

report16

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trim, no alpha	2
right_end = 0.5, order = 5	3
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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))
}

```

```

length_trim <- 1 + right_end
kbw <- length_trim/(order-1)
knots <- seq(-1,right_end,kbw)
bsd.sq <- (0.67*kbw)^2
gausskern <- lapply(knots, function(mu) return(function(x) return(exp(-0.5*(x-mu)^2/bsd.sq))))
get.poly.mat <- function(y) return(sapply(gausskern, function(f) f(y)))

get.miss.reject.x <- function(b, n, x, a, shapes=c(1,1), jbw=0.16,
                                length_trim, positive=FALSE){
  n.hits <- 0
  n.miss <- 0
  Poly.miss <- NULL
  Half.miss <- NULL
  w.miss <- NULL
  x.miss <- NULL
  y.miss <- NULL

  xa <- c(x %*% a)
  if(positive) xa <- pmax(0, xa)

  nremain <- n
  ixremain <- 1:n
  while(nremain > 0){
    z <- length_trim*rbeta(nremain, shapes[1], shapes[2])-1

```

trim, no alpha

right_end = 0.5, order = 5

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

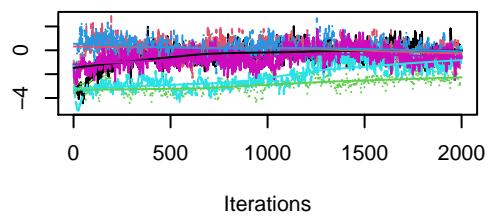
data_trim05 <- get.trim.data(0.5)

noa_o5_multi_trimr05 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x, b=b_init[,i], burn=0, nsamp=2000,
                        thin=1, order = order, right_end = 0.5)

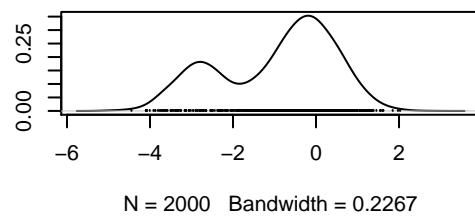
load("./report/report16/noa_o5_multi_trimr05.RData")

noa_o5_multi_trimr05_coda <- multi_chain_coda_noa(noa_o5_multi_trimr05, burn = 0, N_para, p, order = or
plot(noa_o5_multi_trimr05_coda)
```

