

report17

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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(right_end){
  vote <- subset(vote, from_requirement_threshold < right_end/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

right_end = 0.5, order = 8, new basis functions

```

set.seed(123)
order <- 8
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))

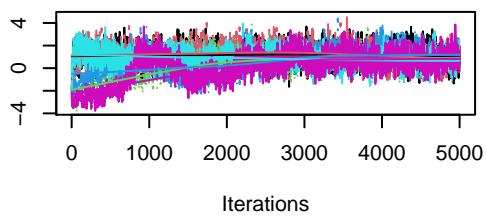
data_trim05 <- get.trim.data(0.5)

noa_o5_multi_trimr05_new <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x, b=b_init[, , i], burn=0, nsamp=5000,
                        thin=1, order = order, right_end = 0.5)

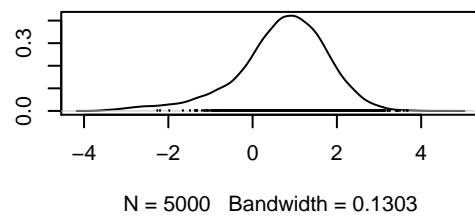
load("./report/report16/noa_o5_multi_trimr05_new.RData")
p <- 6
order <- 8
noa_o5_multi_trimr05_new_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05_new, burn = 0, N_para, p, or
plot(noa_o5_multi_trimr05_new_coda)

