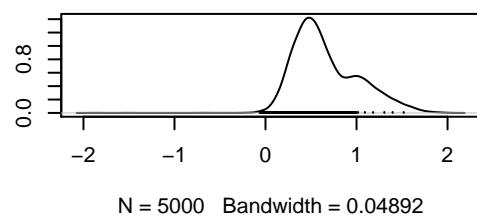
Density of b22



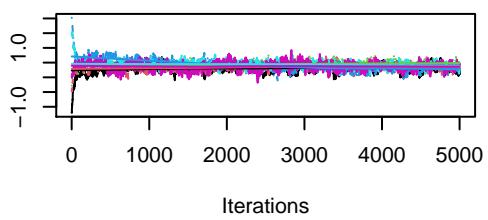
Trace of b23



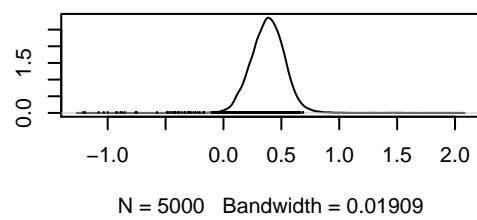
Density of b23



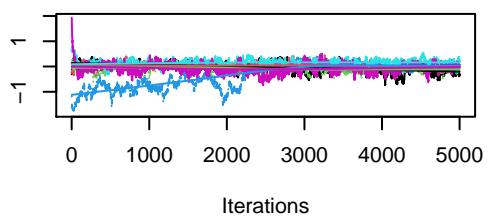
Trace of b24



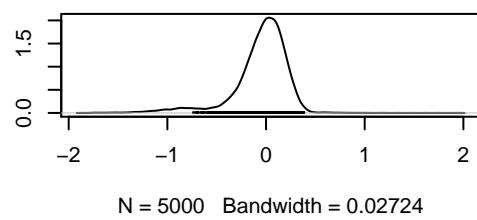
Density of b24



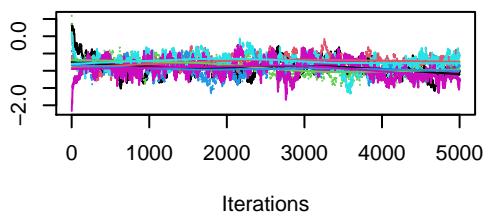
Trace of b25



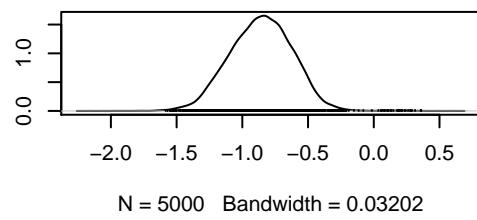
Density of b25



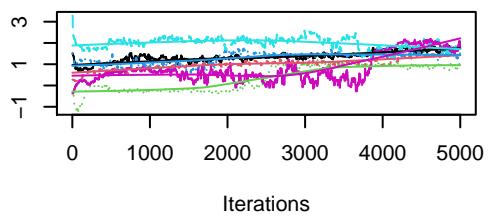
Trace of b26



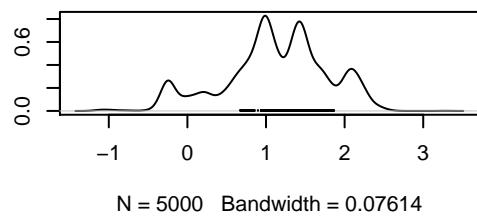
Density of b26



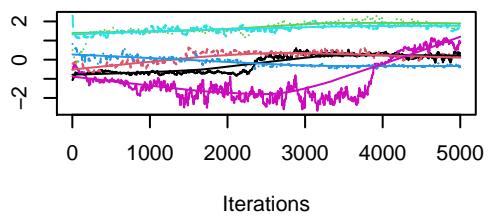