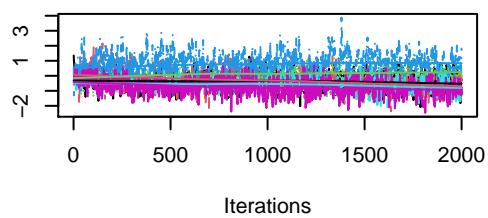
Trace of b_{11}



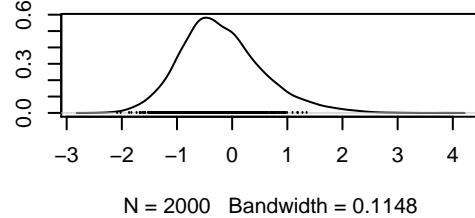
Density of b_{11}



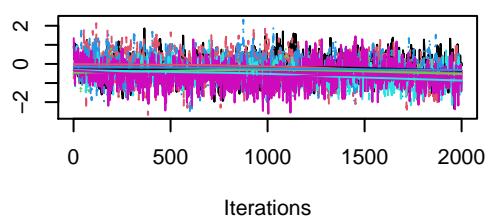
Trace of b_{12}



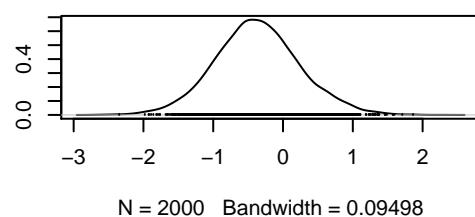
Density of b_{12}



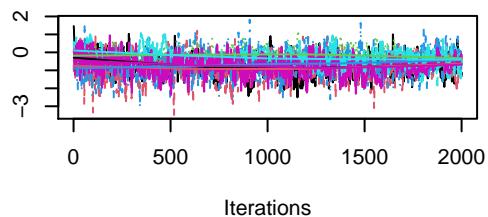
Trace of b_{13}



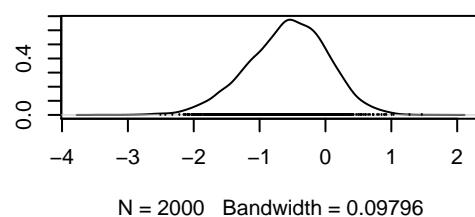
Density of b_{13}



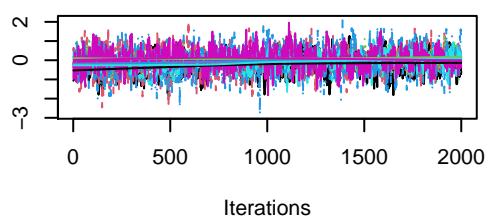
Trace of b_{14}



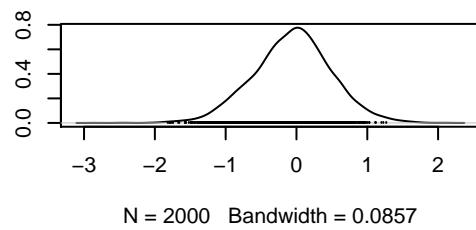
Density of b_{14}



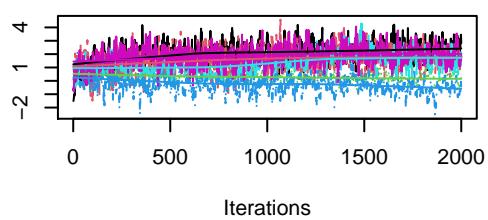
Trace of b15



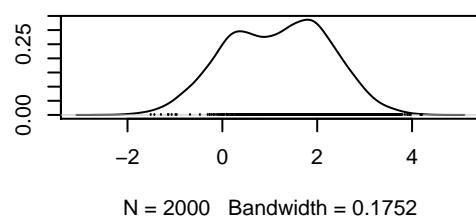
Density of b15



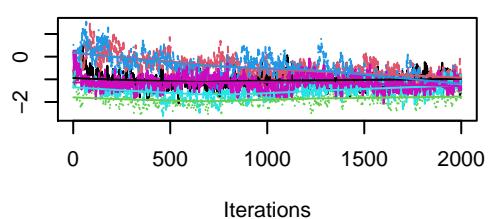
Trace of b16



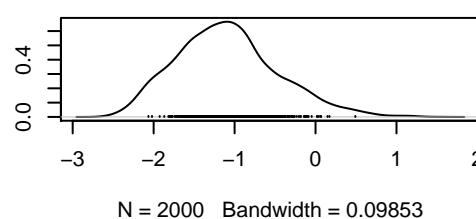
Density of b16



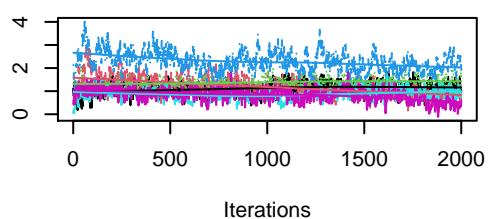
Trace of b21



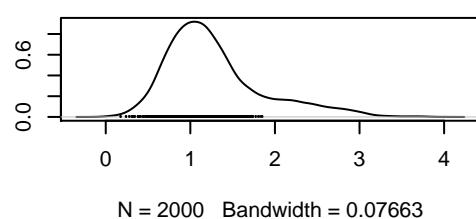
Density of b21



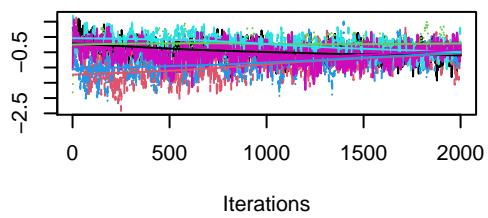
Trace of b22



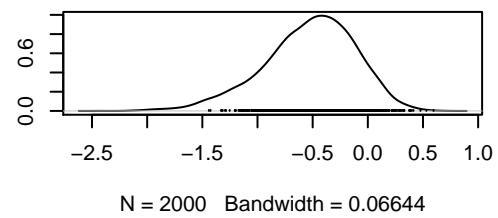
Density of b22



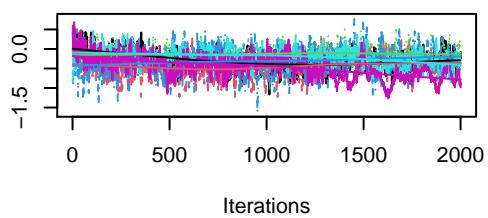
Trace of b23



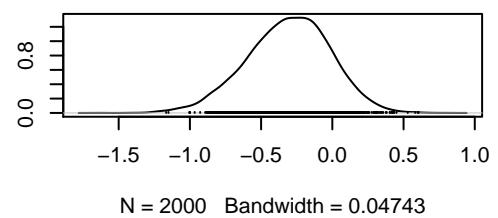
Density of b23



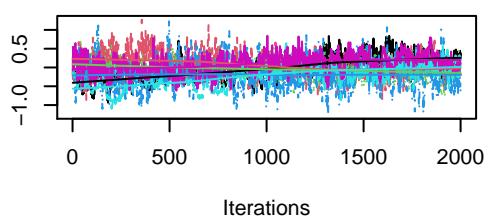
Trace of b24



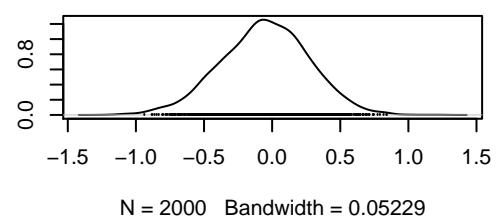
Density of b24



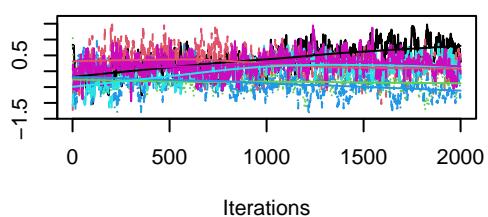
Trace of b25



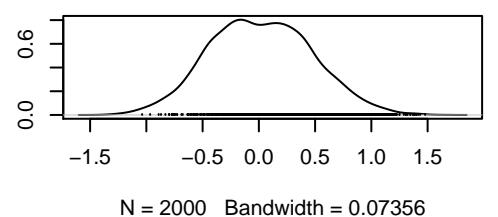
Density of b25



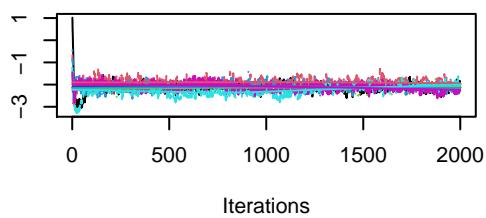
Trace of b26



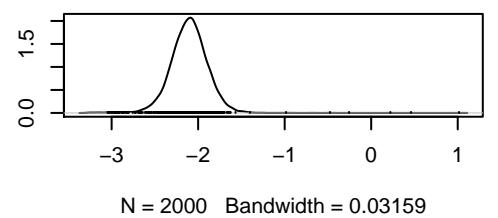
Density of b26



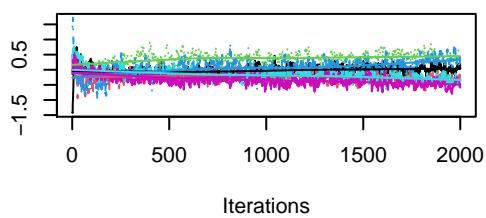
Trace of b31



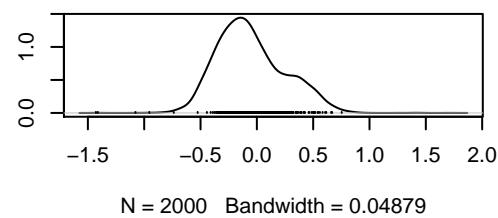
Density of b31



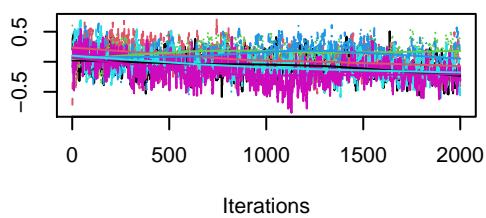
Trace of b32



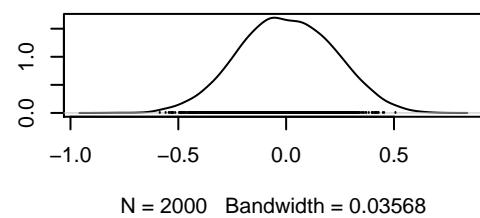
Density of b32



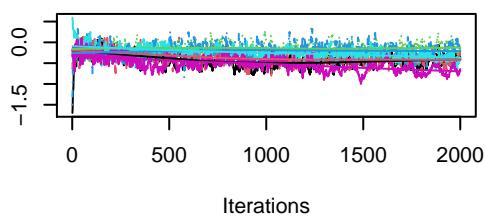
Trace of b33



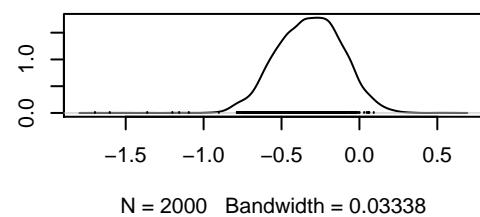
Density of b33



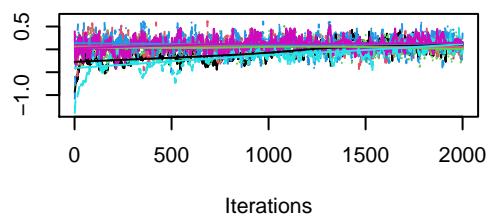
Trace of b34



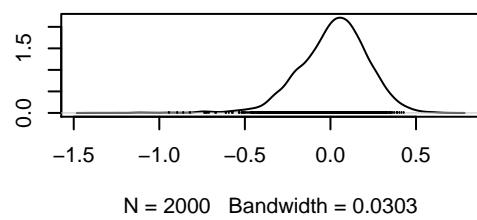
Density of b34



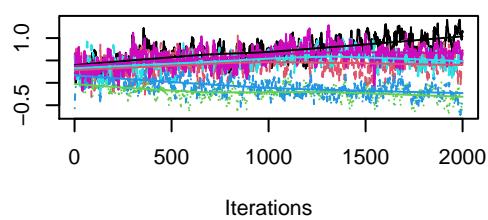