```

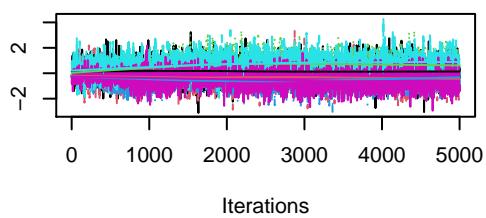
Trace of b_{11}



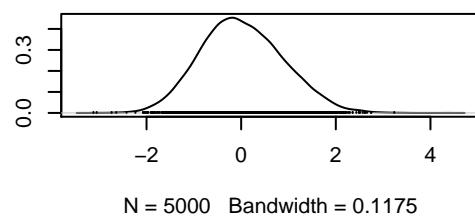
Density of b_{11}



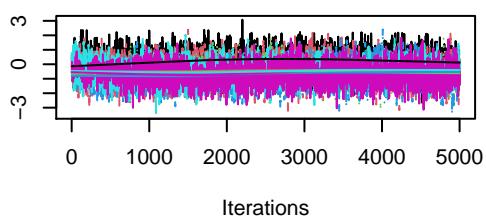
Trace of b_{12}



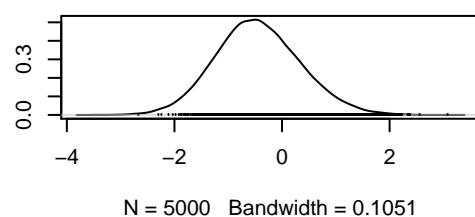
Density of b_{12}



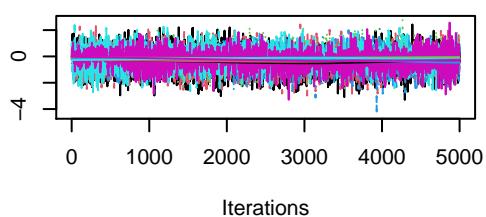
Trace of b_{13}



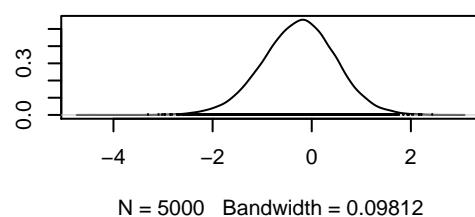
Density of b_{13}



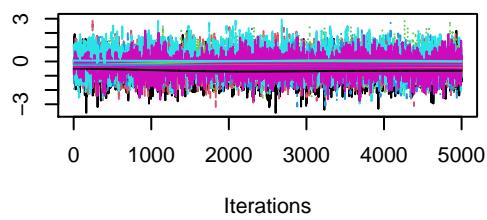
Trace of b_{14}



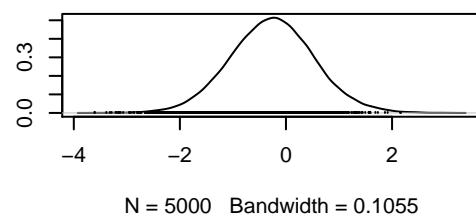
Density of b_{14}



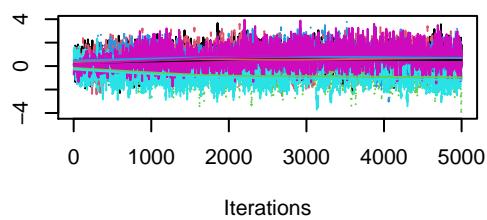
Trace of b15



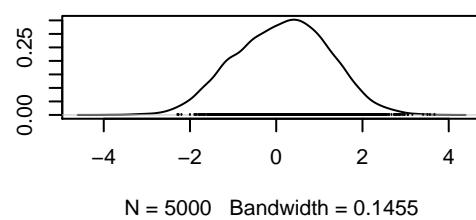
Density of b15



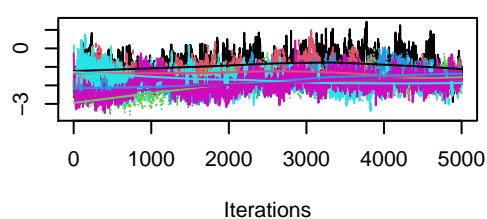
Trace of b16



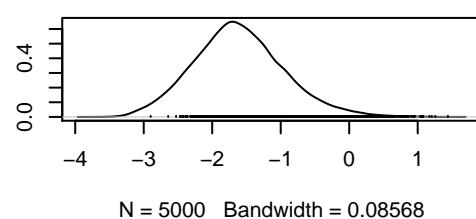
Density of b16



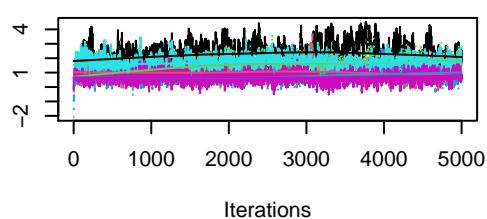
Trace of b21



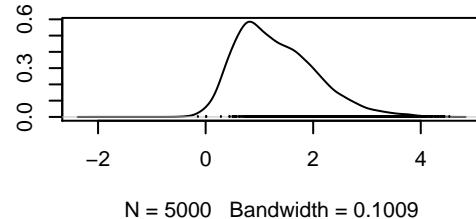
Density of b21



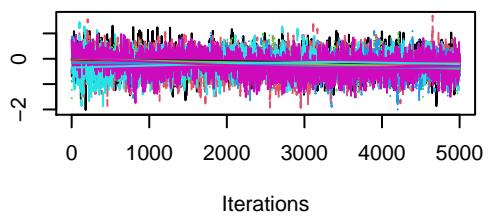
Trace of b22



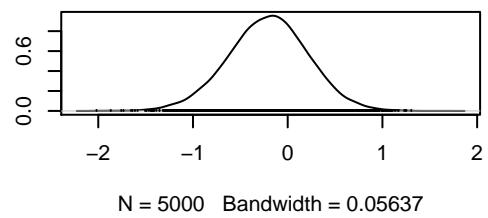
Density of b22



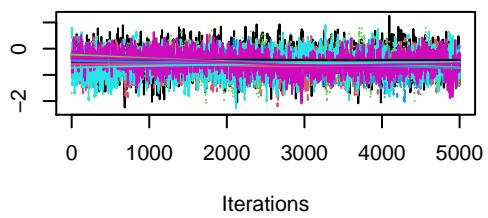
Trace of b23



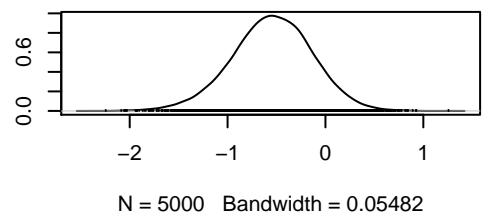
Density of b23



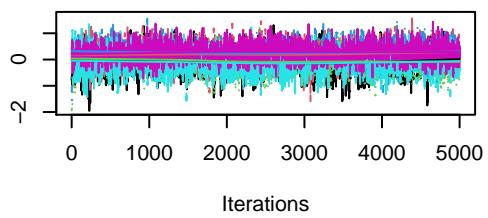
Trace of b24



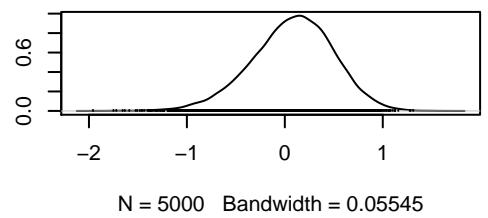
Density of b24



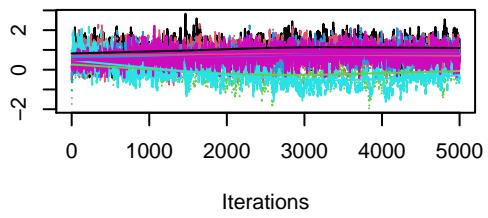
Trace of b25



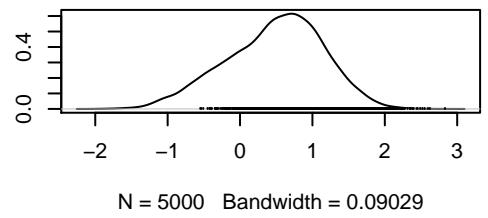
Density of b25



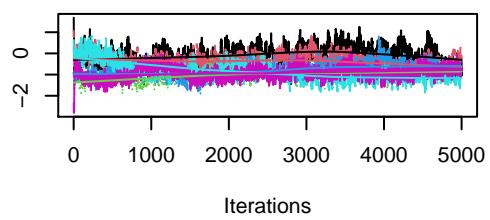
Trace of b26



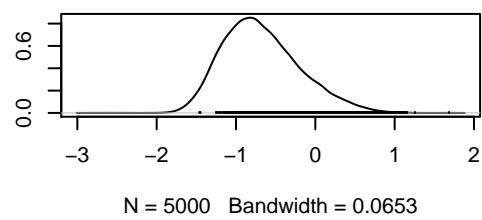
Density of b26



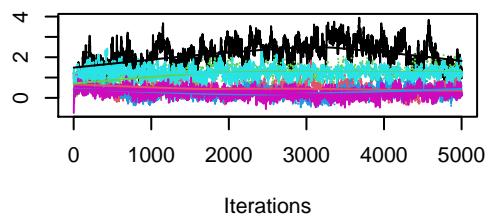
Trace of b31



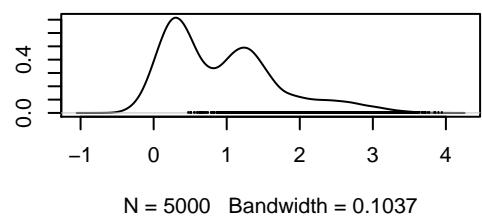
Density of b31



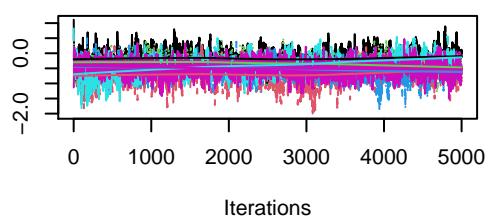
Trace of b32



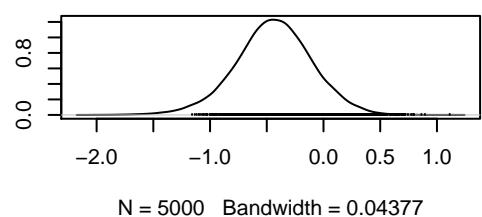
Density of b32



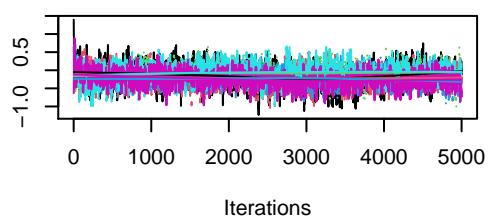
Trace of b33



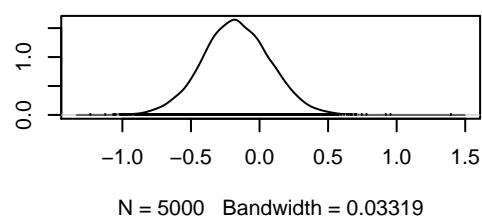
Density of b33



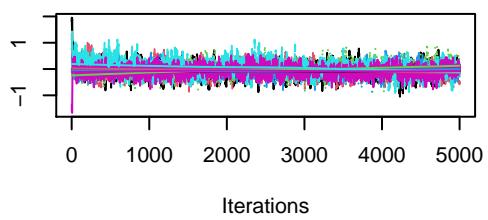
Trace of b34



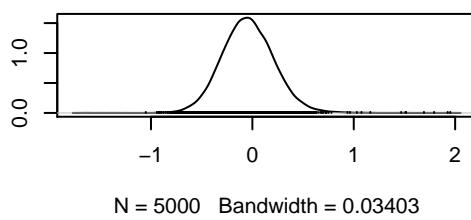
Density of b34



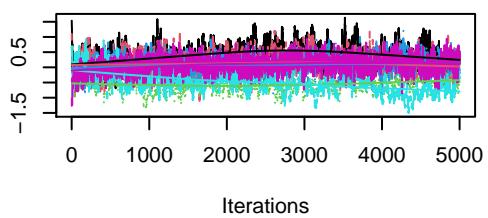
Trace of b35



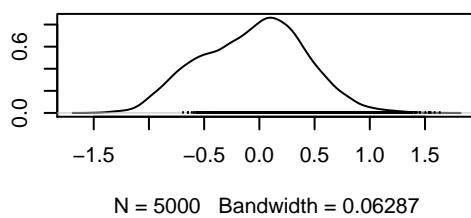
Density of b35



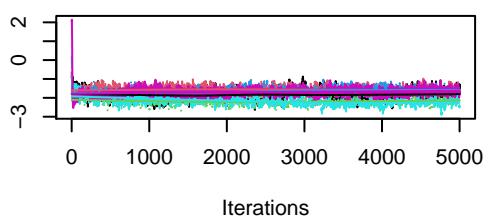
Trace of b36



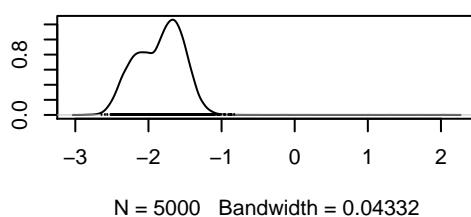
Density of b36



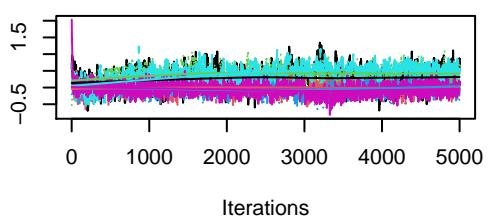
Trace of b41



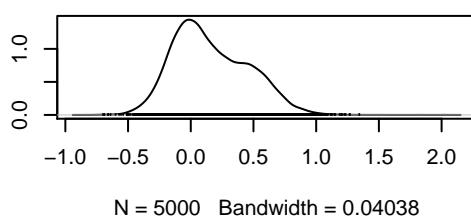
Density of b41

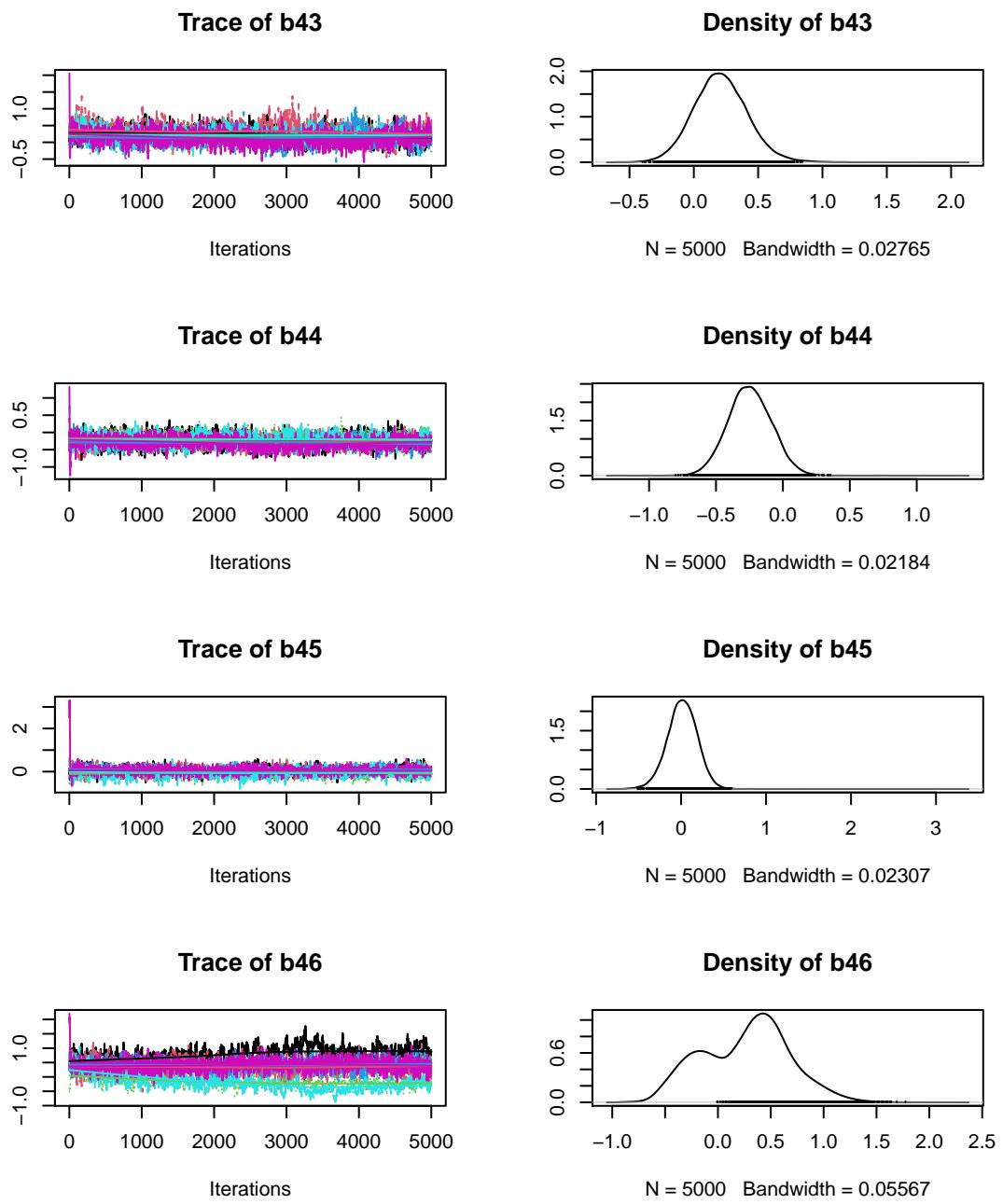


Trace of b42

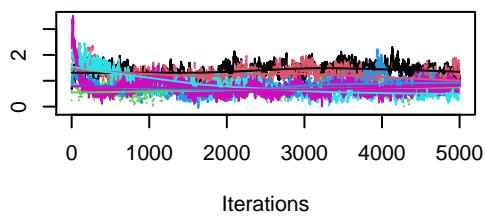


Density of b42

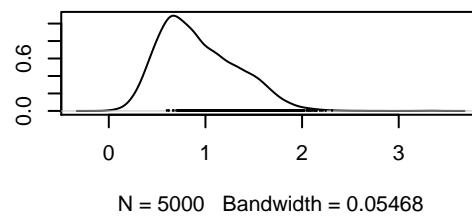




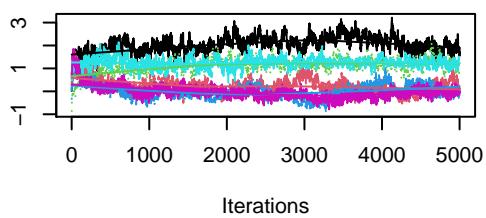
Trace of b51