Trace of a1



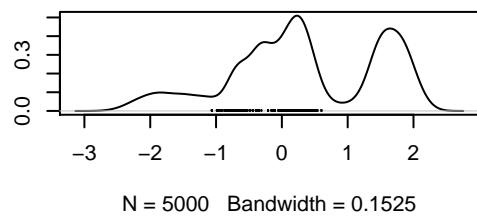
Density of a1



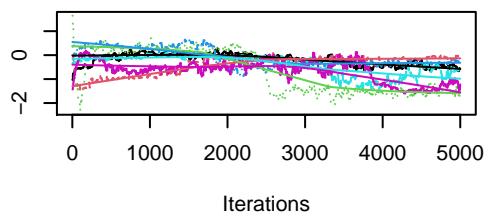
Trace of a2



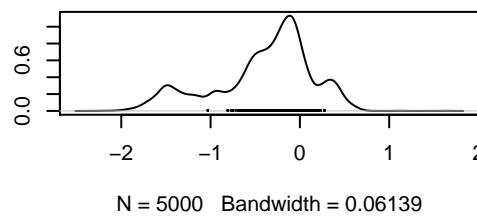
Density of a2



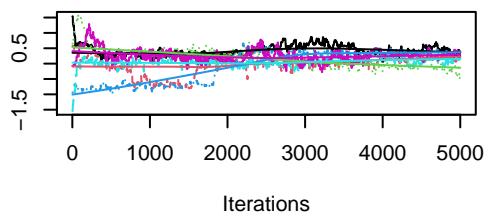
Trace of a3



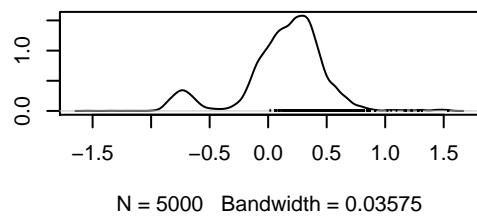
Density of a3

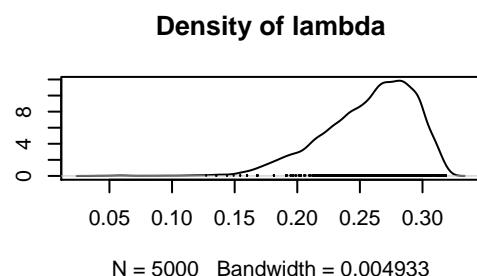
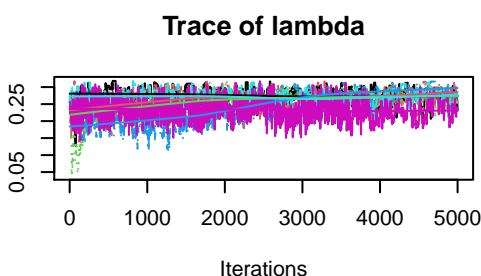
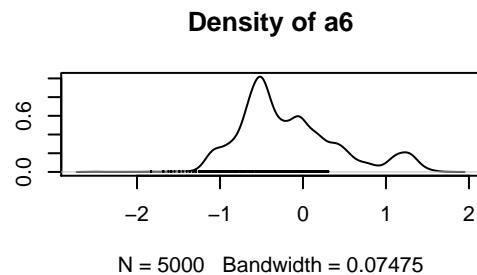
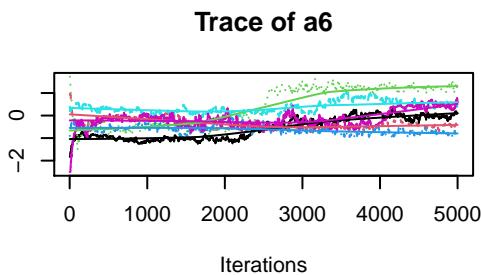
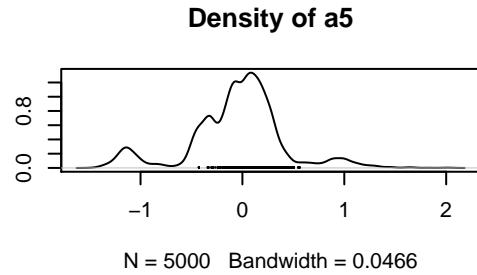
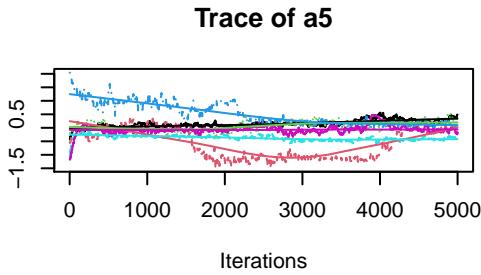