Trace of b35



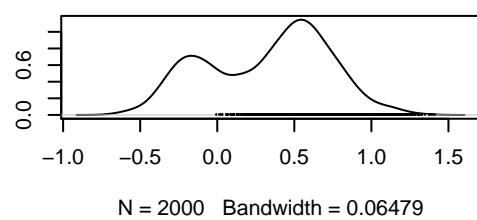
Density of b35



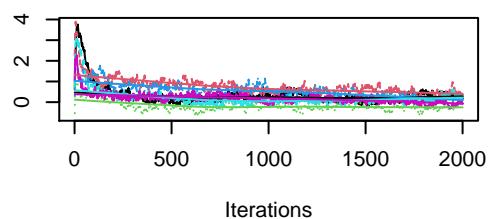
Trace of b36



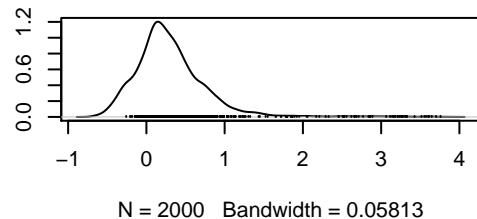
Density of b36



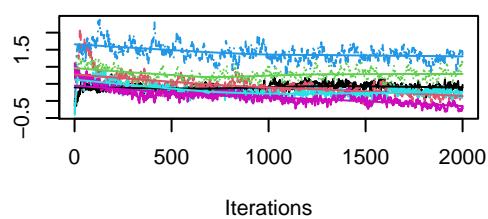
Trace of b41



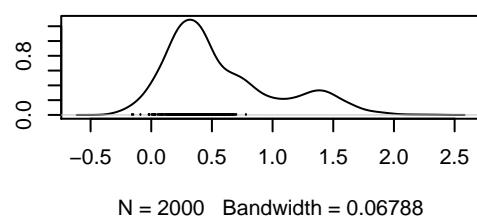
Density of b41



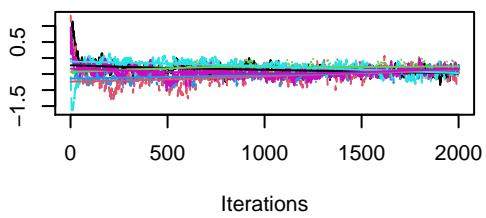
Trace of b42



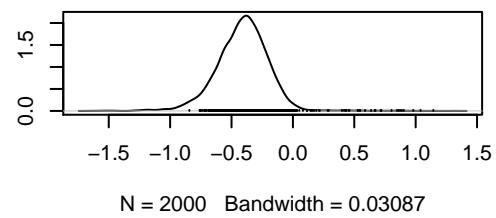
Density of b42



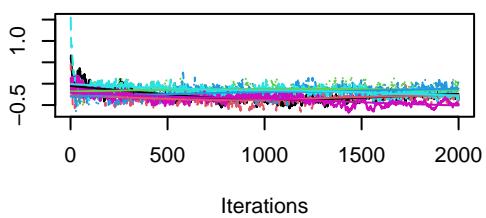
Trace of b43



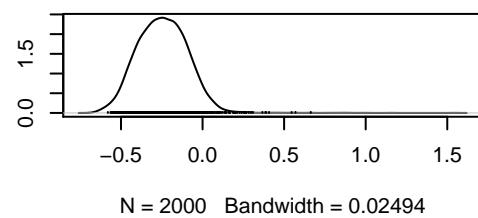
Density of b43



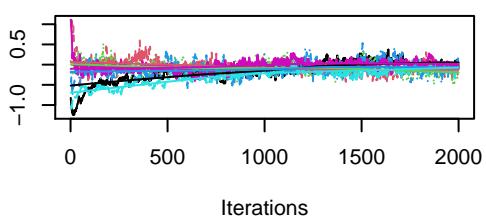
Trace of b44



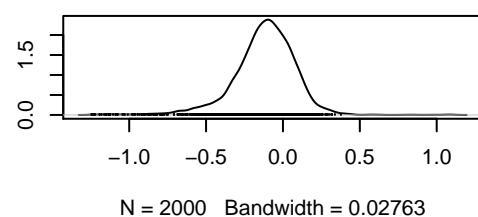
Density of b44



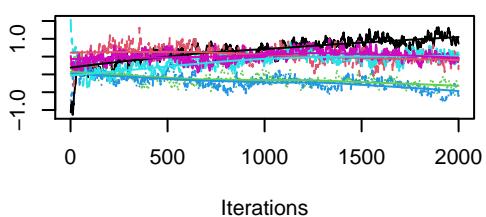
Trace of b45



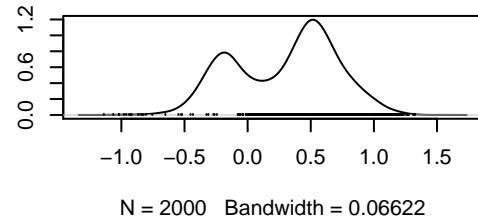
Density of b45



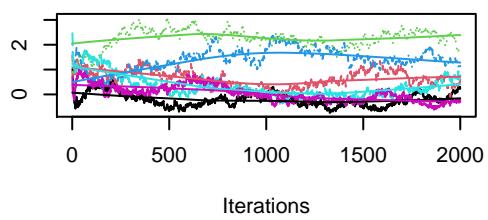
Trace of b46



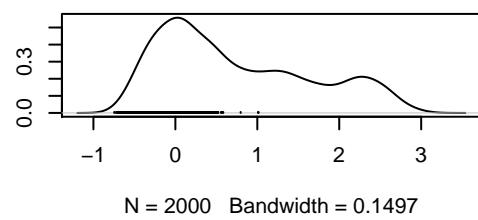
Density of b46



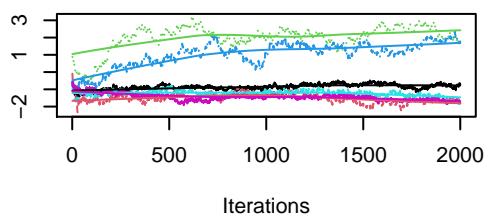
Trace of b51



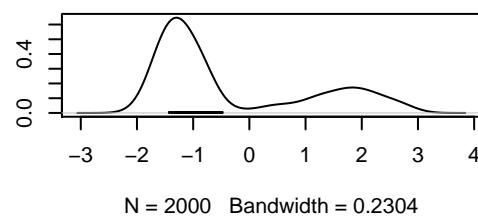
Density of b51



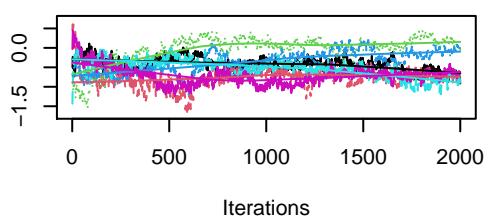
Trace of b52



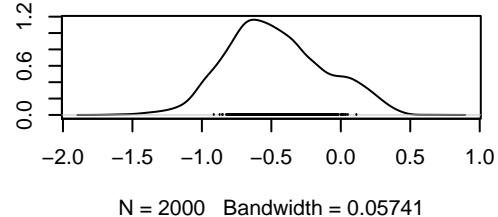
Density of b52



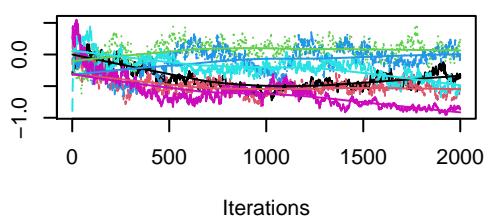
Trace of b53



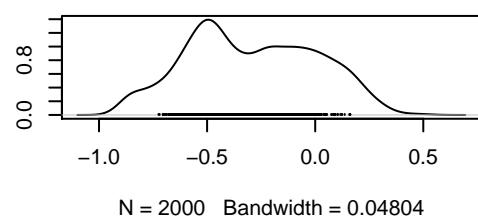
Density of b53

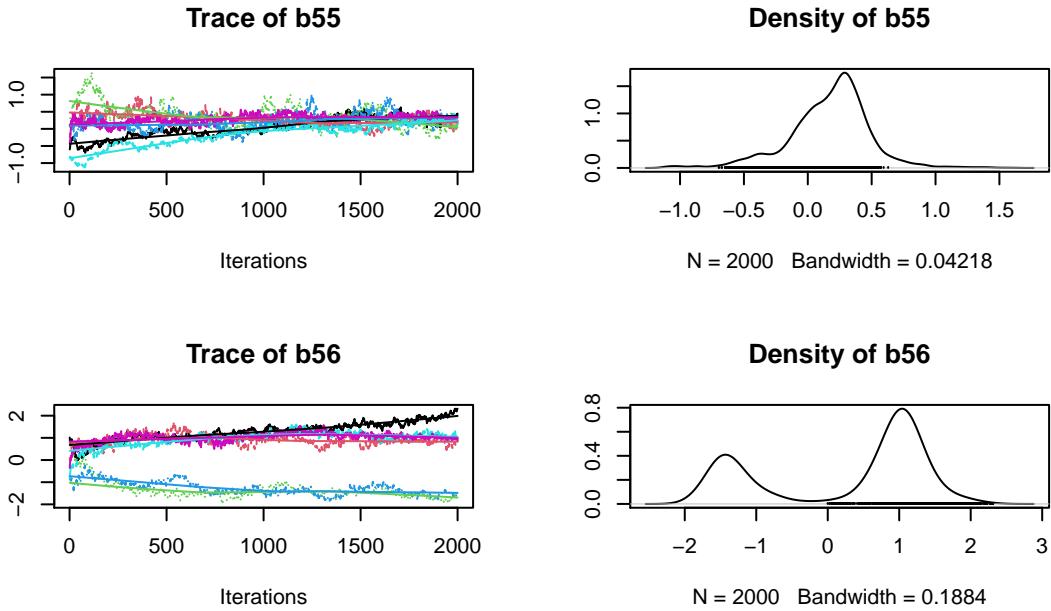


Trace of b54



Density of b54





`right_end = 0.5, order = 10`

```

set.seed(123)
order <- 10
b_init <- replicate(N_para, matrix(rnorm(n = order*p, sd=3), order, p))

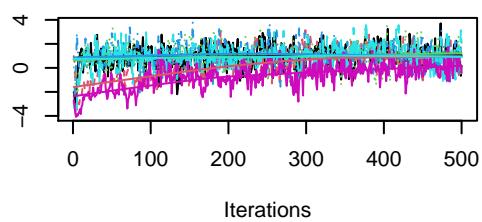
noa_o10_multi_trimr05 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim05$y, x=data_trim05$x, b=b_init[,,i], burn=0, nsamp=500,
                        thin=1, order = order, right_end = 0.5)

load("./report/report16/noa_o10_multi_trimr05.RData")

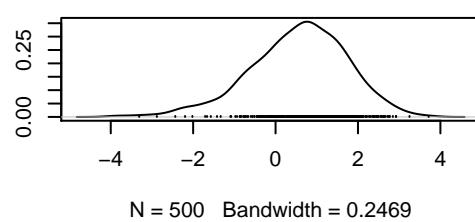
noa_o10_multi_trimr05_coda <- multi_chain_coda_noa(noa_o10_multi_trimr05, burn = 0, N_para, p, order = order)
plot(noa_o10_multi_trimr05_coda)