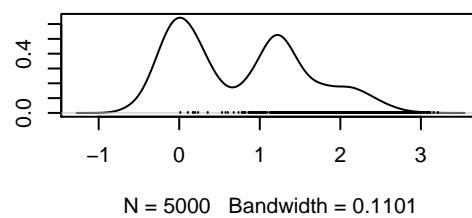
Density of b51



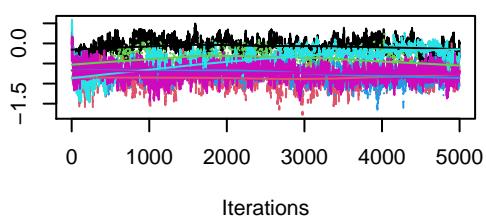
Trace of b52



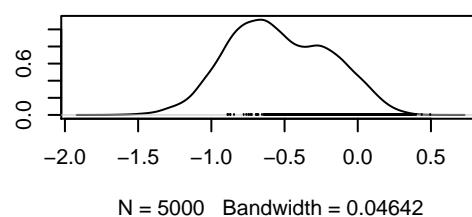
Density of b52



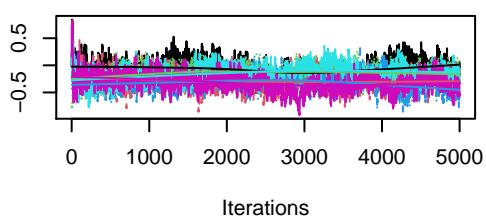
Trace of b53



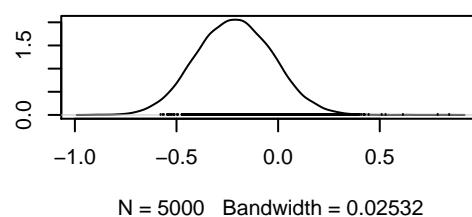
Density of b53



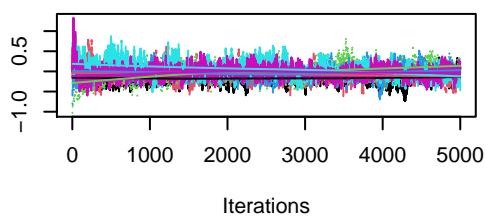
Trace of b54



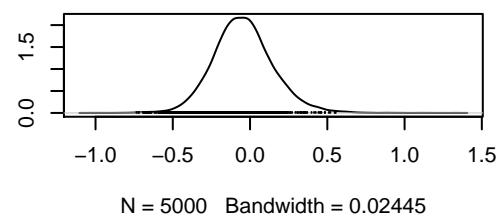
Density of b54



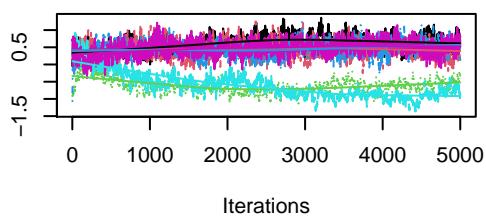
Trace of b55



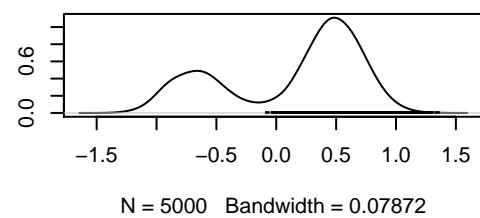
Density of b55



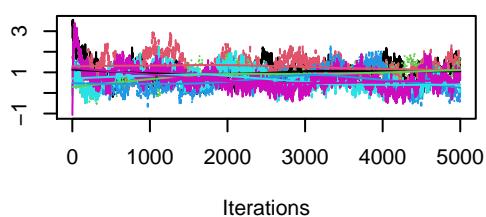
Trace of b56



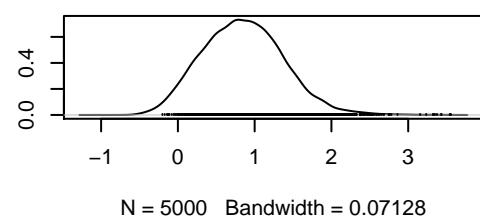
Density of b56



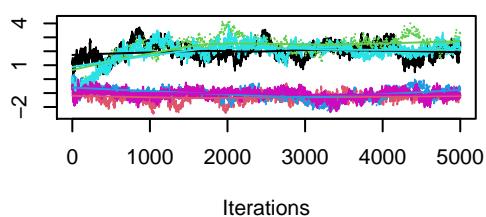
Trace of b61



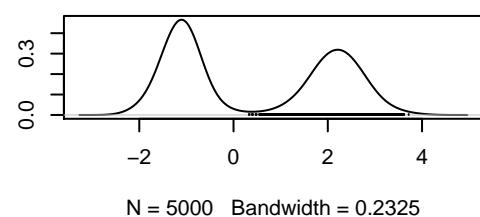
Density of b61



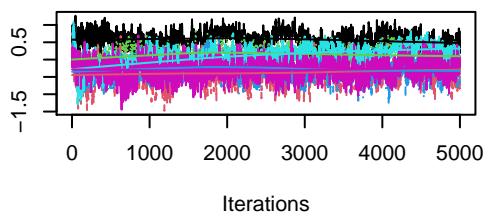
Trace of b62



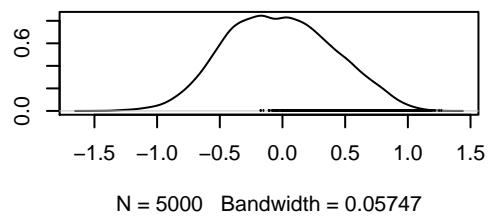
Density of b62



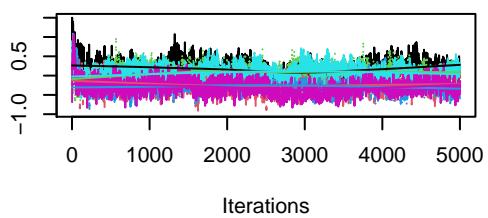
Trace of b63



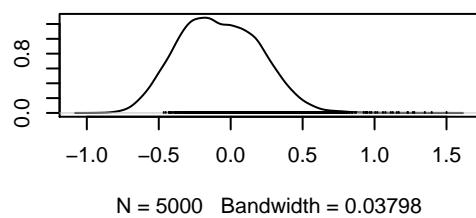
Density of b63



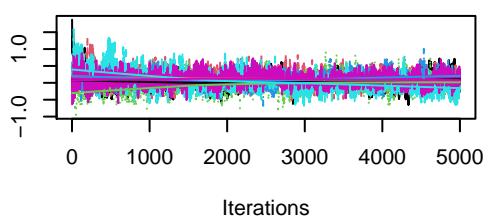
Trace of b64



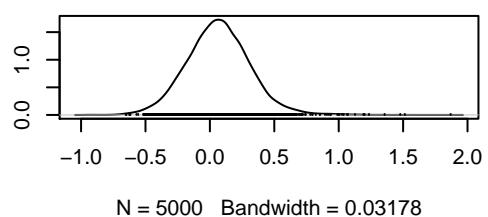
Density of b64



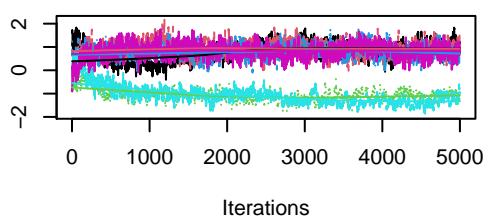
Trace of b65



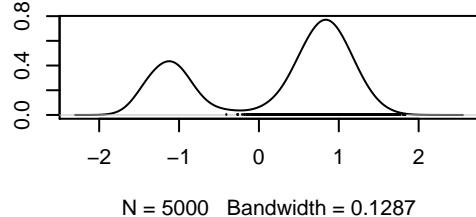
Density of b65



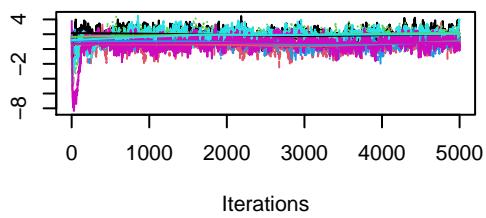
Trace of b66



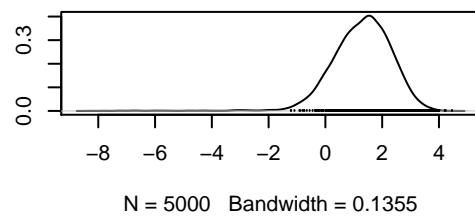
Density of b66



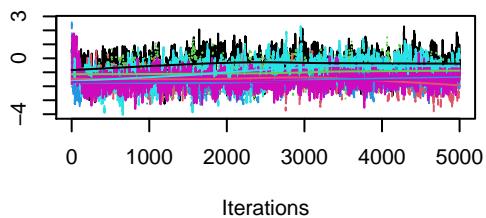
Trace of b71



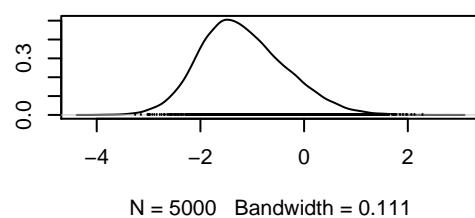
Density of b71



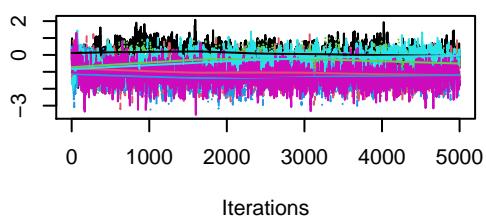
Trace of b72



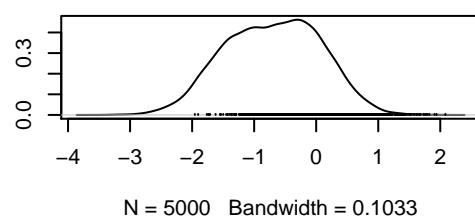
Density of b72



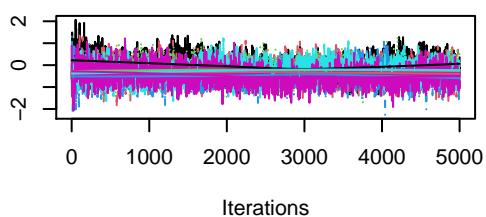
Trace of b73



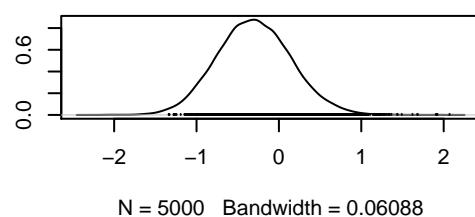
Density of b73



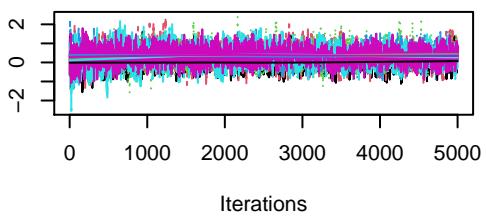
Trace of b74



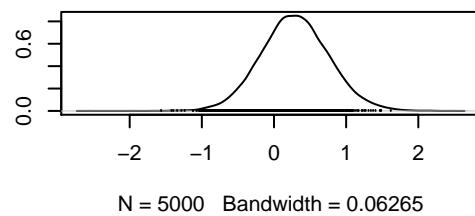
Density of b74



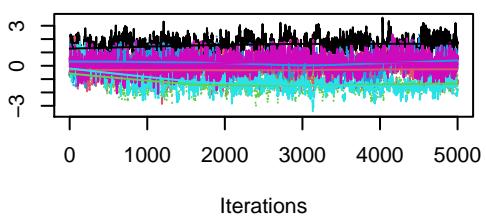
Trace of b75



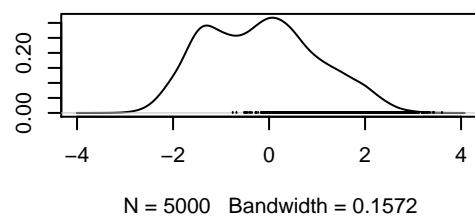
Density of b75



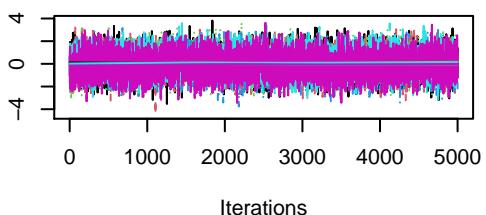
Trace of b76



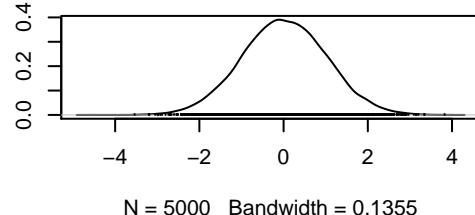
Density of b76



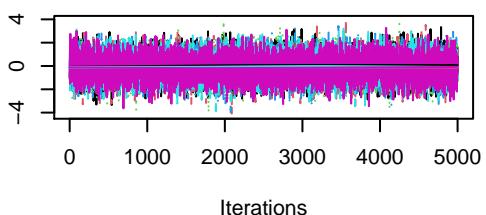
Trace of b81



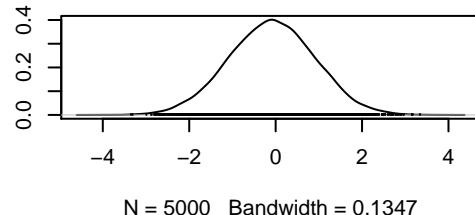
Density of b81

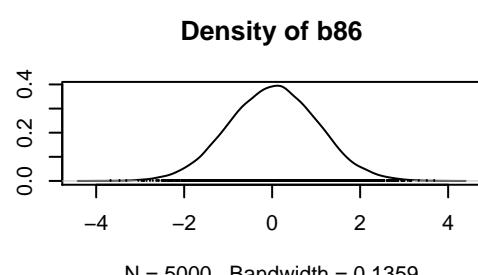
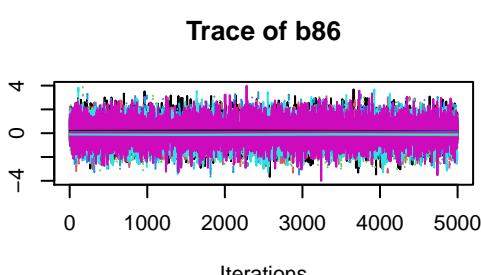
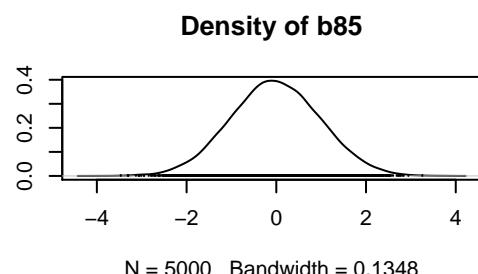
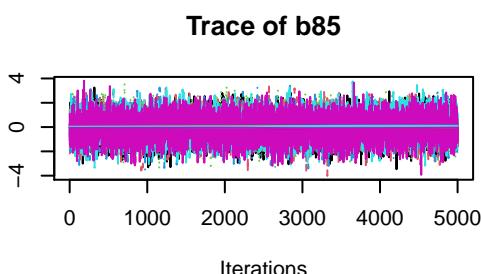
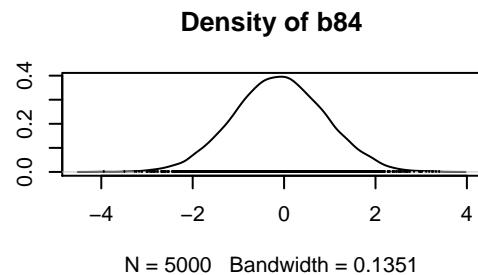
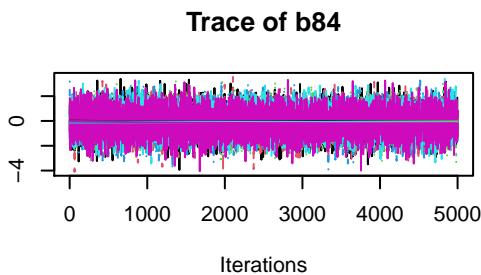
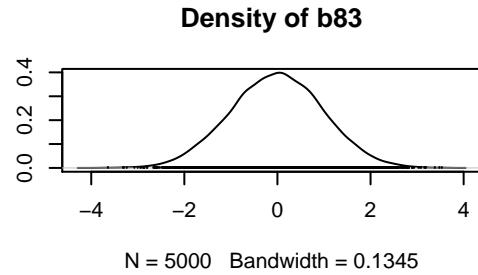
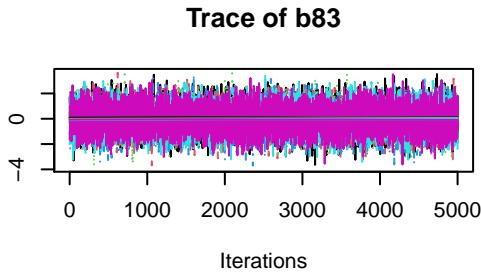