Trace of a4



Density of a4





trim = 0.5, order = 3, update.jbw

```

set.seed(123)
order <- 3
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)

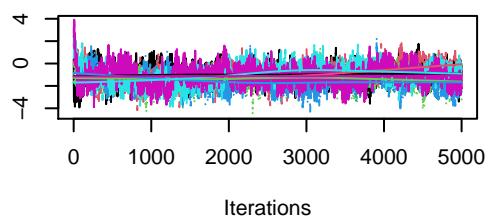
multi_adapt_poly_trim05_o3_jbw <- foreach(i = 1:N_para) %dorng%
  bdregjump_adapt_poly_trim(y=data_trim05$y, x=data_trim05$x, b=b_init[,i],
    burn=0, nsamp=5000, thin=1, trim = 0.5, order = 3,
    jump=list(a=a_init[,i], prec = 1, positive=pos.est,
    persistence=0.8, update.jbw=TRUE))

load("./report/report18/multi_adapt_poly_trim05_o3_jbw.RData")
multi_adapt_poly_trim05_o3_jbw_coda <- multi_chain_coda(multi_adapt_poly_trim05_o3_jbw, burn = 0, N_para)

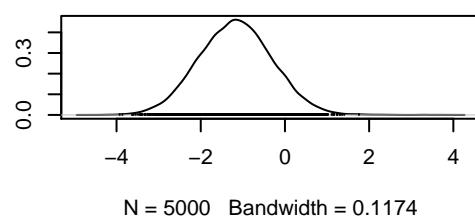
plot(multi_adapt_poly_trim05_o3_jbw_coda)