```

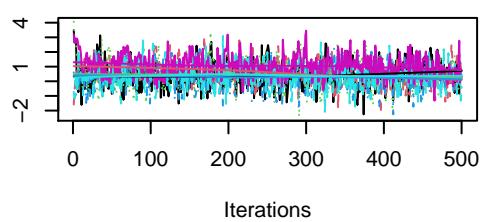
Trace of b_{11}



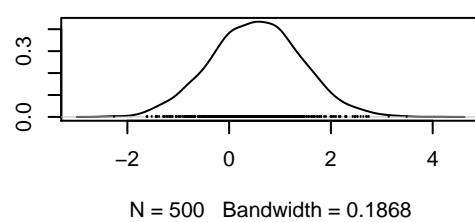
Density of b_{11}



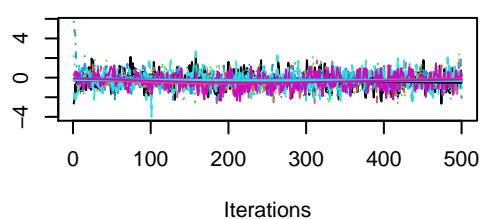
Trace of b_{12}



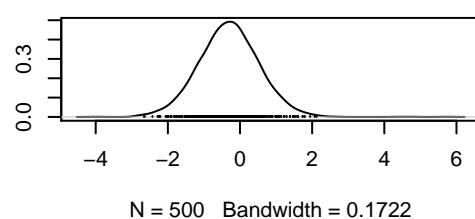
Density of b_{12}



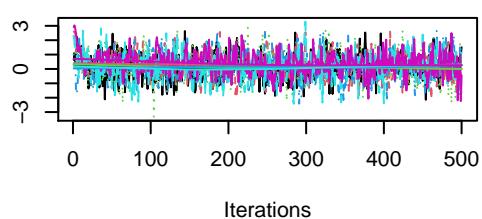
Trace of b_{13}



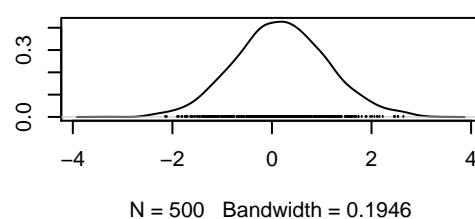
Density of b_{13}



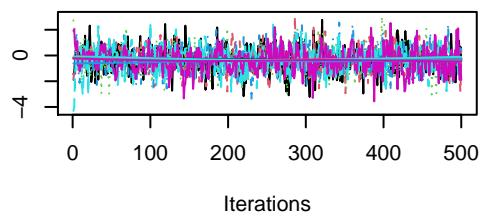
Trace of b_{14}



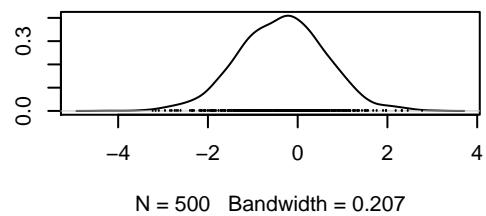
Density of b_{14}



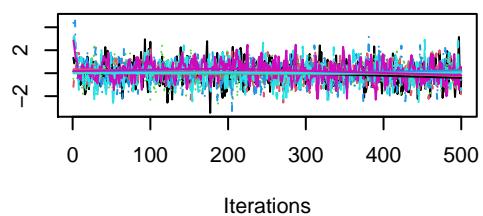
Trace of b15



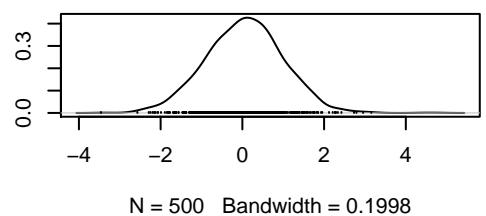
Density of b15



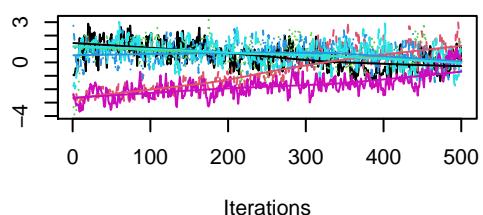
Trace of b16



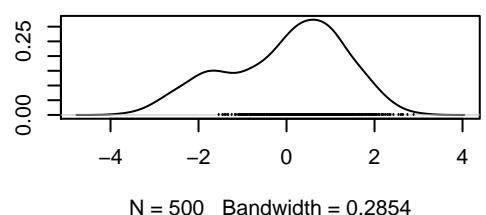
Density of b16



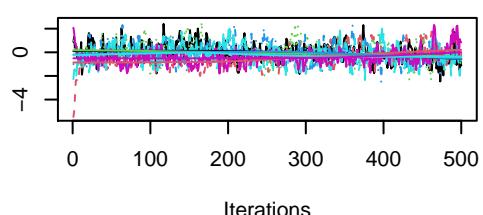
Trace of b21



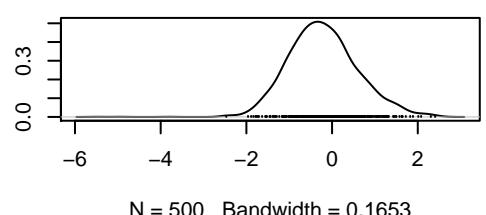
Density of b21



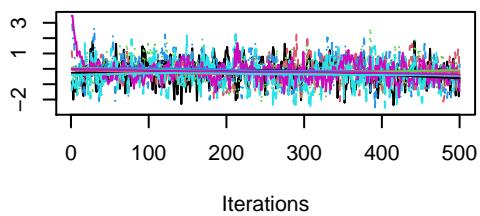
Trace of b22



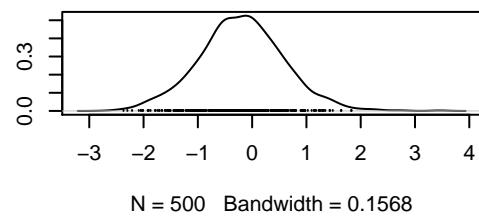
Density of b22



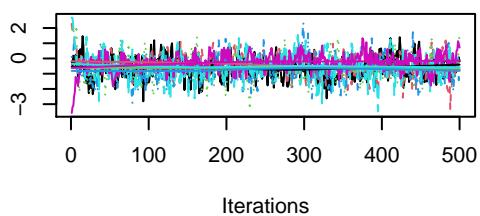
Trace of b23



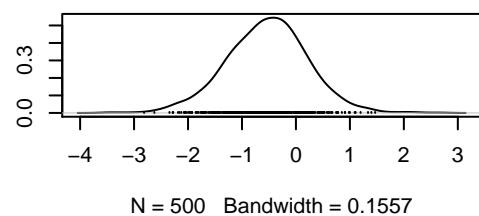
Density of b23



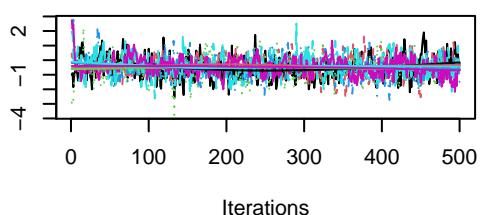
Trace of b24



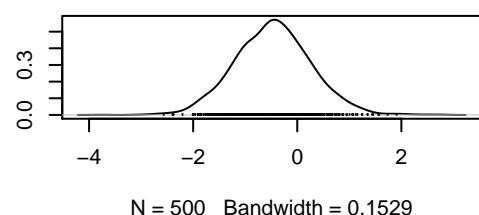
Density of b24



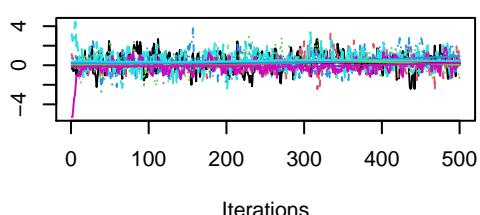
Trace of b25



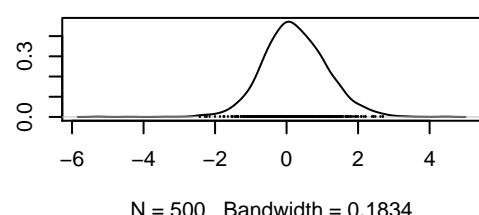
Density of b25



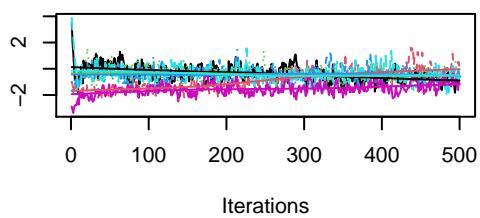
Trace of b26



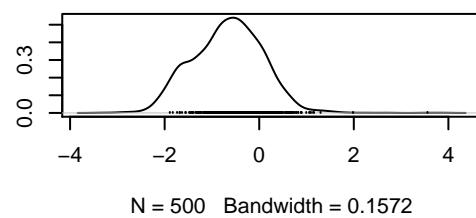
Density of b26



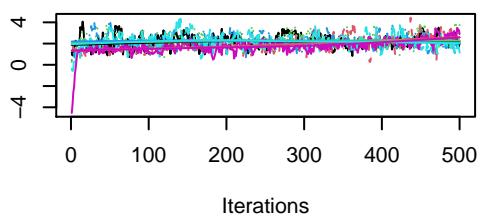
Trace of b31



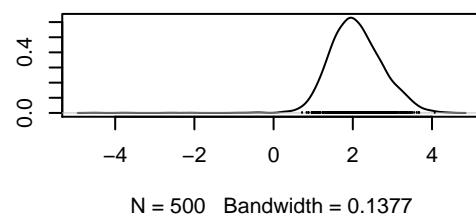
Density of b31



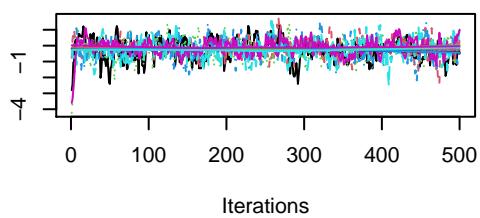
Trace of b32



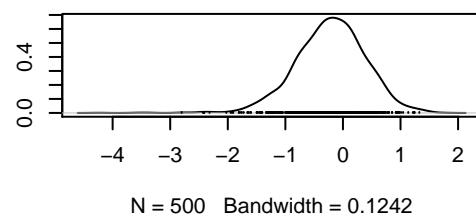
Density of b32



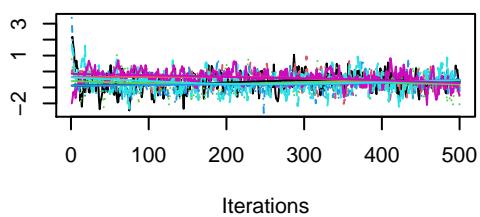
Trace of b33



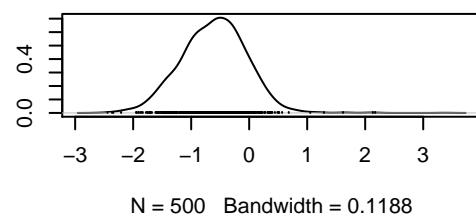
Density of b33



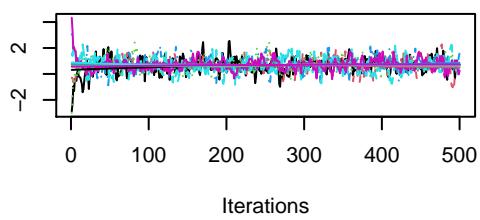
Trace of b34



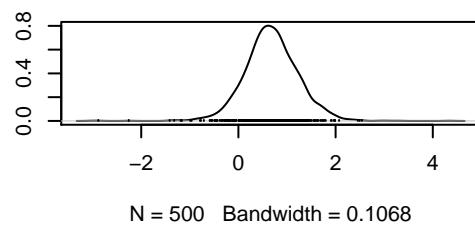
Density of b34



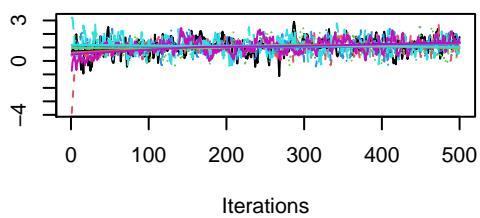
Trace of b35



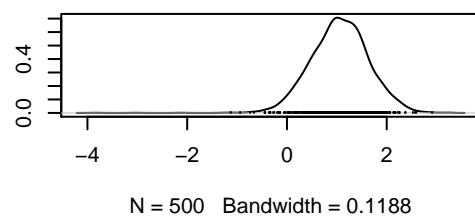
Density of b35



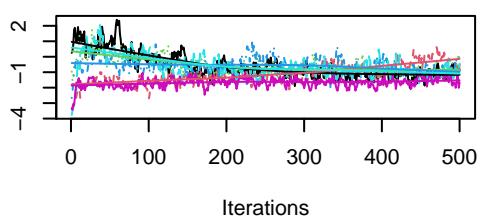
Trace of b36



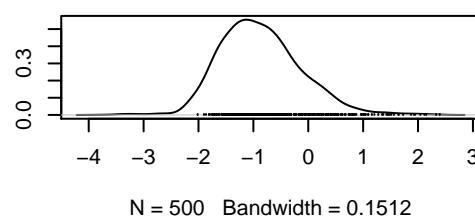
Density of b36



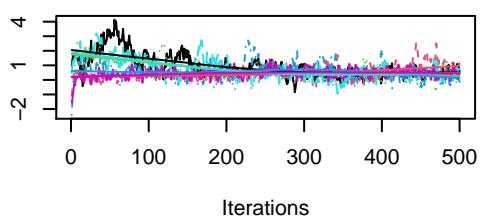
Trace of b41



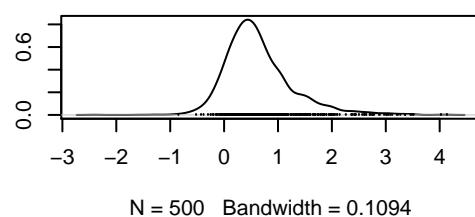
Density of b41