Trace of b82



Density of b82





right_end = 0.5, order = 5, new basis functions, only intercept

```
set.seed(123)
order <- 5
p <- 1
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))

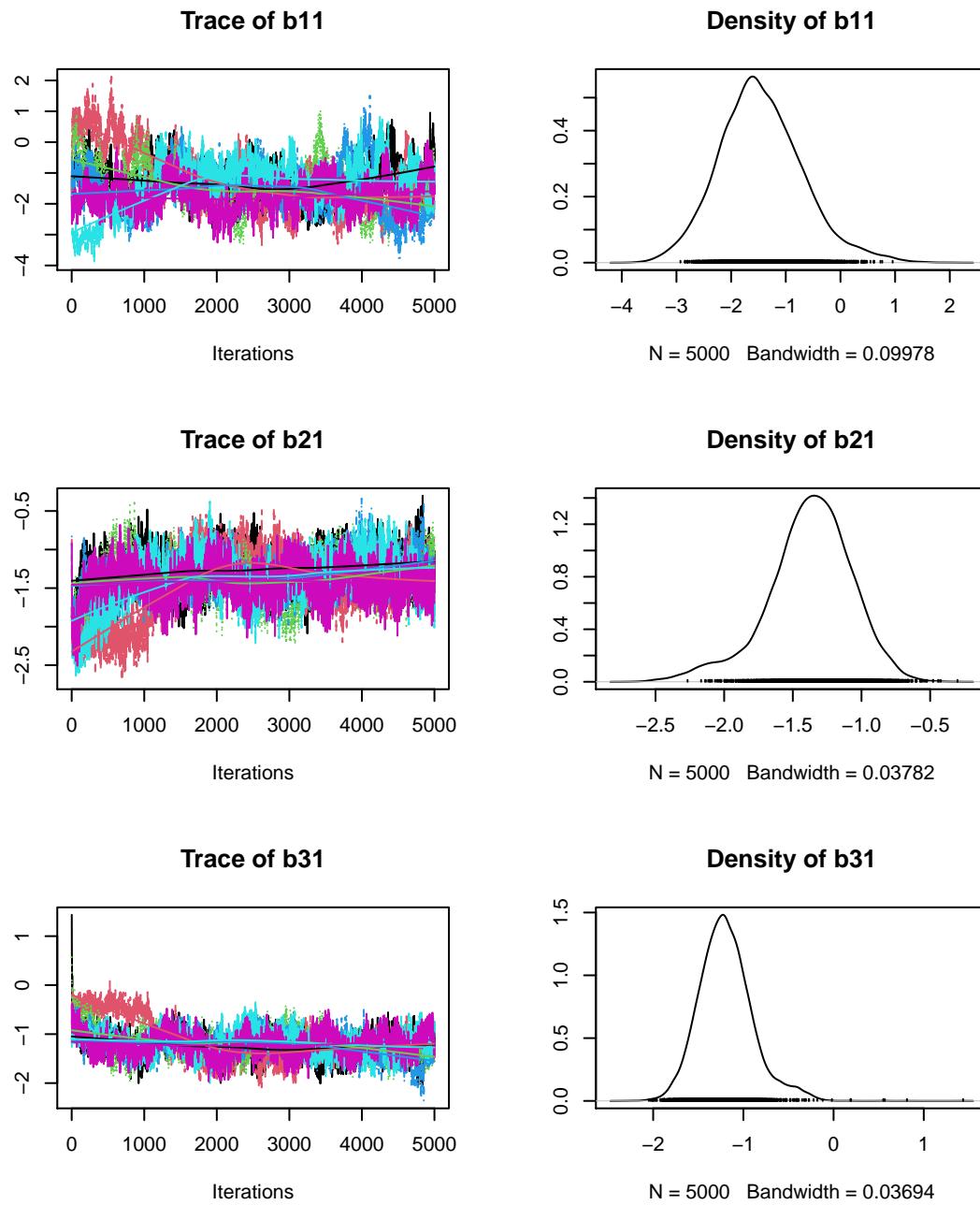
data_trim05 <- get.trim.data(0.5)
```

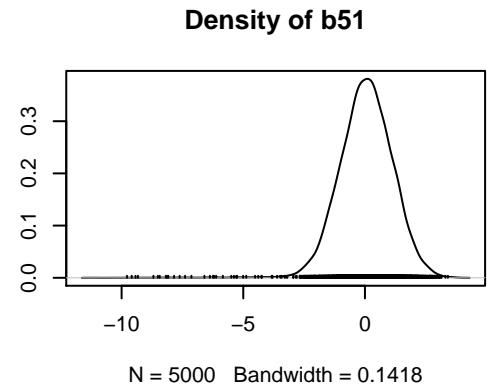
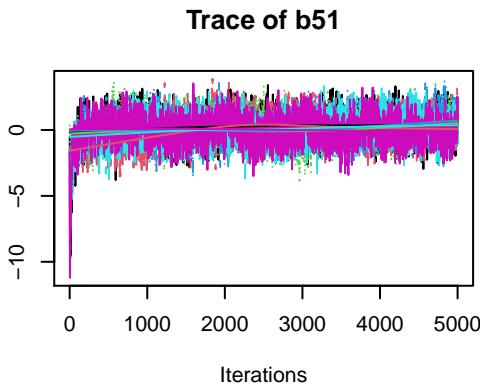
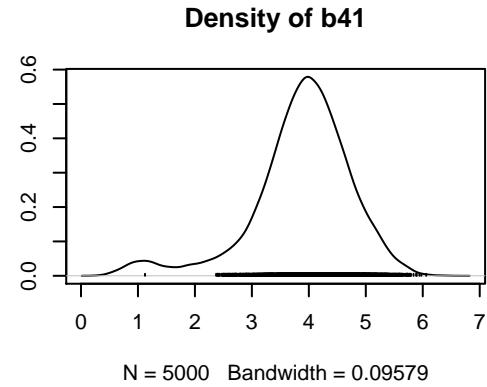
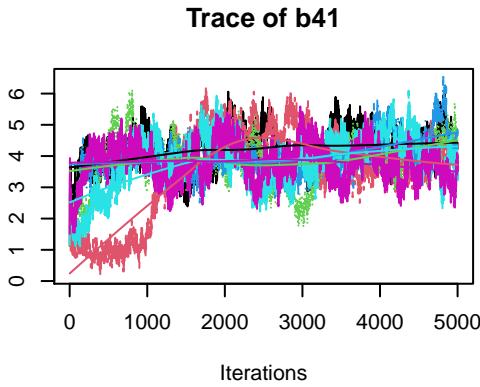
```

noa_o5_multi_trimr05_new_inter <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x[,1], b=b_init[,,i], burn=0, nsamp=5000,
                        thin=1, order = order, right_end = 0.5)

load("./report/report16/noa_o5_multi_trimr05_new_inter.RData")
noa_o5_multi_trimr05_new_inter_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05_new_inter, burn = 0, N =
plot(noa_o5_multi_trimr05_new_inter_coda)

```





right_end = 0.5, order = 5, new basis functions, one predictor

2

```

set.seed(123)
order <- 5
p <- 2
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=1), order, p))

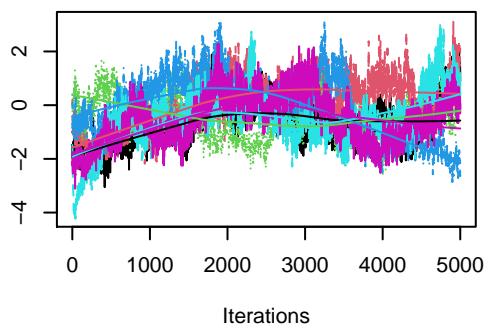
data_trim05 <- get.trim.data(0.5)

noa_o5_multi_trimr05_new_inter_onep_2 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x[,c(1,2)], b=b_init[,,i], burn=0, nsamp=5000,
                        thin=1, order = order, right_end = 0.5)

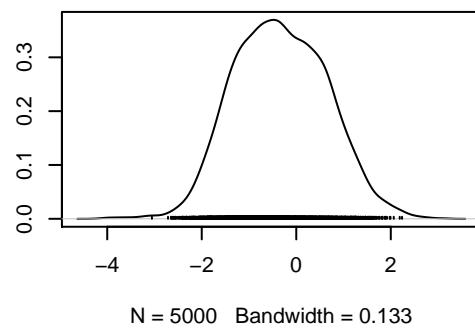
load("./report/report16/noa_o5_multi_trimr05_new_inter_onep_2.RData")
order <- 5
p <- 2
noa_o5_multi_trimr05_new_inter_onep_2_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05_new_inter_onep_
plot(noa_o5_multi_trimr05_new_inter_onep_2_coda)