```

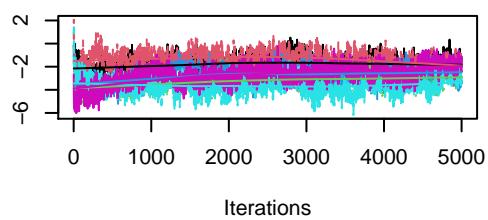
Trace of b_{11}



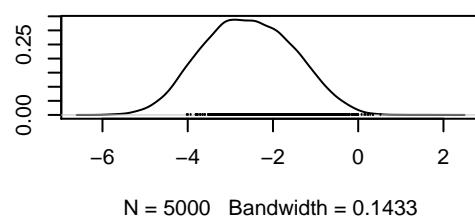
Density of b_{11}



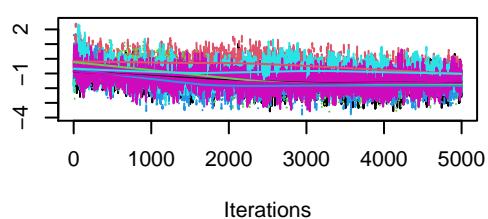
Trace of b_{12}



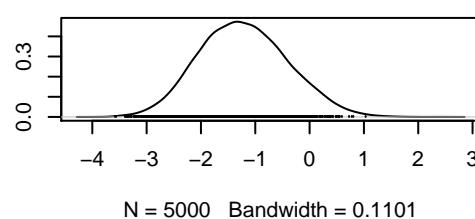
Density of b_{12}



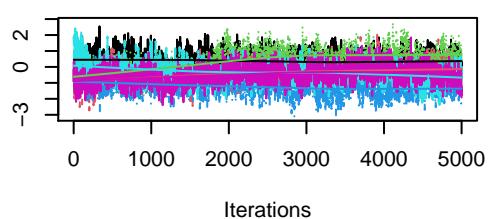
Trace of b_{13}



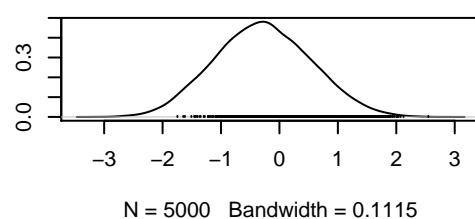
Density of b_{13}



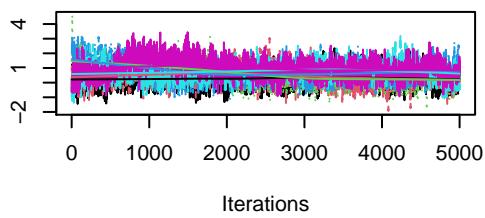
Trace of b_{14}



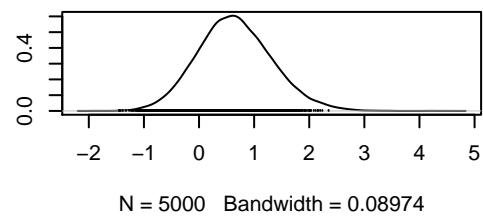
Density of b_{14}



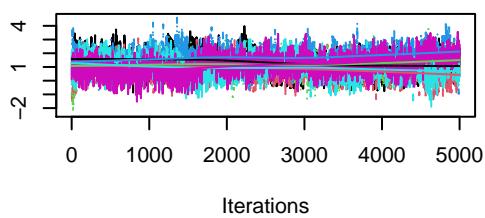
Trace of b15



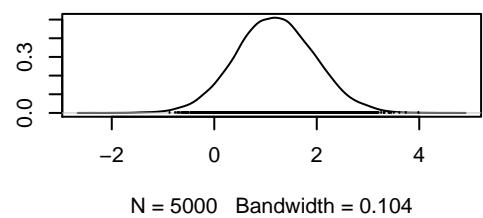
Density of b15



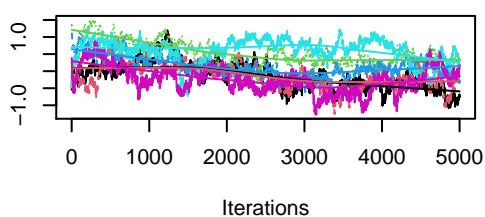
Trace of b16



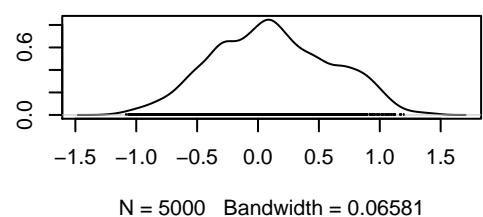