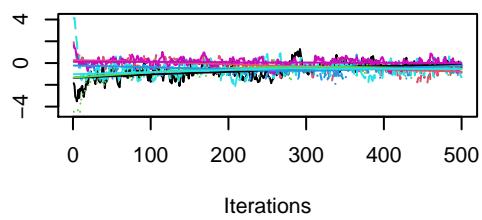
Trace of b42



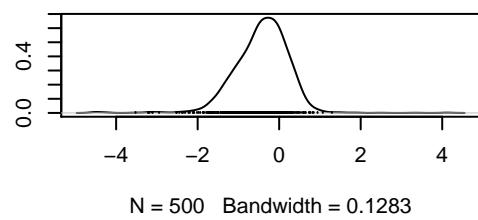
Density of b42



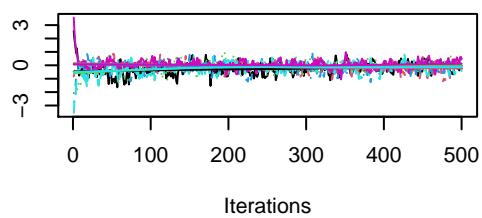
Trace of b43



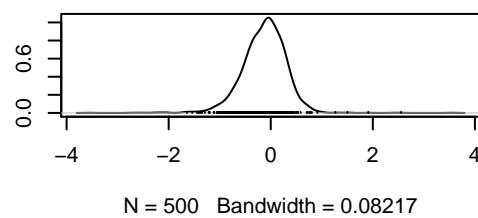
Density of b43



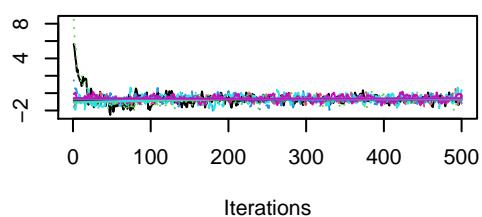
Trace of b44



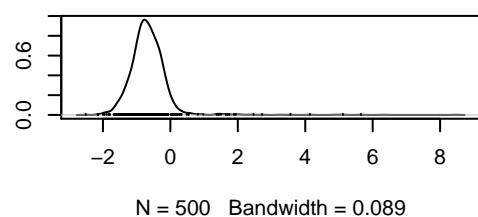
Density of b44



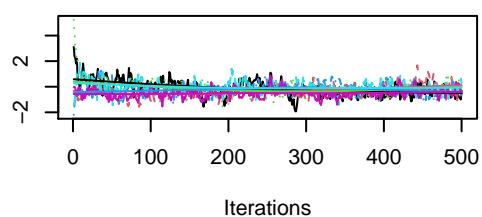
Trace of b45



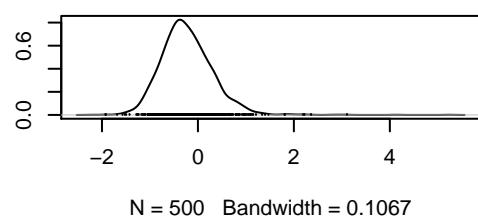
Density of b45



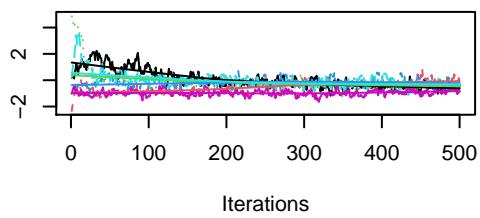
Trace of b46



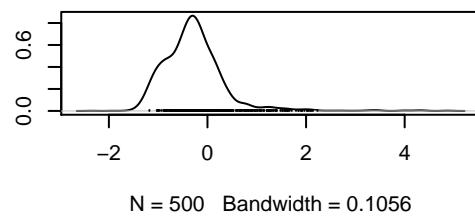
Density of b46



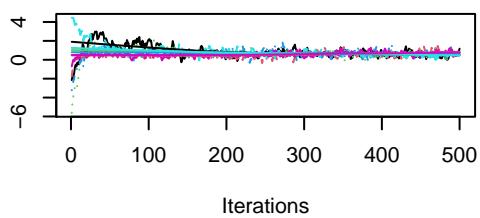
Trace of b51



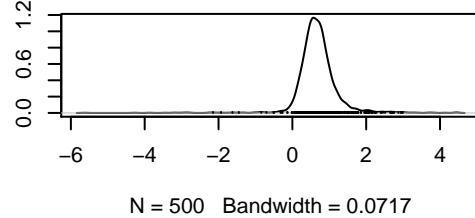
Density of b51



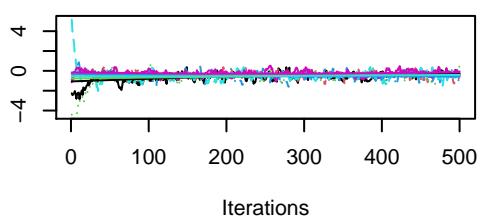
Trace of b52



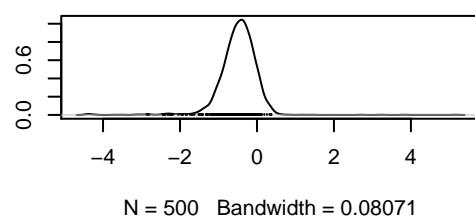
Density of b52



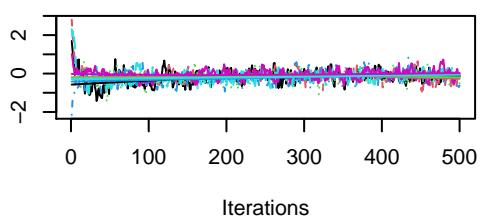
Trace of b53



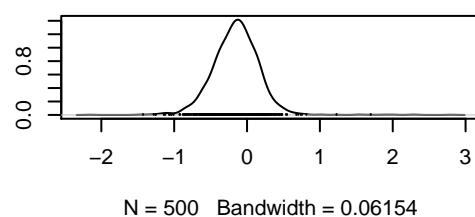
Density of b53



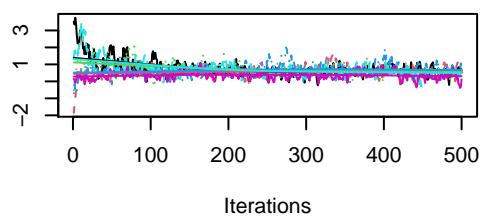
Trace of b54



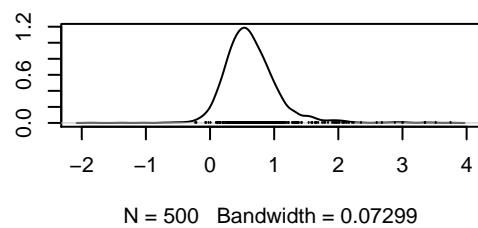
Density of b54



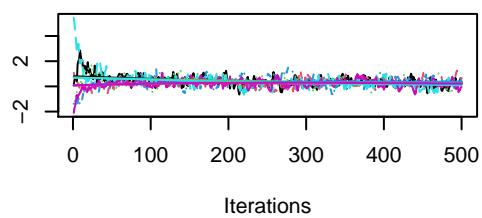
Trace of b55



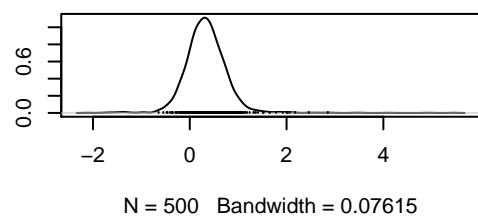
Density of b55



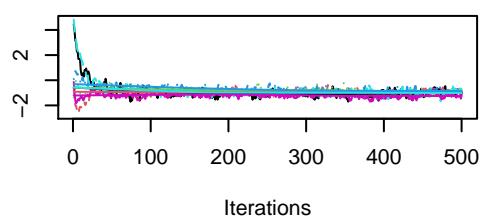
Trace of b56



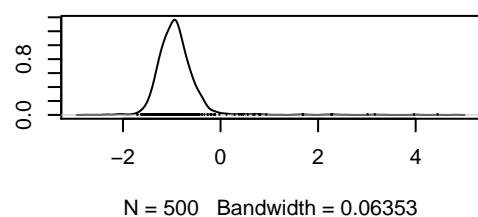
Density of b56



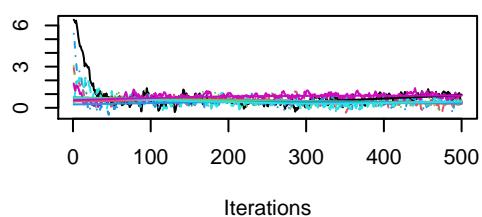
Trace of b61



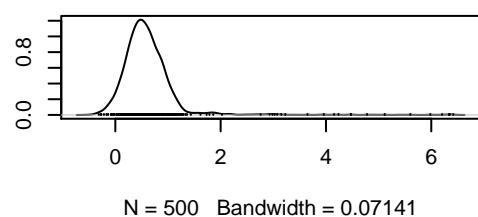
Density of b61



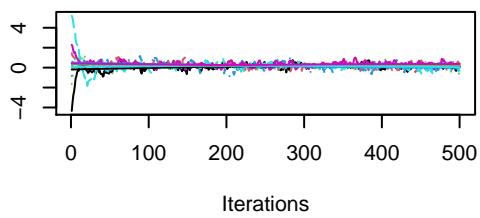
Trace of b62



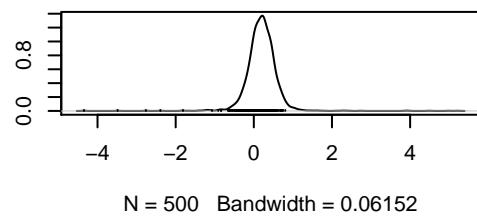
Density of b62



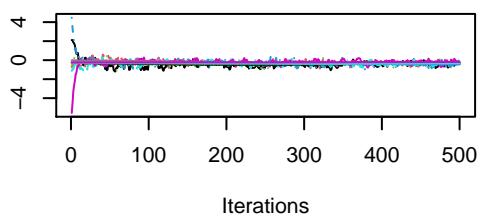
Trace of b63



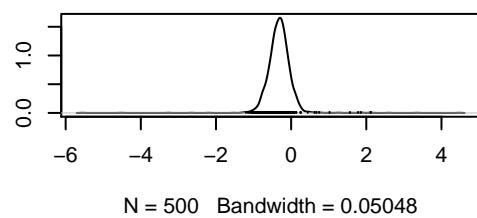
Density of b63



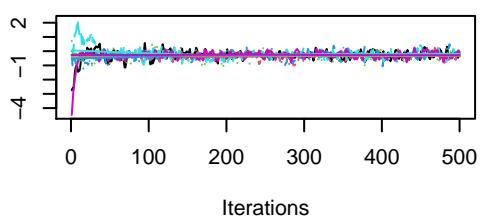
Trace of b64



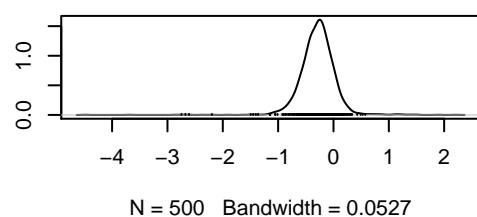
Density of b64



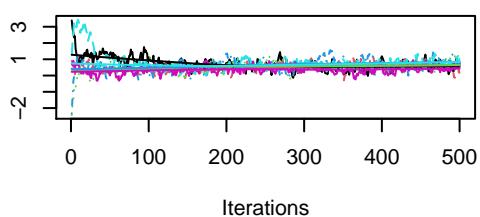
Trace of b65



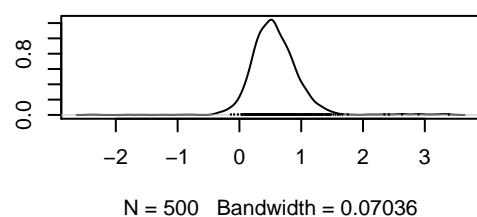
Density of b65



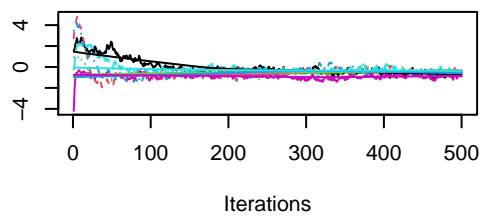
Trace of b66



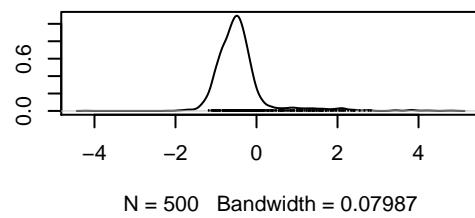
Density of b66



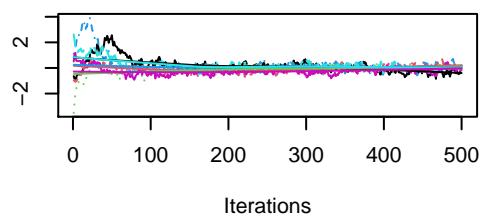
Trace of b71



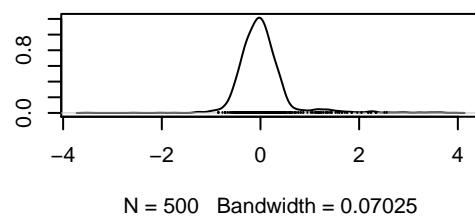
Density of b71



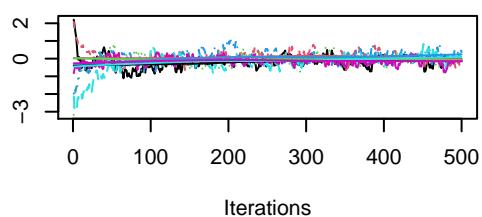
Trace of b72



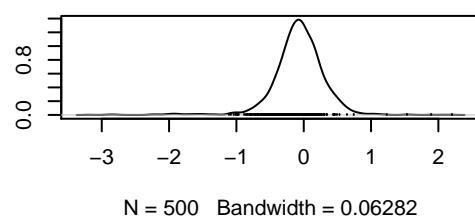
Density of b72



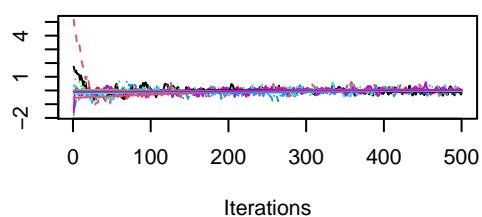
Trace of b73