```

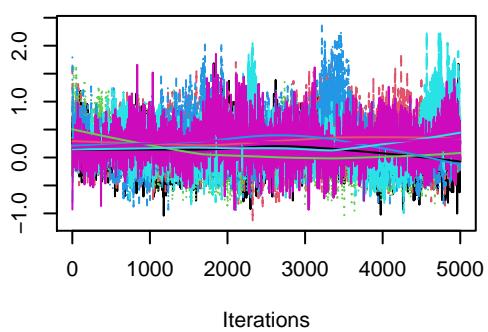
Trace of b_{11}



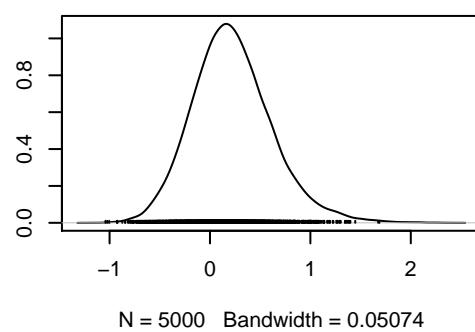
Density of b_{11}



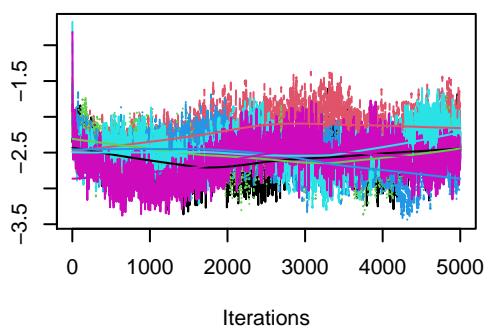
Trace of b_{12}



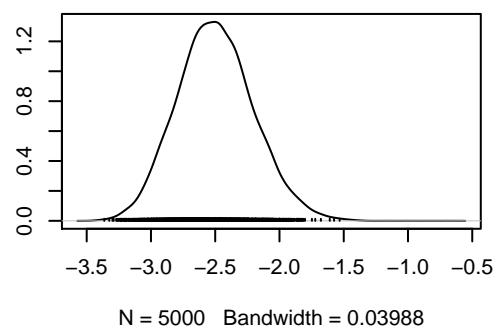
Density of b_{12}



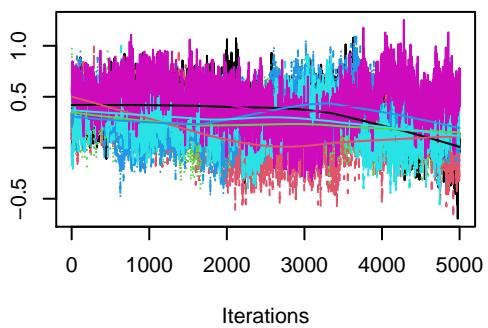
Trace of b_{21}



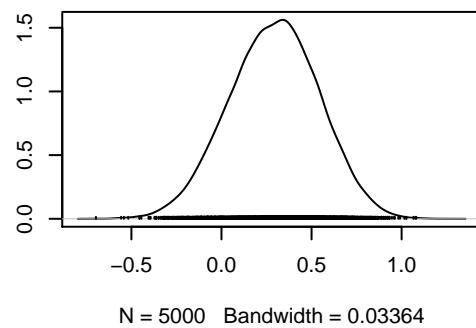
Density of b_{21}



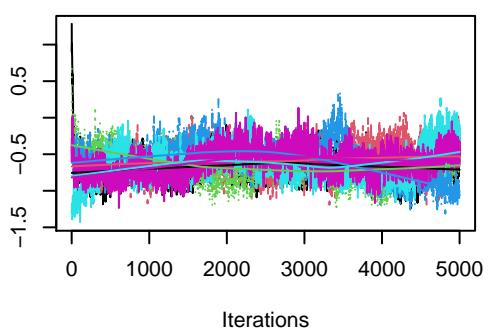
Trace of b22



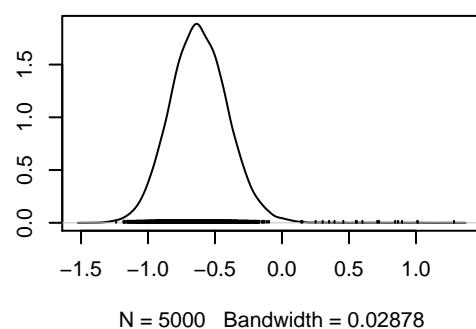
Density of b22



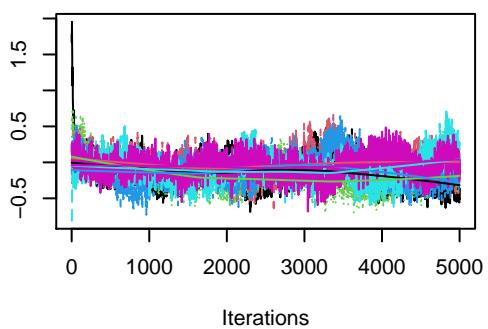
Trace of b31



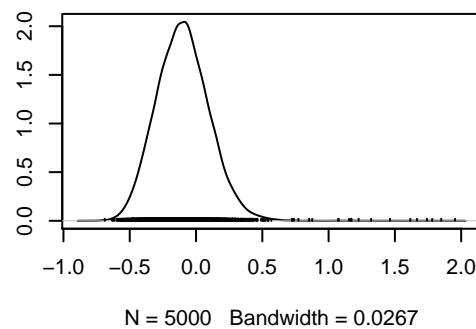
Density of b31



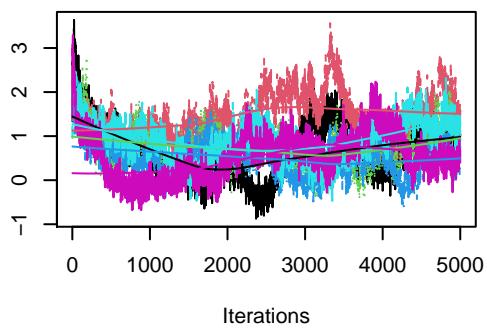
Trace of b32



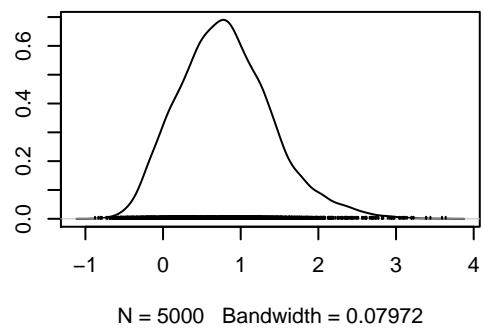
Density of b32



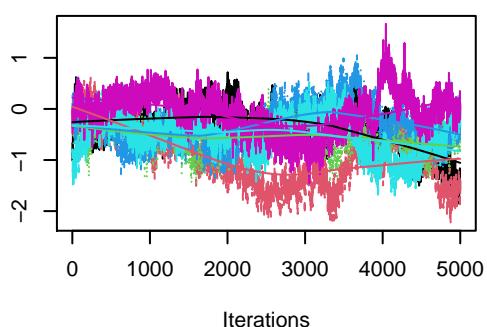
Trace of b41



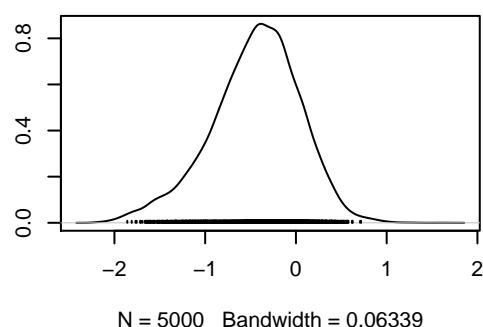
Density of b41



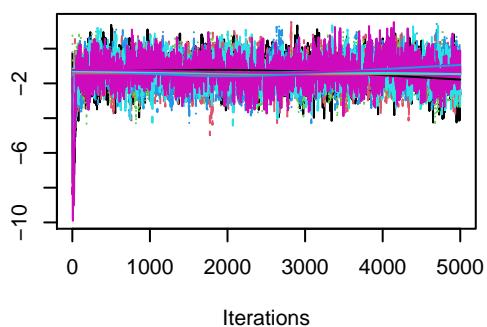
Trace of b42



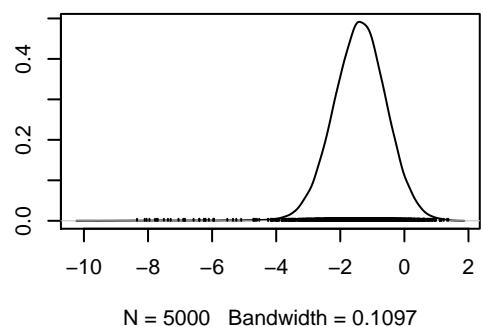
Density of b42



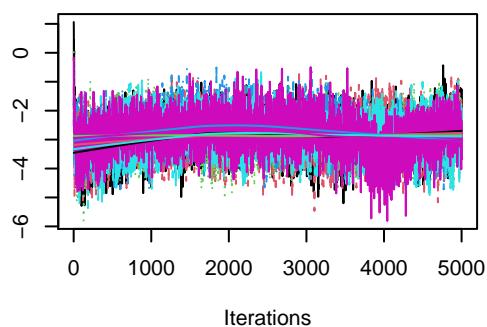
Trace of b51



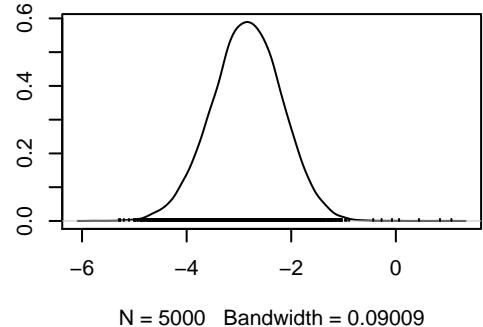
Density of b51



Trace of b52



Density of b52

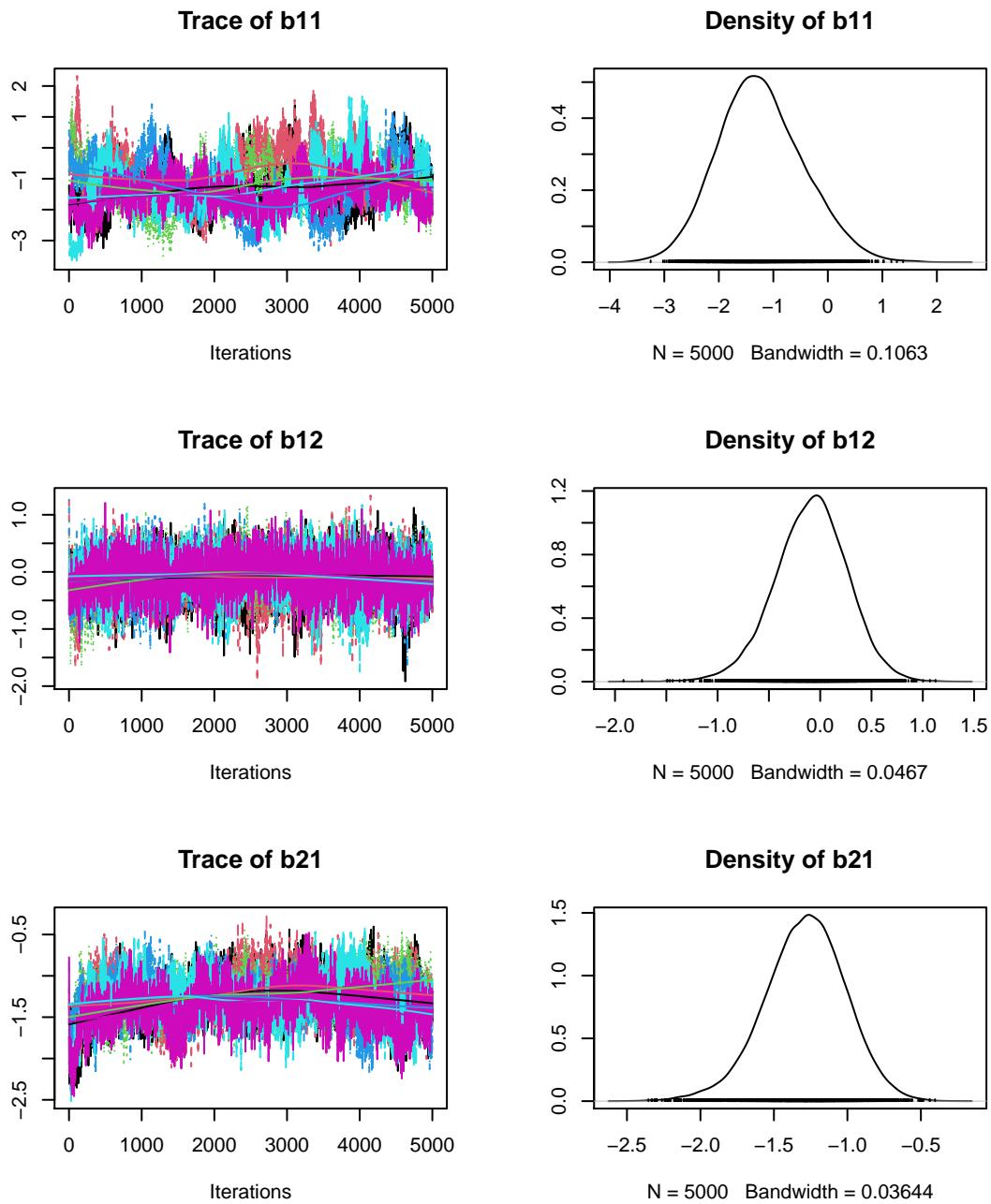


```

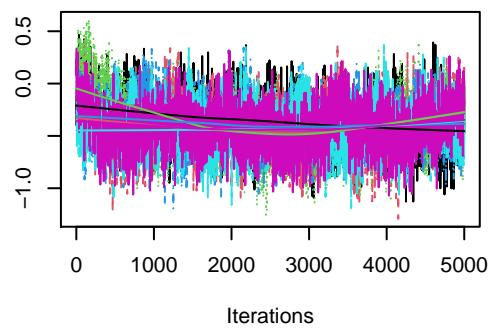
noa_o5_multi_trimr05_new_inter_onep_3 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x[,c(1,3)], b=b_init[,i], burn=0, nsamp=5000,
                        thin=1, order = order, right_end = 0.5)

load("./report/report16/noa_o5_multi_trimr05_new_inter_onep_3.RData")
noa_o5_multi_trimr05_new_inter_onep_3_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05_new_inter_onep_3)
plot(noa_o5_multi_trimr05_new_inter_onep_3_coda)

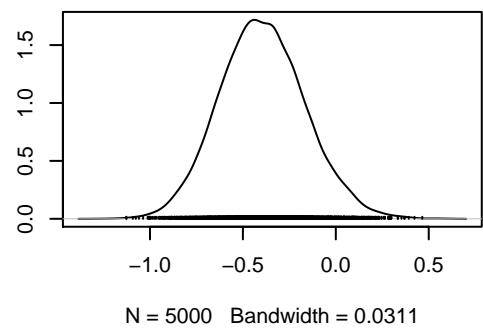
```