Density of b16



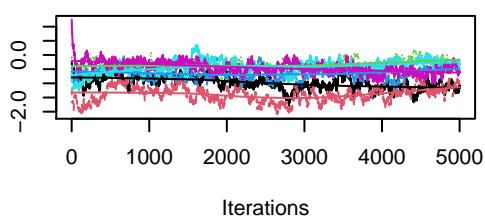
Trace of b21



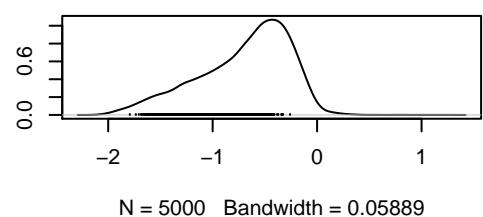
Density of b21



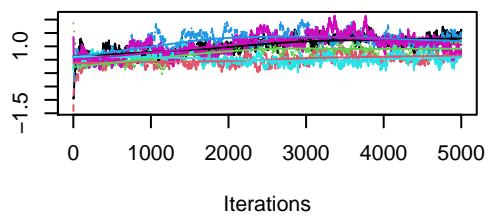
Trace of b22



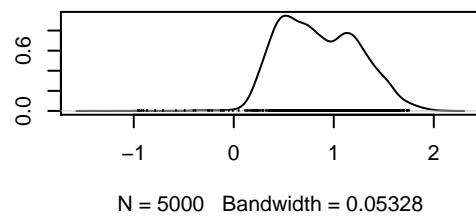
Density of b22



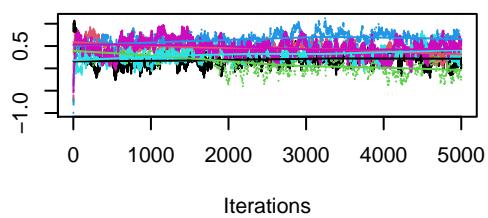
Trace of b23



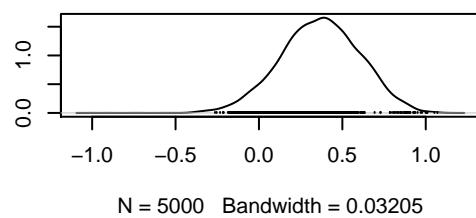
Density of b23



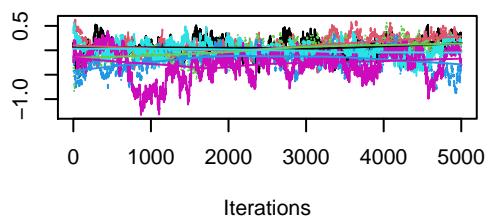
Trace of b24



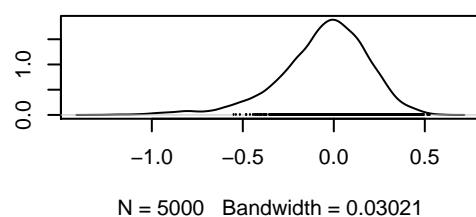
Density of b24



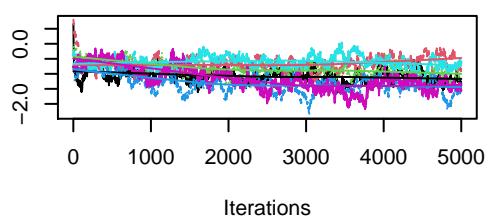
Trace of b25



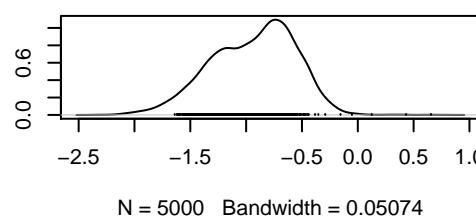
Density of b25



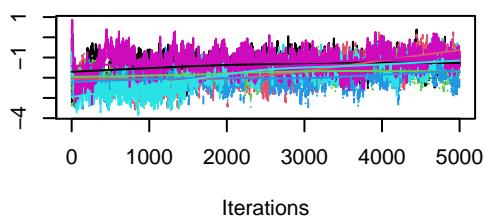
Trace of b26



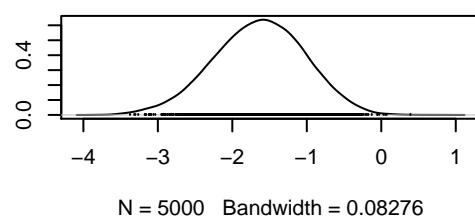