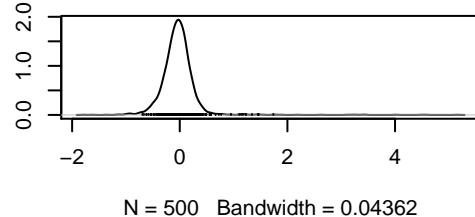
Density of b73



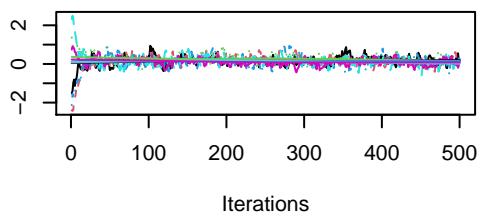
Trace of b74



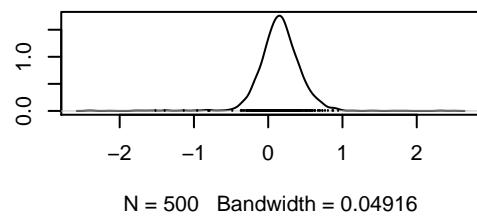
Density of b74



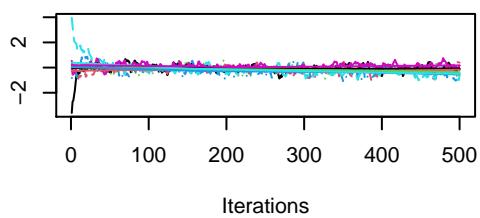
Trace of b75



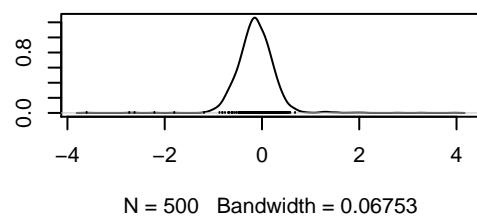
Density of b75



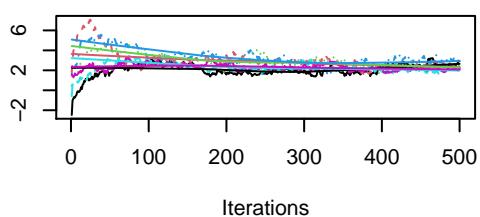
Trace of b76



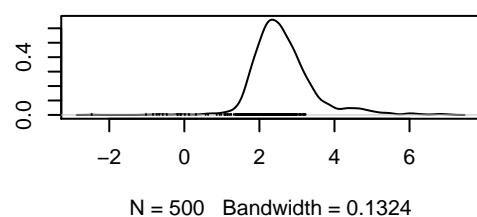
Density of b76



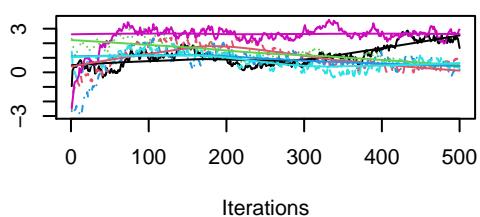
Trace of b81



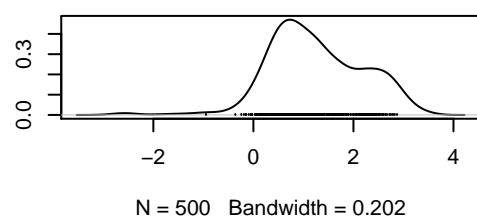
Density of b81



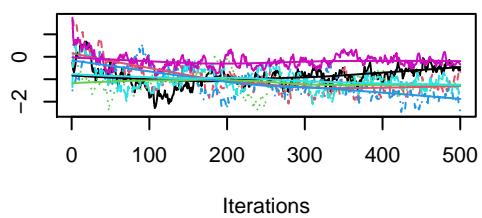
Trace of b82



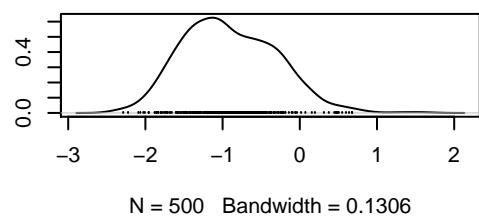
Density of b82



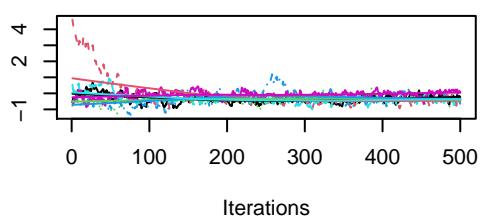
Trace of b83



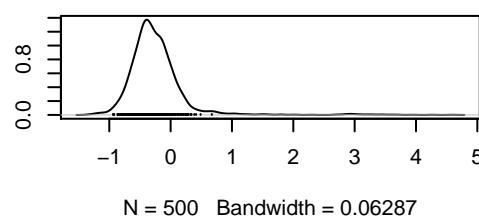
Density of b83



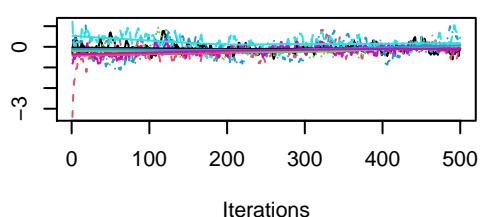
Trace of b84



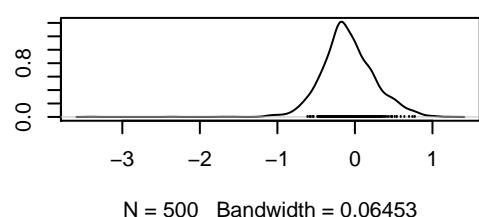
Density of b84



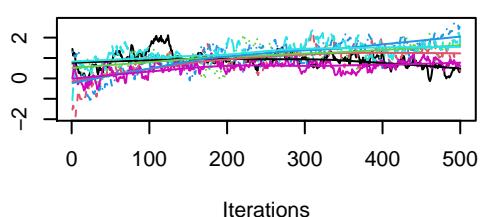
Trace of b85



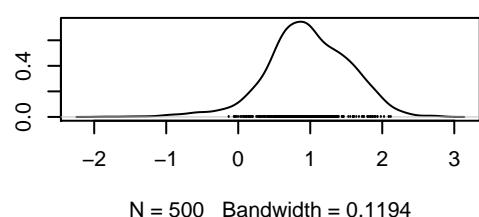
Density of b85



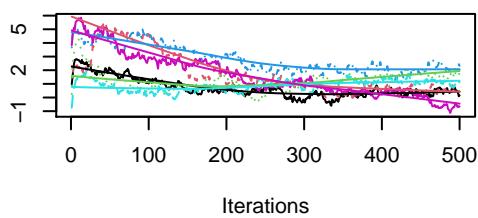
Trace of b86



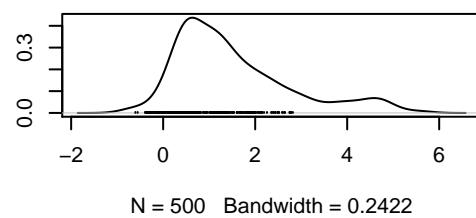
Density of b86



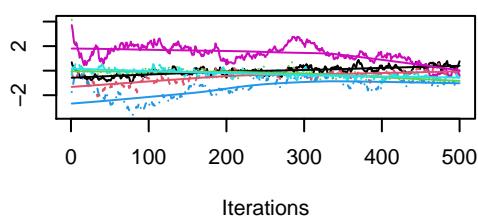
Trace of b91



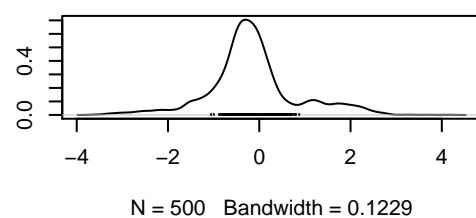
Density of b91



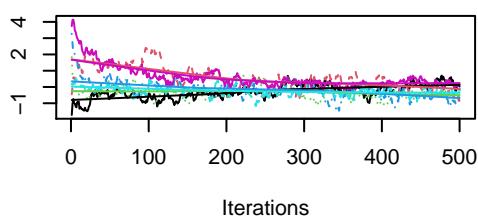
Trace of b92



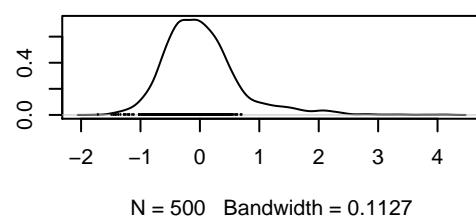
Density of b92



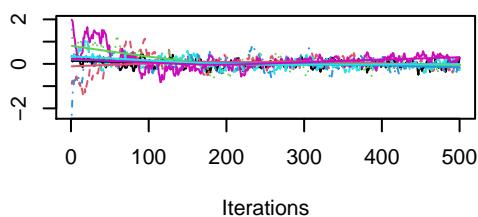
Trace of b93



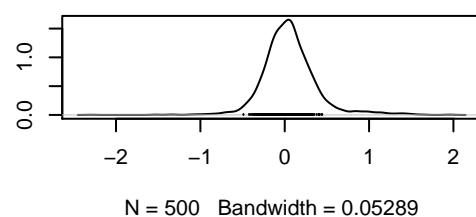
Density of b93



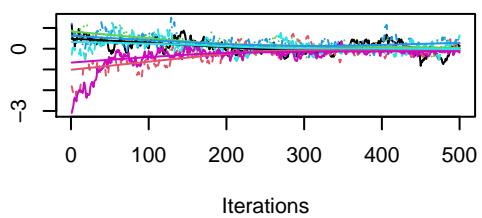
Trace of b94



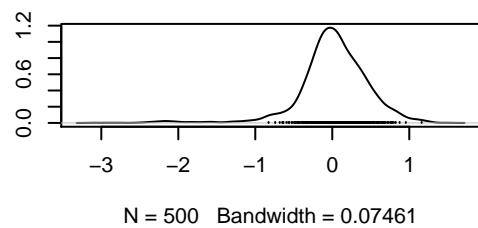
Density of b94



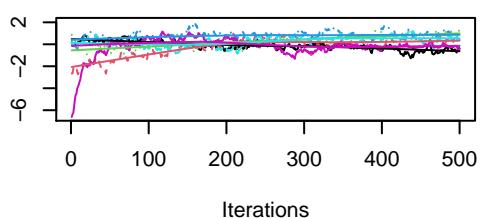
Trace of b95



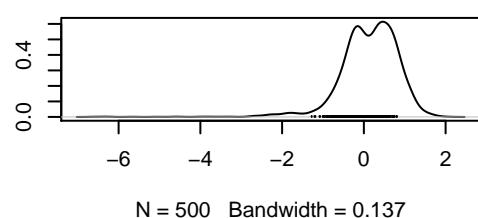
Density of b95



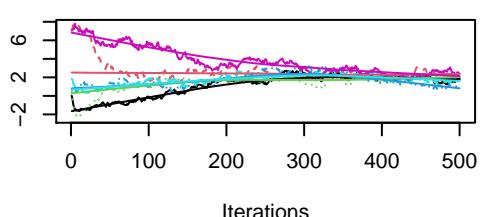
Trace of b96



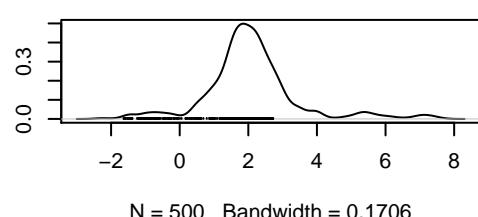
Density of b96



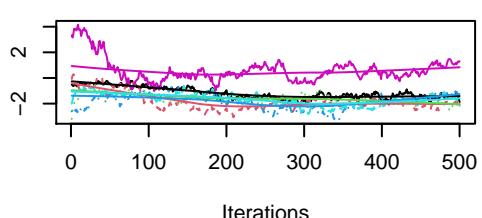
Trace of b101



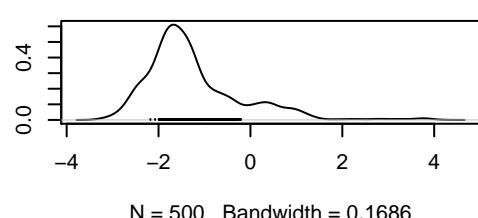
Density of b101

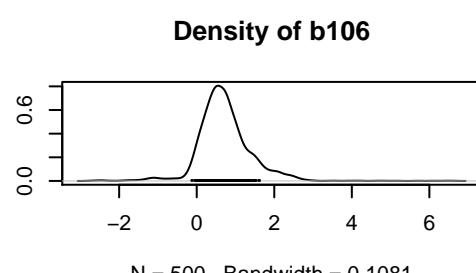
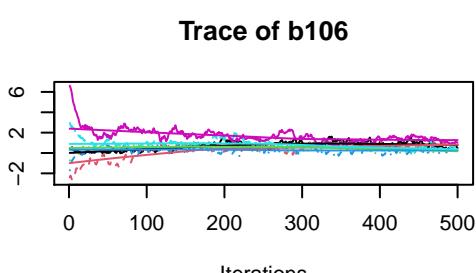
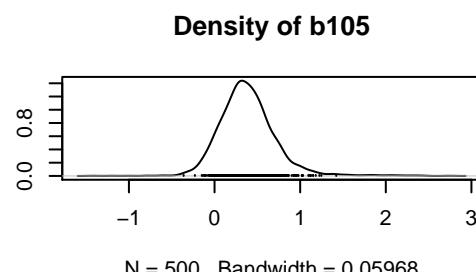
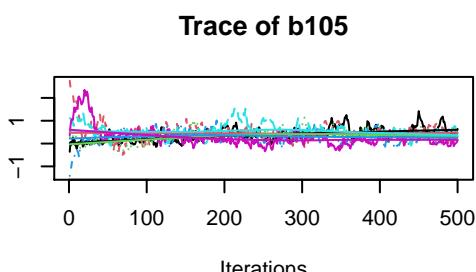
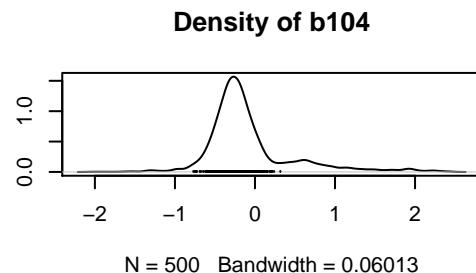
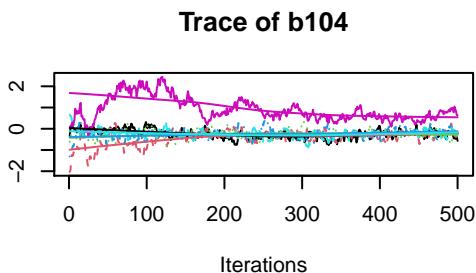
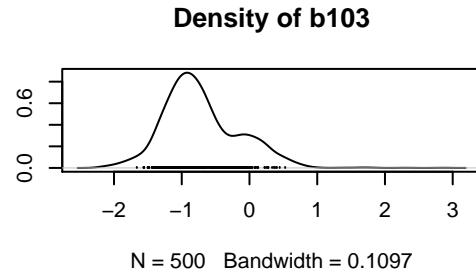
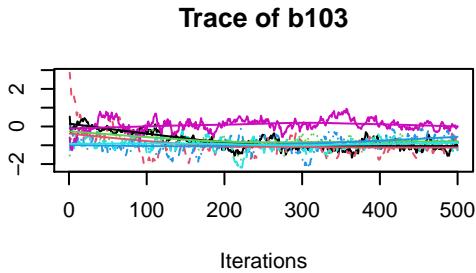