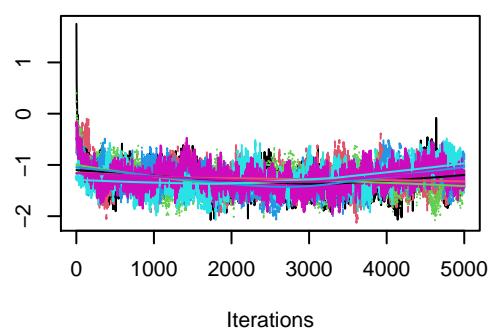
Trace of b22



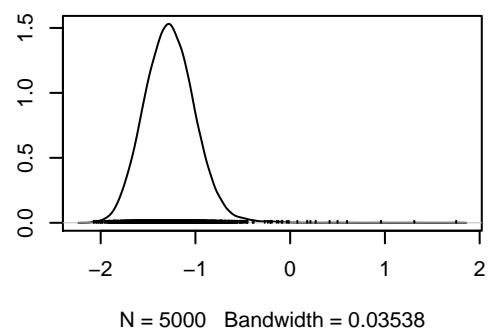
Density of b22



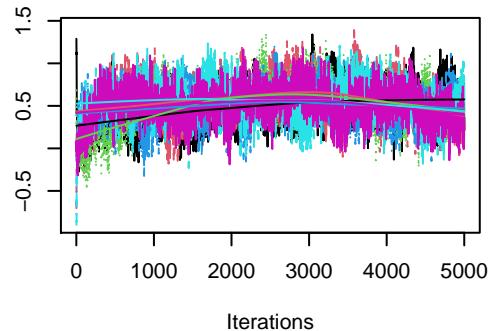
Trace of b31



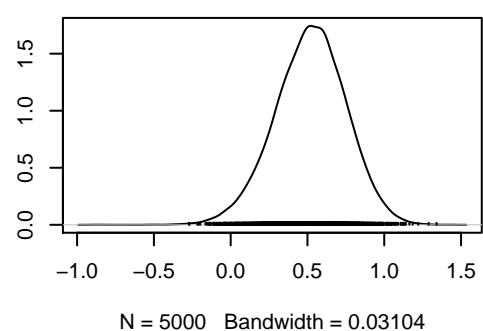
Density of b31



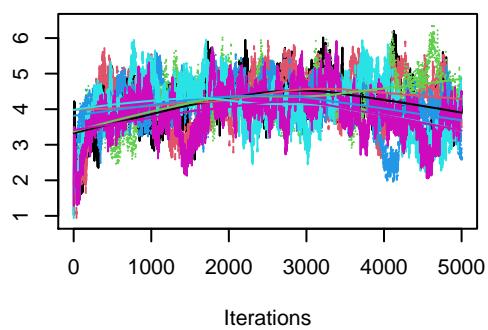
Trace of b32



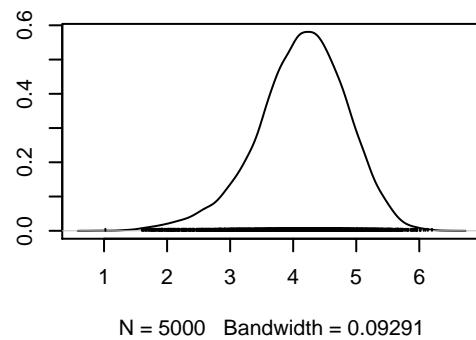
Density of b32



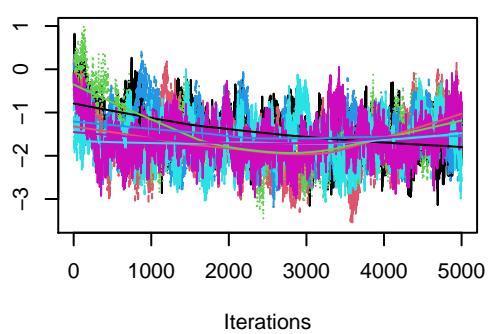
Trace of b41



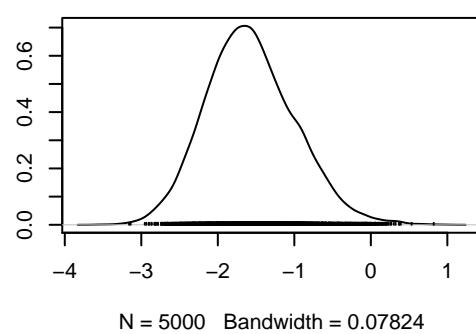
Density of b41



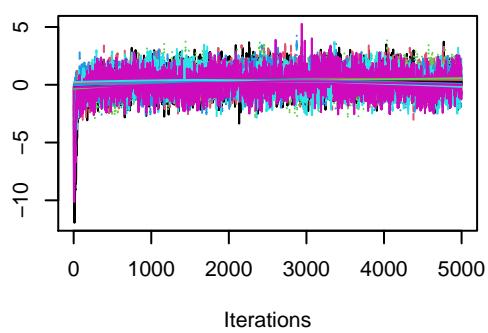
Trace of b42



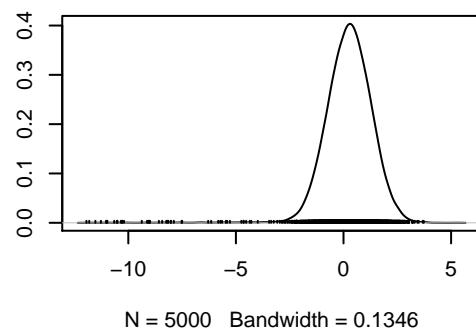
Density of b42



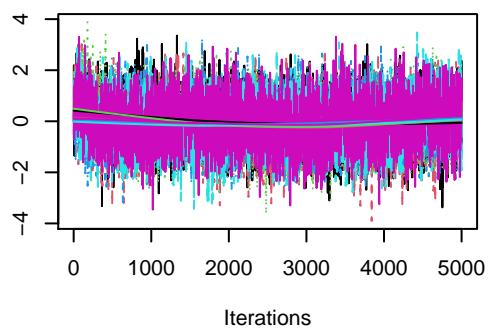
Trace of b51



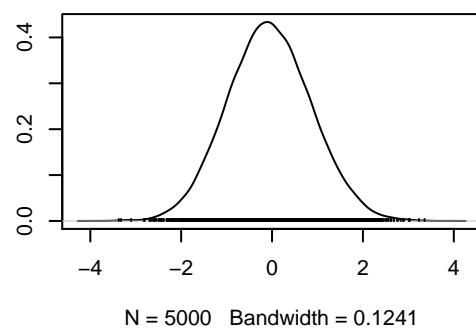
Density of b51



Trace of b52



Density of b52

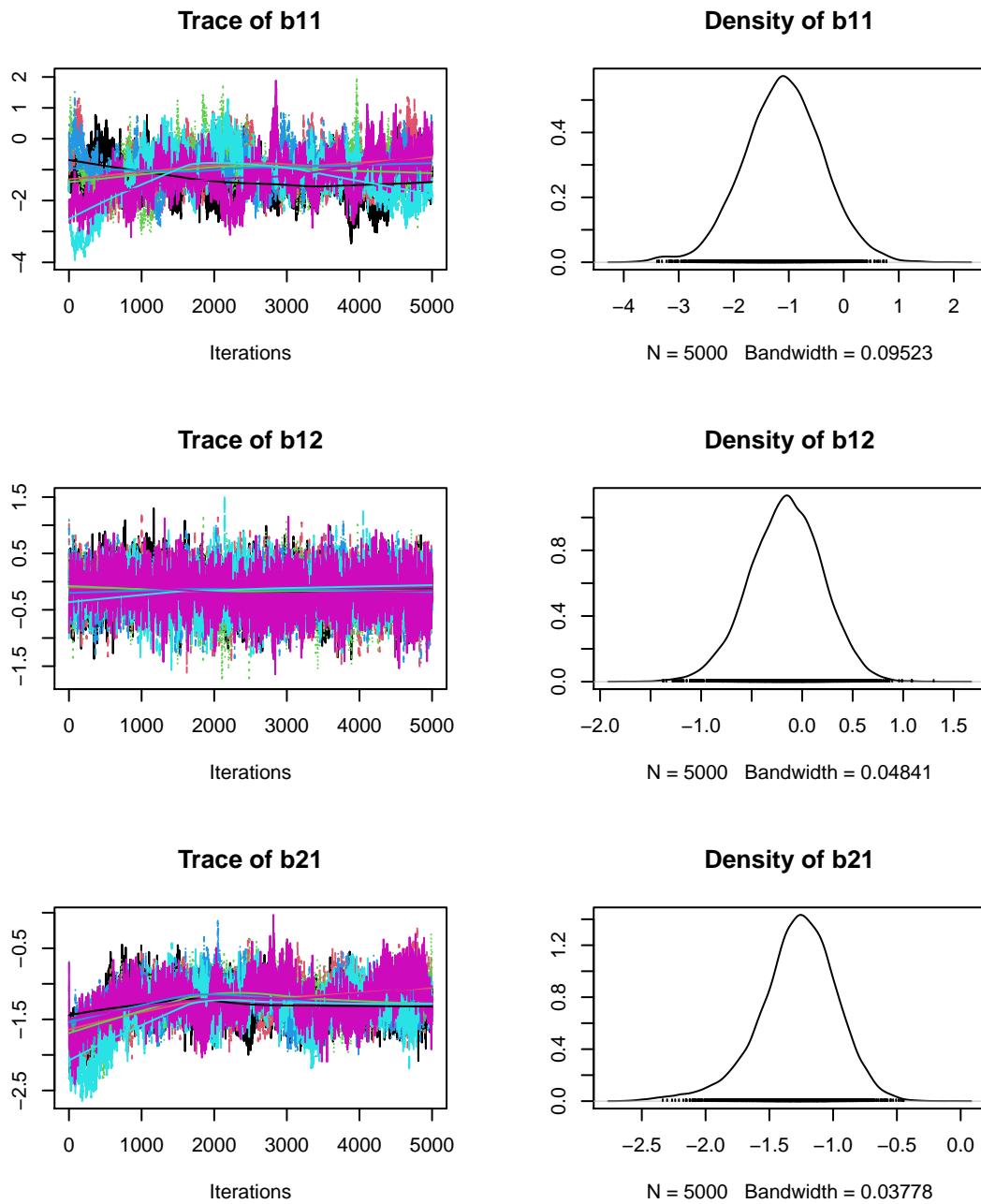


```

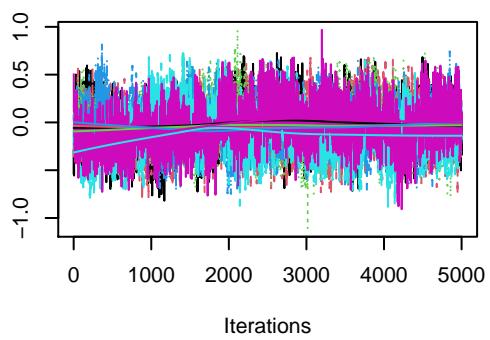
noa_o5_multi_trimr05_new_inter_onep_4 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x[,c(1,4)], b=b_init[,i], burn=0, nsamp=5000,
                        thin=1, order = order, right_end = 0.5)

load("./report/report16/noa_o5_multi_trimr05_new_inter_onep_4.RData")
noa_o5_multi_trimr05_new_inter_onep_4_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05_new_inter_onep_4)
plot(noa_o5_multi_trimr05_new_inter_onep_4_coda)

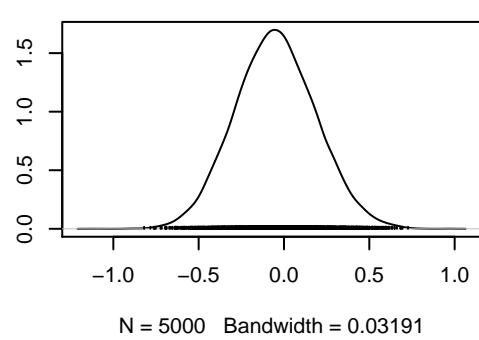
```