Density of b26



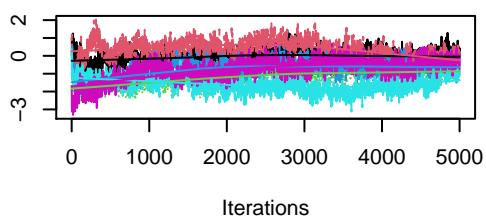
Trace of b31



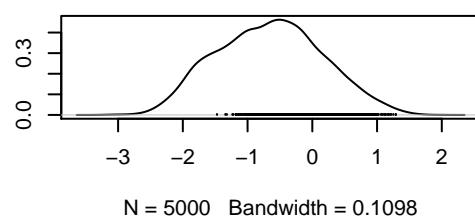
Density of b31



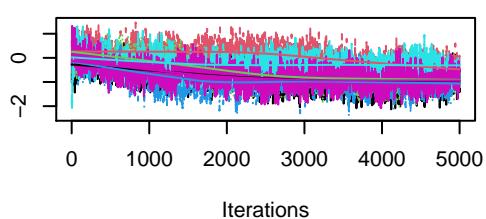
Trace of b32



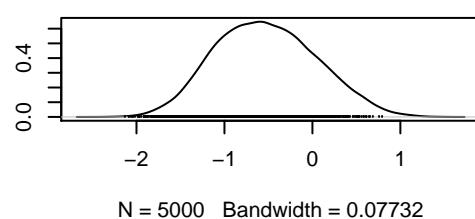
Density of b32



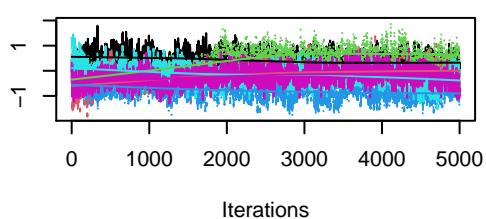
Trace of b33



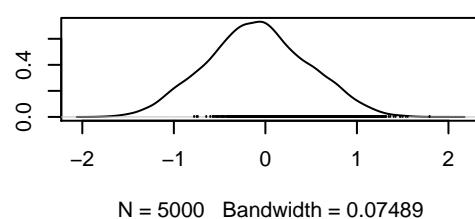
Density of b33



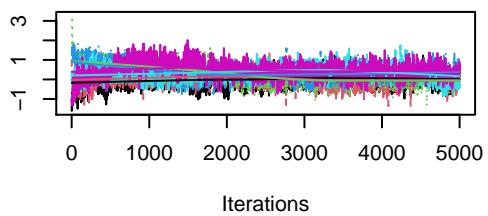
Trace of b34



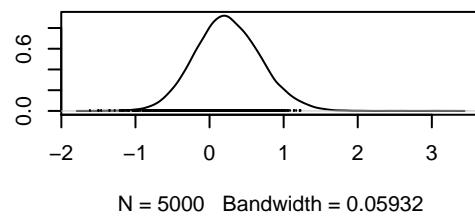
Density of b34



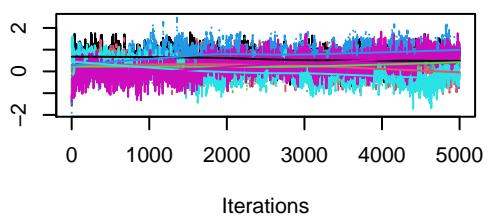
Trace of b35



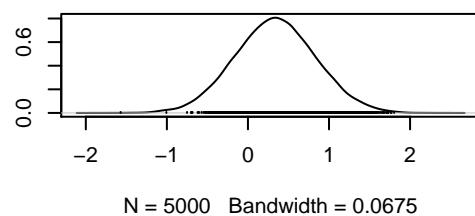
Density of b35



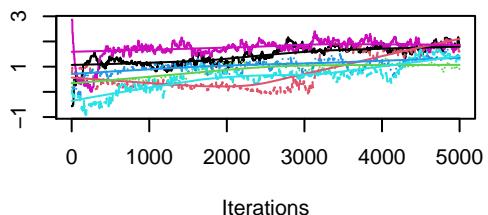
Trace of b36



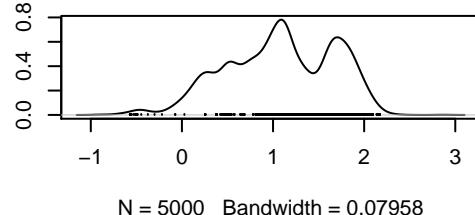