Trace of b102



Density of b102





right_end = 0, order = 5

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

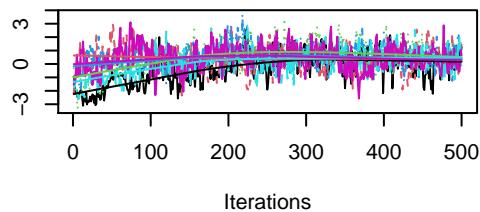
data_trim0 <- get.trim.data(0)

noa_o5_multi_trimr0 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim0$y, x=data_trim0$x, b=b_init[,,i], burn=0, nsamp=500,
                        thin=1, order = order, right_end = 0)
```

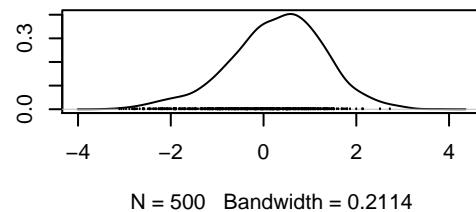
```
load("./report/report16/noa_o5_multi_trimr0.RData")
```

```
noa_o5_multi_trimr0_coda <- multi_chain_coda_noa(noa_o5_multi_trimr0, burn = 0, N_para, p, order = order)
plot(noa_o5_multi_trimr0_coda)
```

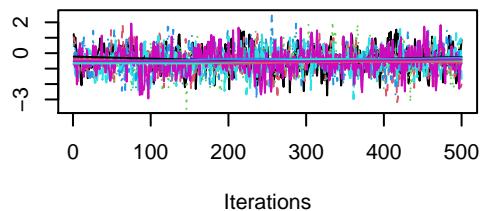
Trace of b11



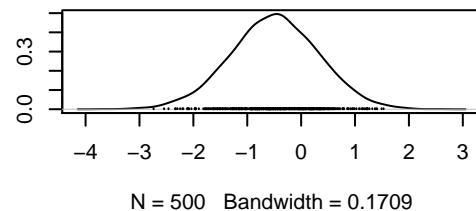
Density of b11



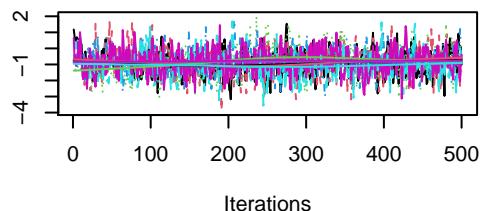
Trace of b12



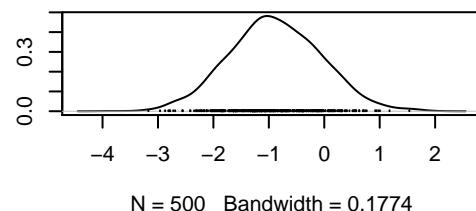
Density of b12



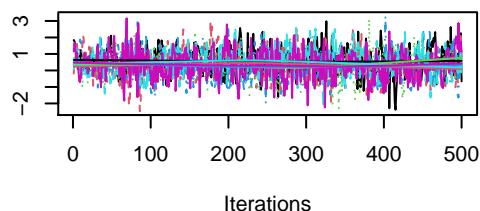
Trace of b13



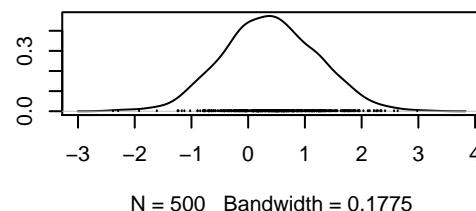
Density of b13



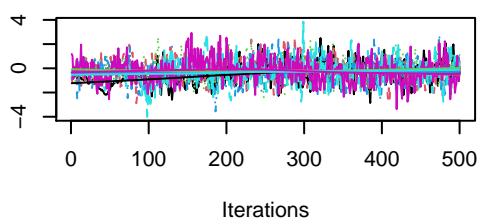
Trace of b14



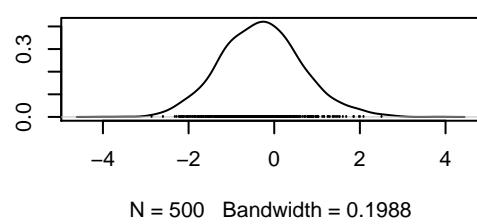
Density of b14



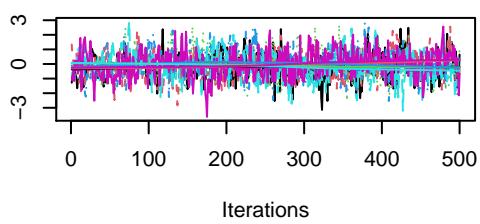
Trace of b15



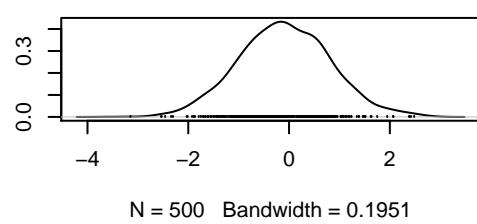
Density of b15



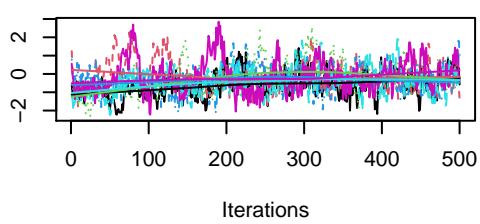
Trace of b16



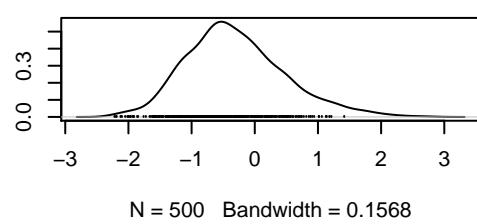
Density of b16



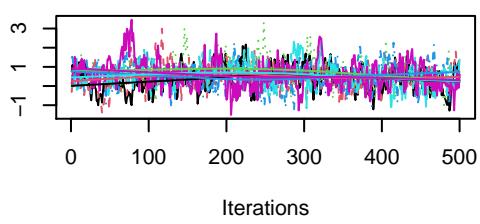
Trace of b21



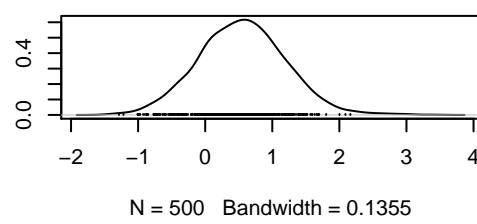
Density of b21



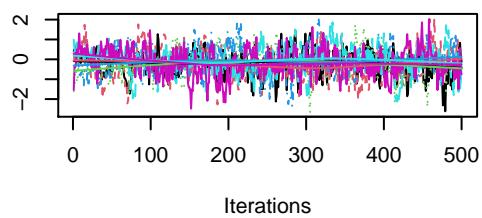
Trace of b22



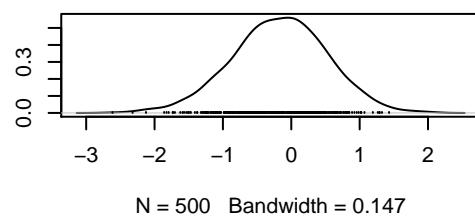
Density of b22



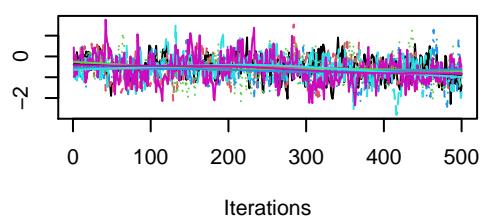
Trace of b23



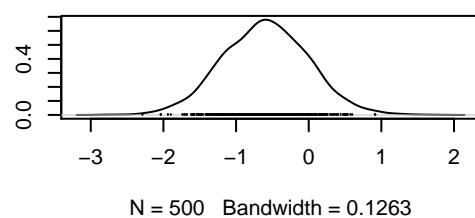
Density of b23



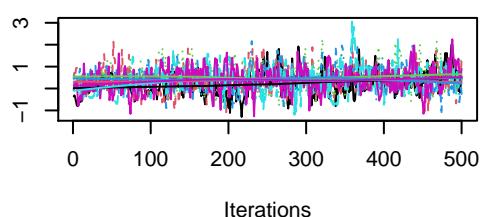
Trace of b24



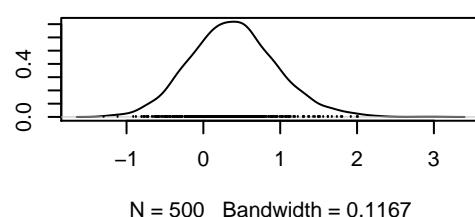
Density of b24



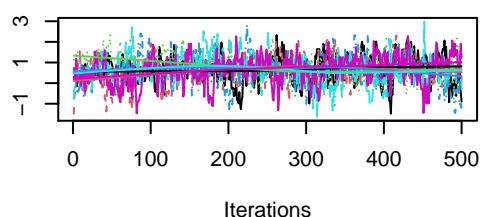
Trace of b25



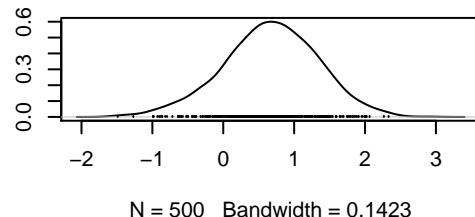