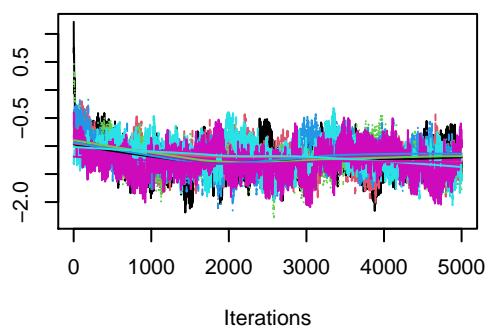
Trace of b22



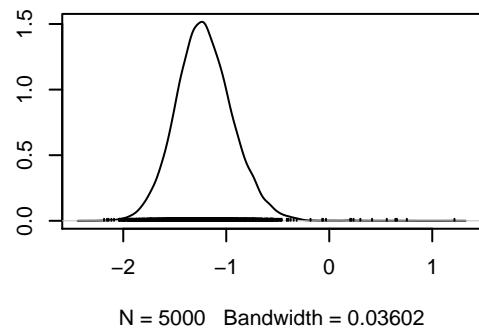
Density of b22



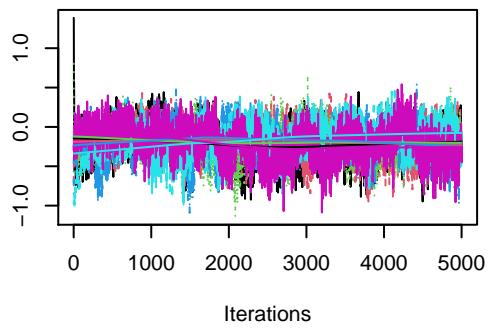
Trace of b31



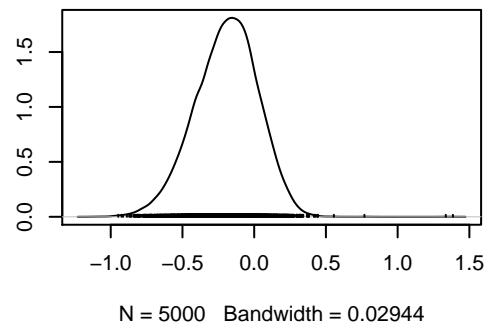
Density of b31

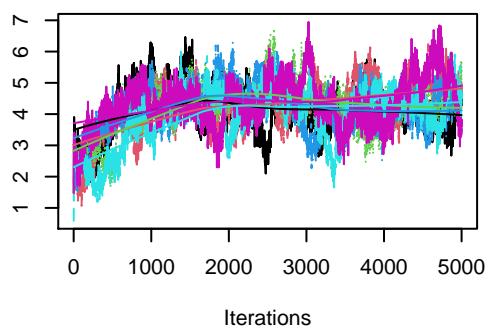
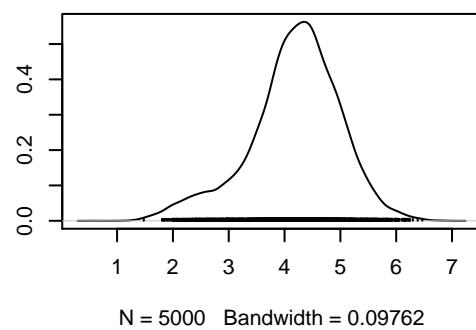
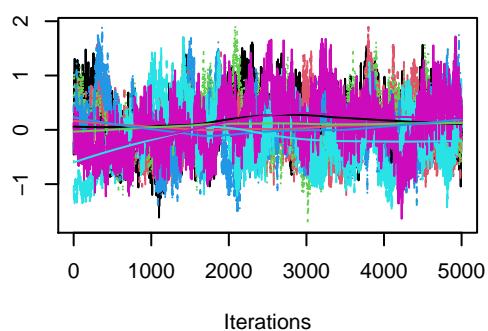
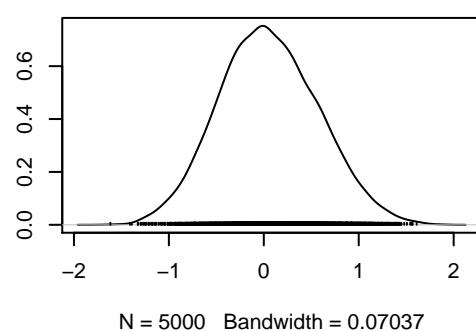
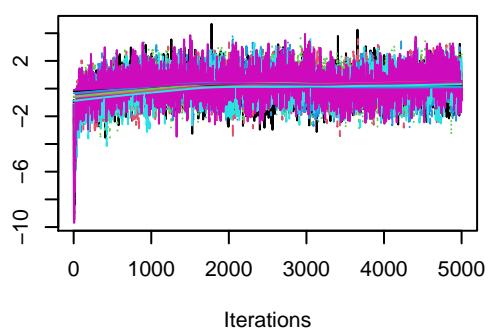
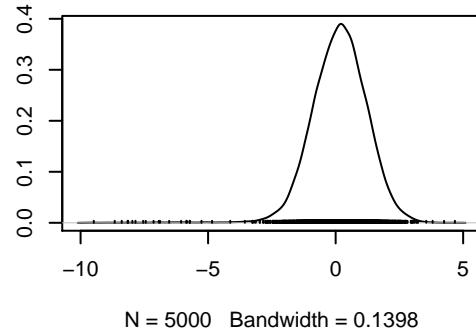
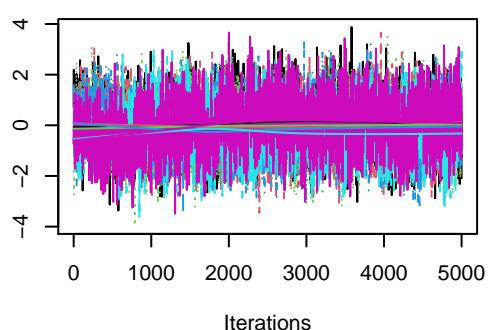
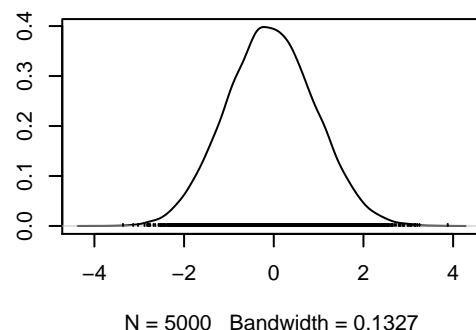


Trace of b32



Density of b32



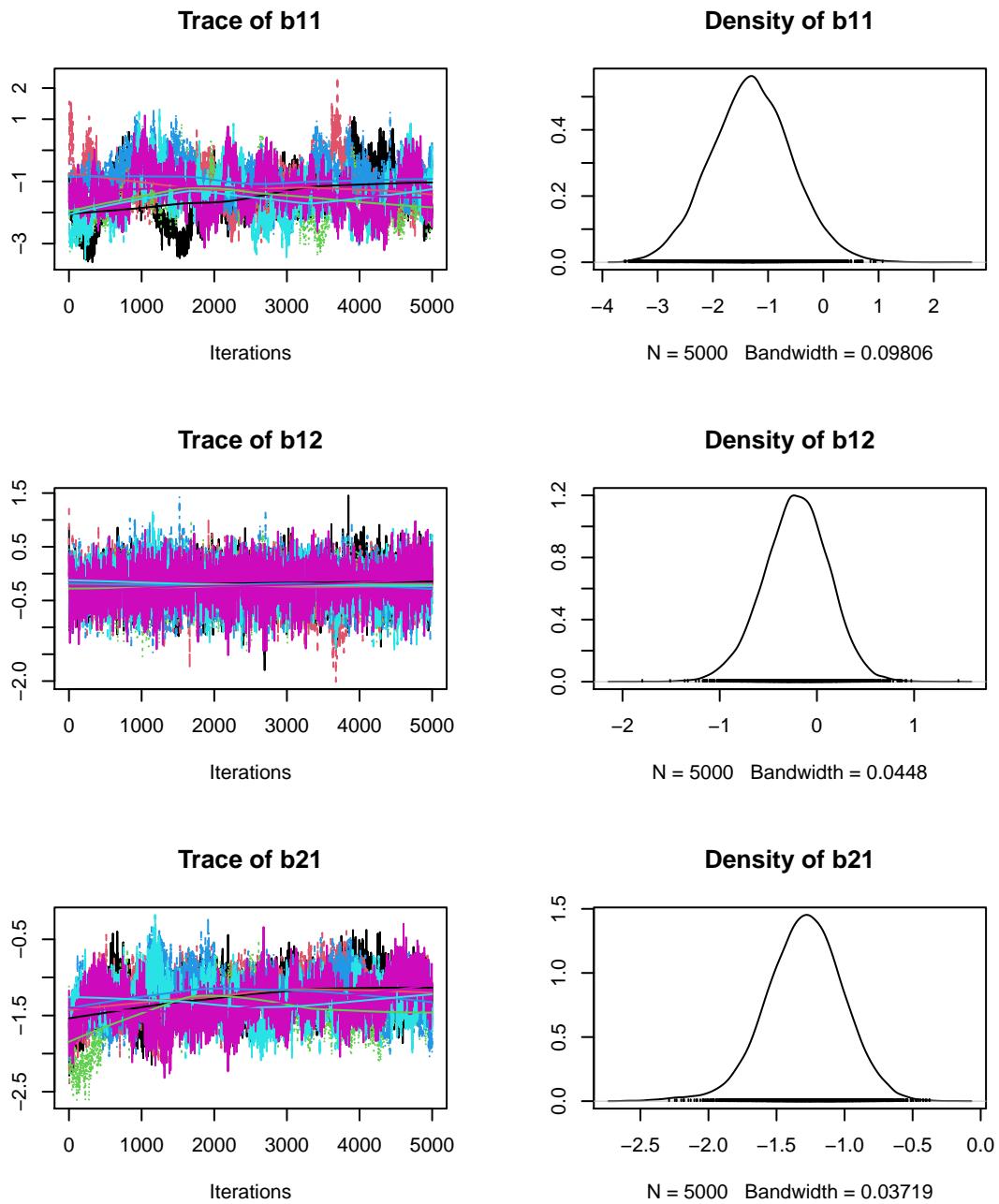
Trace of b41**Density of b41****Trace of b42****Density of b42****Trace of b51****Density of b51****Trace of b52****Density of b52**

```

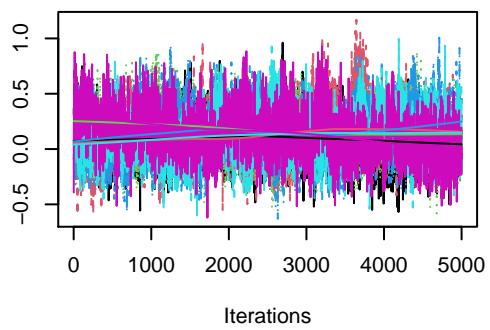
noa_o5_multi_trimr05_new_inter_onep_5 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x[,c(1,5)], b=b_init[,i], burn=0, nsamp=5000,
                        thin=1, order = order, right_end = 0.5)

load("./report/report16/noa_o5_multi_trimr05_new_inter_onep_5.RData")
noa_o5_multi_trimr05_new_inter_onep_5_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05_new_inter_onep_5)
plot(noa_o5_multi_trimr05_new_inter_onep_5_coda)

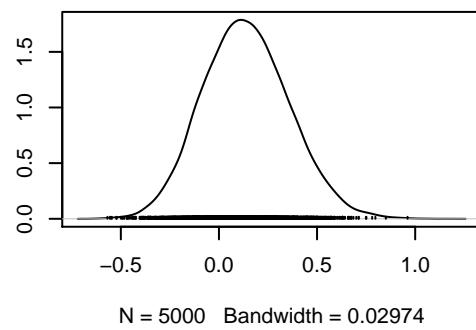
```



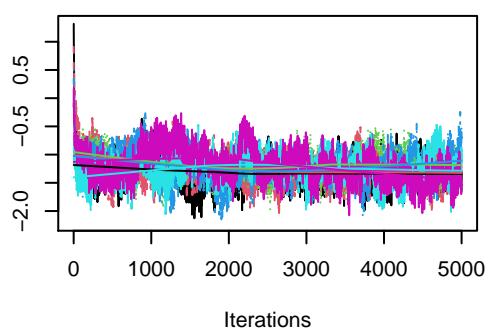
Trace of b22



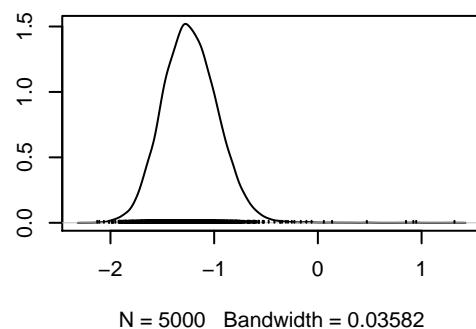
Density of b22



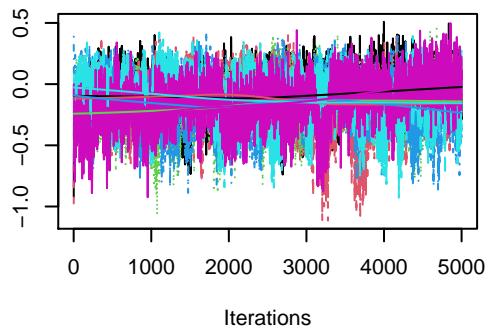
Trace of b31



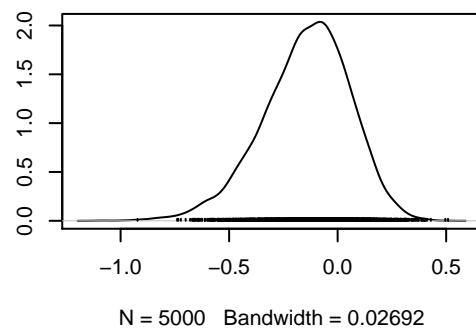
Density of b31

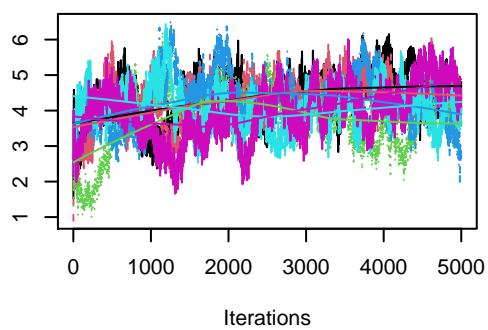
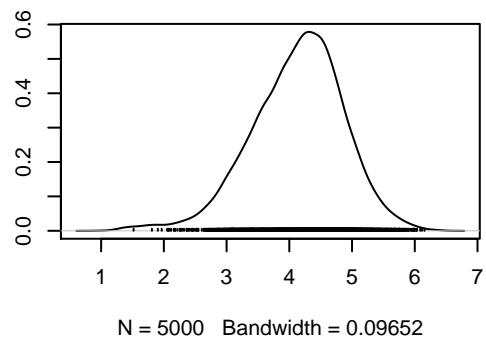
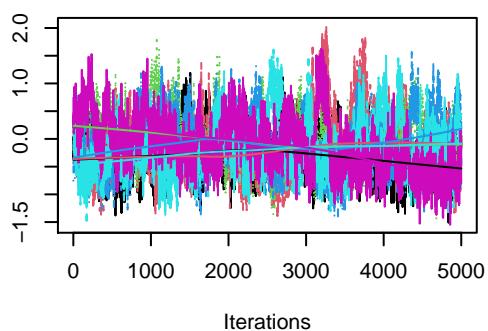
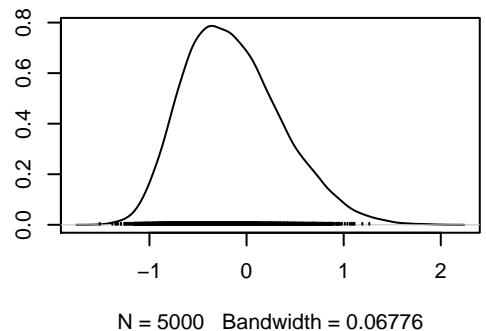
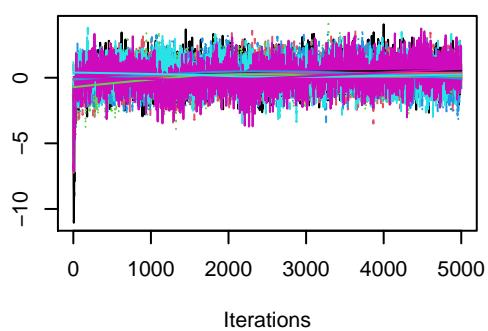
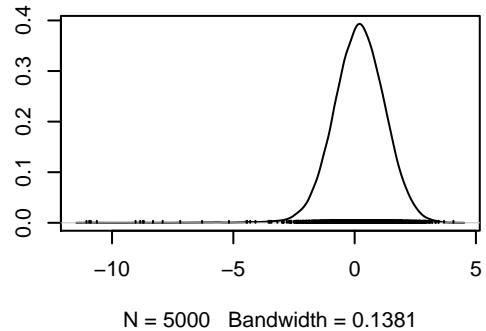
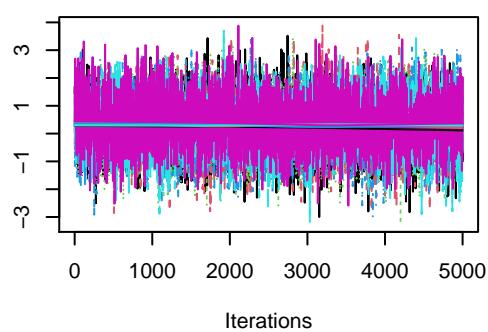
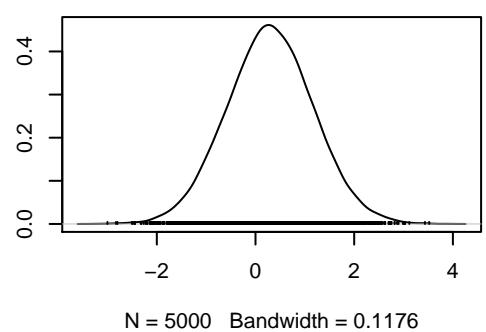