Density of b36



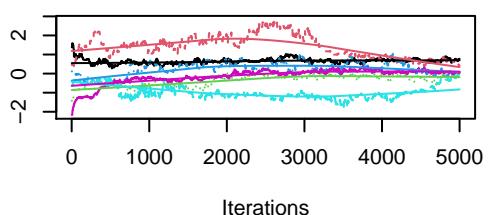
Trace of a1



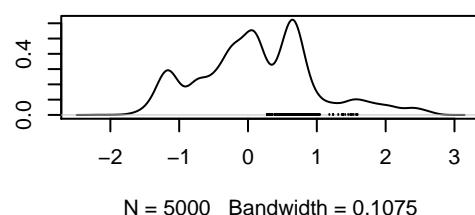
Density of a1

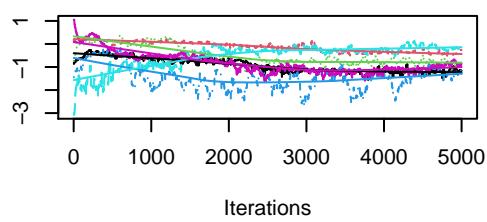
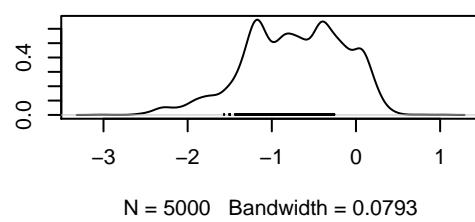
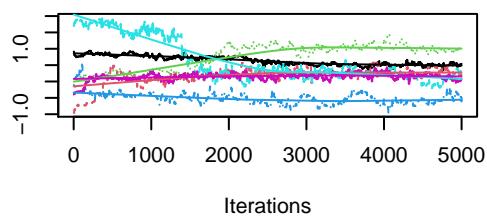
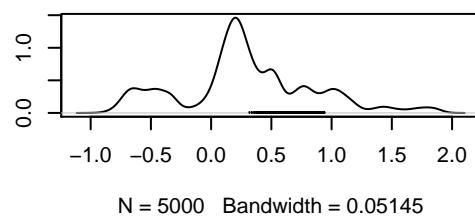
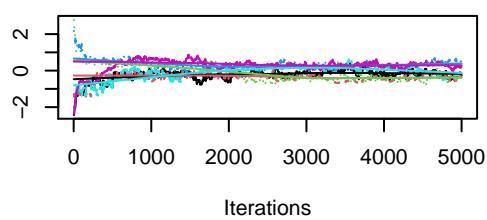
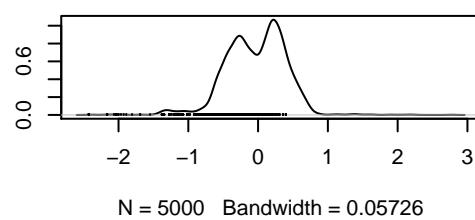
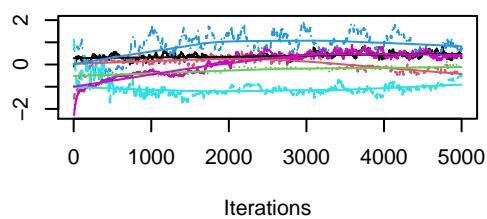
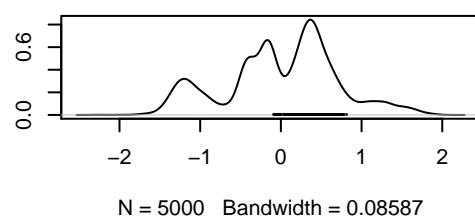
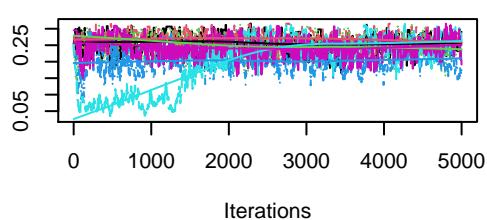


Trace of a2



Density of a2



Trace of a3**Density of a3****Trace of a4****Density of a4****Trace of a5****Density of a5****Trace of a6****Density of a6****Trace of lambda****Density of lambda**