Trace of b32



Density of b32



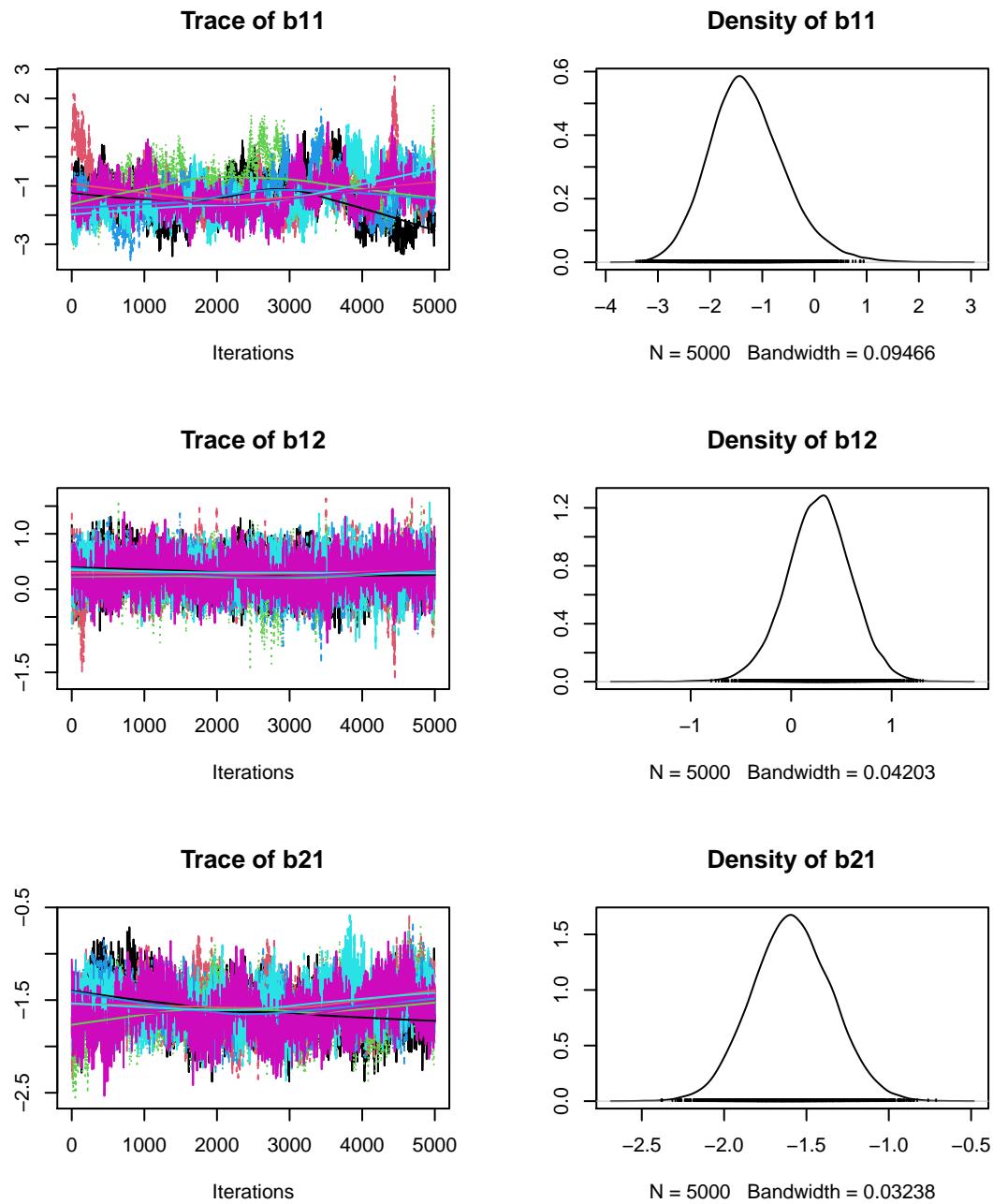
Trace of b41**Density of b41****Trace of b42****Density of b42****Trace of b51****Density of b51****Trace of b52****Density of b52**

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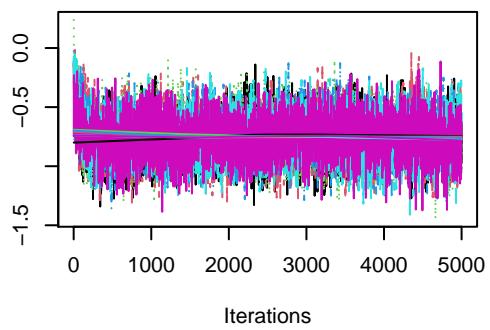
noa_o5_multi_trimr05_new_inter_onep_6 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x[,c(1,6)], b=b_init[,i], burn=0, nsamp=5000,
                        thin=1, order = order, right_end = 0.5)

load("./report/report16/noa_o5_multi_trimr05_new_inter_onep_6.RData")
noa_o5_multi_trimr05_new_inter_onep_6_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05_new_inter_onep_6)
plot(noa_o5_multi_trimr05_new_inter_onep_6_coda)

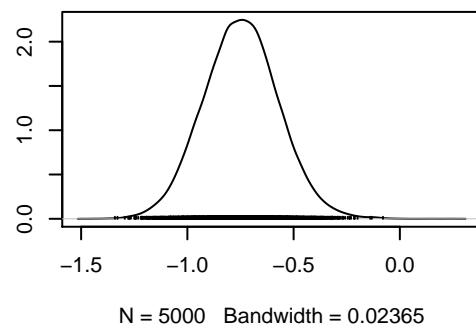
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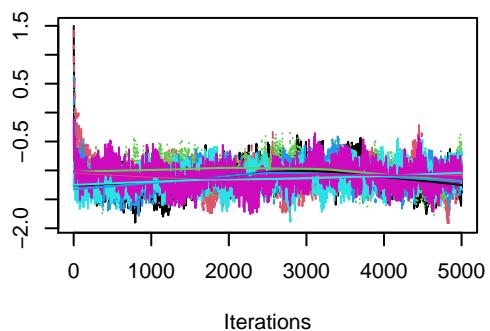
Trace of b22



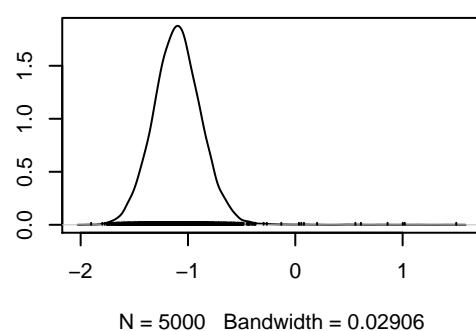
Density of b22



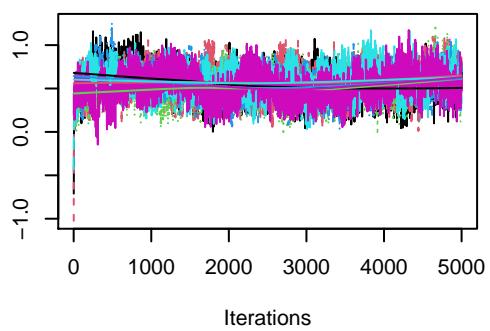
Trace of b31



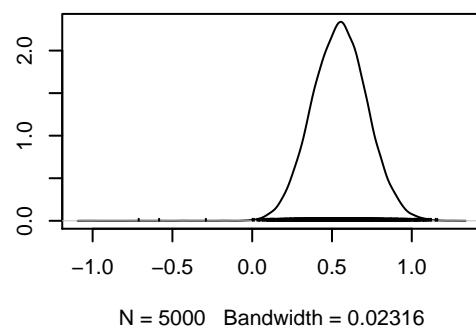
Density of b31

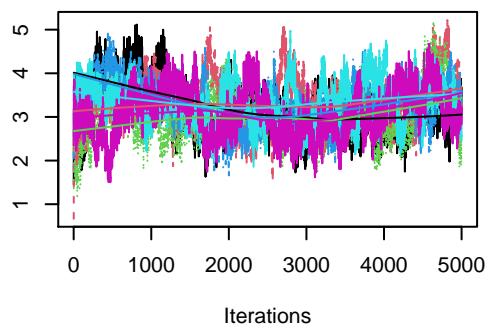
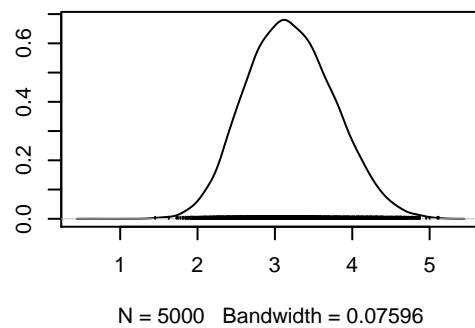
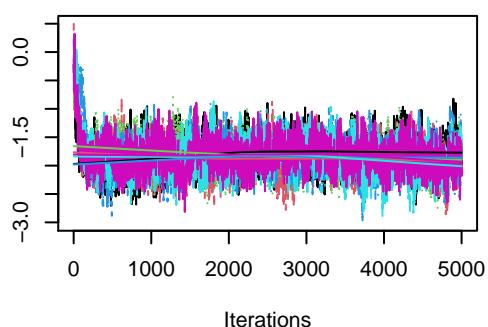
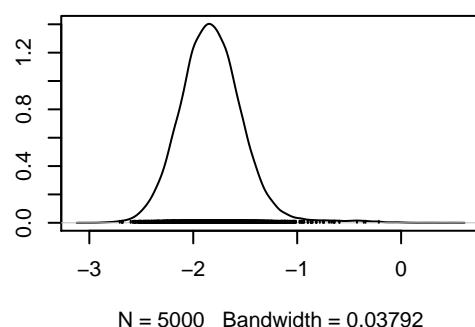
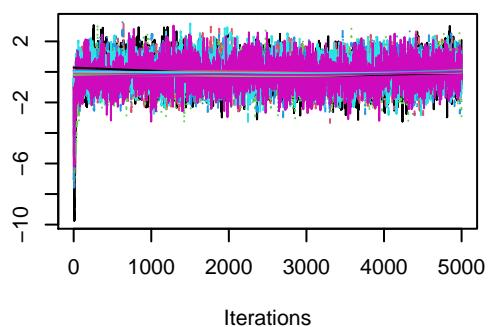
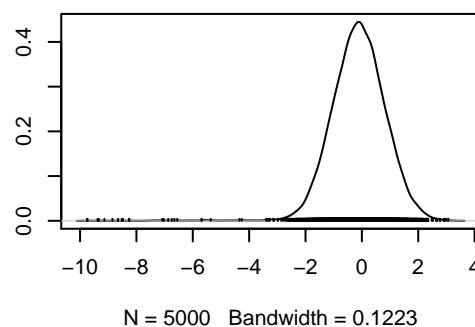
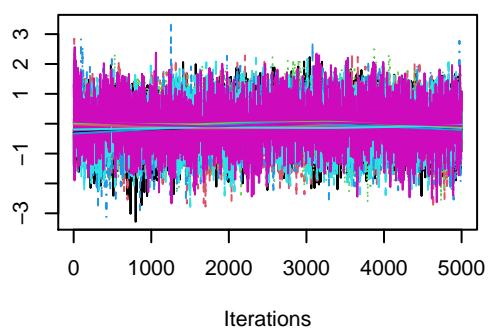


Trace of b32



Density of b32



Trace of b41**Density of b41****Trace of b42****Density of b42****Trace of b51****Density of b51****Trace of b52****Density of b52**