Density of b25



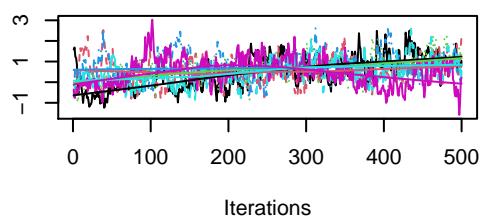
Trace of b26



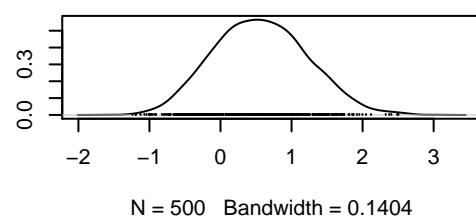
Density of b26



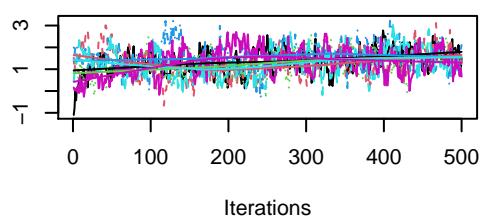
Trace of b31



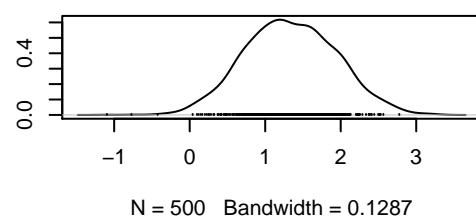
Density of b31



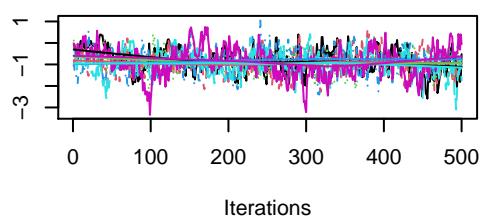
Trace of b32



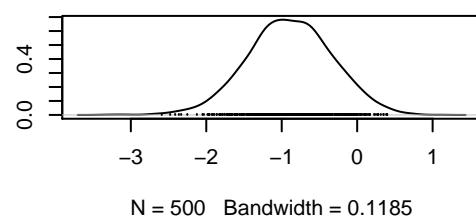
Density of b32



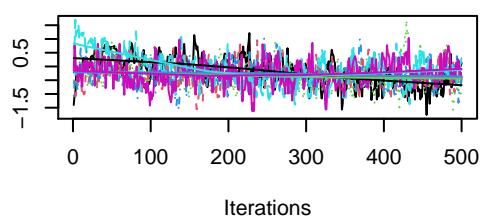
Trace of b33



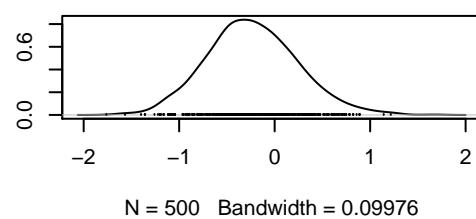
Density of b33



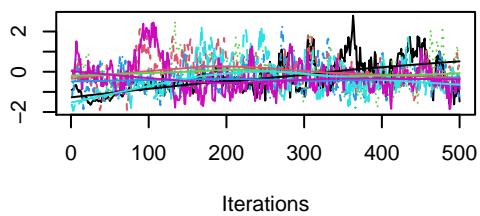
Trace of b34



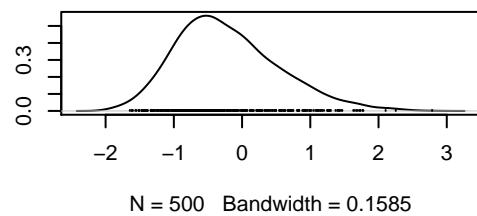
Density of b34



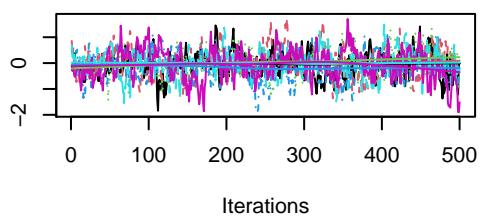
Trace of b35



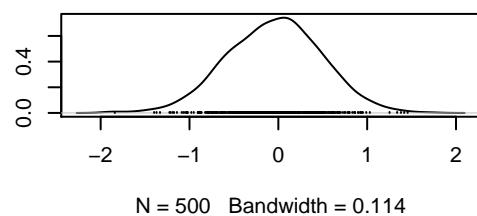
Density of b35



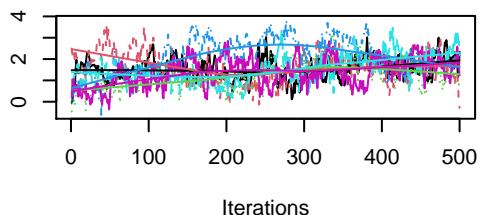
Trace of b36



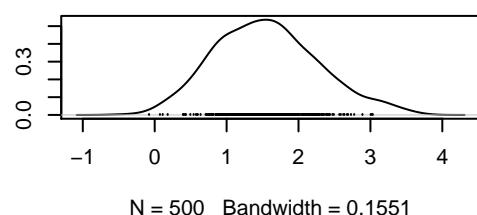
Density of b36



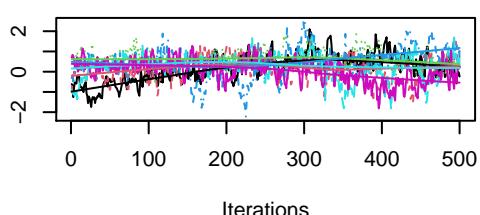
Trace of b41



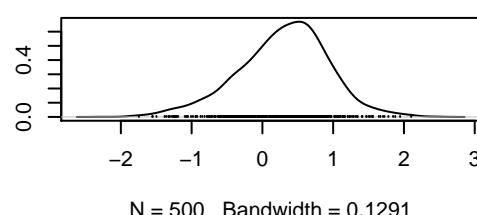
Density of b41



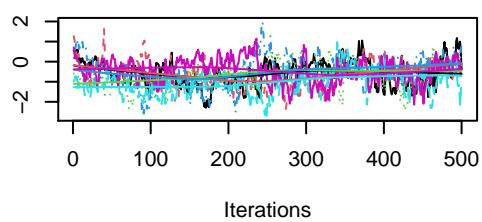
Trace of b42



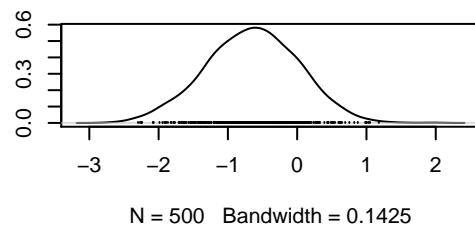
Density of b42



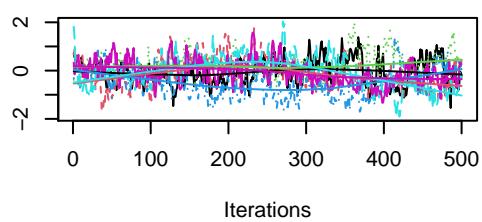
Trace of b43



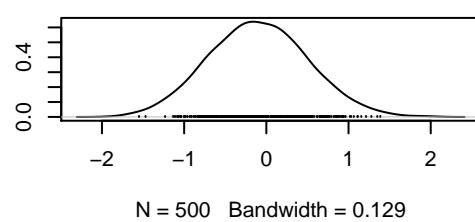
Density of b43



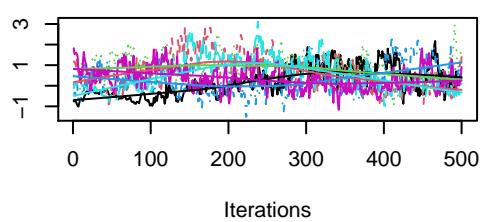
Trace of b44



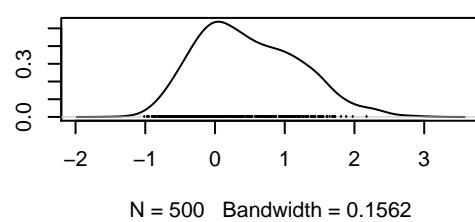
Density of b44



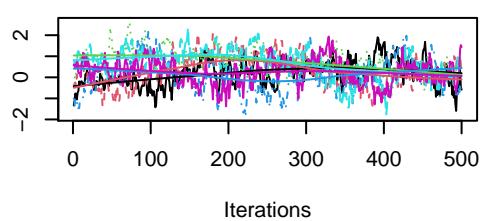
Trace of b45



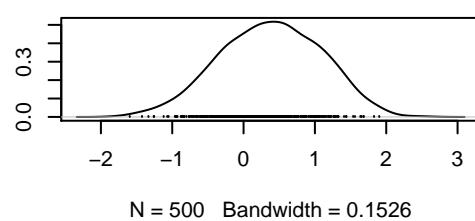
Density of b45



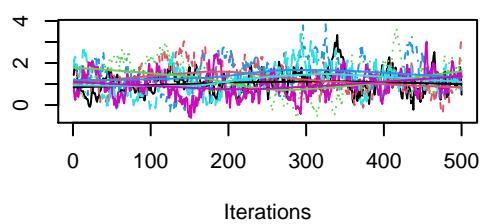
Trace of b46



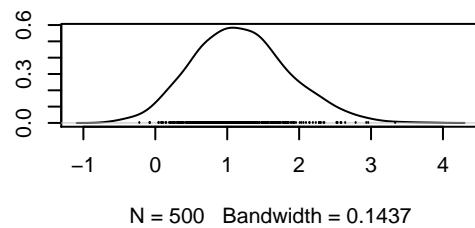
Density of b46



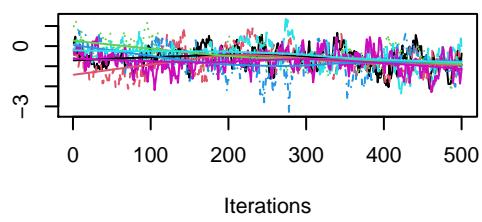
Trace of b51



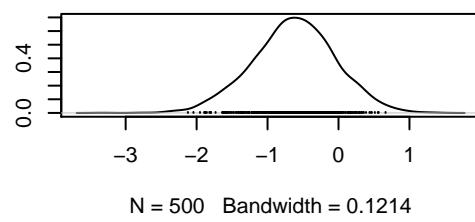
Density of b51



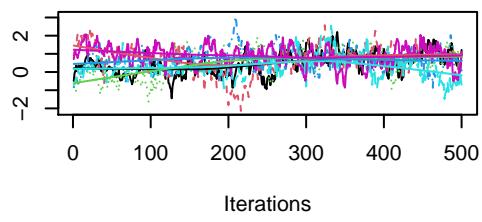
Trace of b52



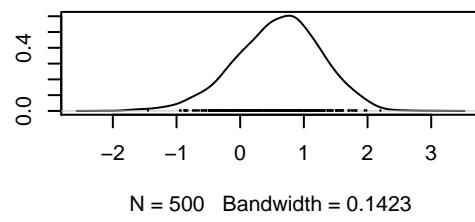
Density of b52



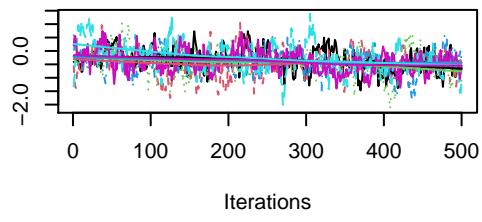
Trace of b53



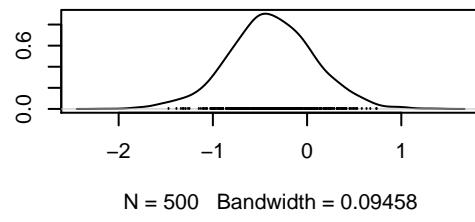
Density of b53

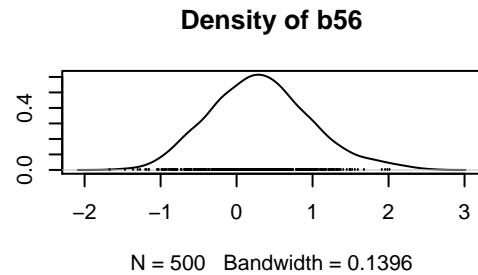
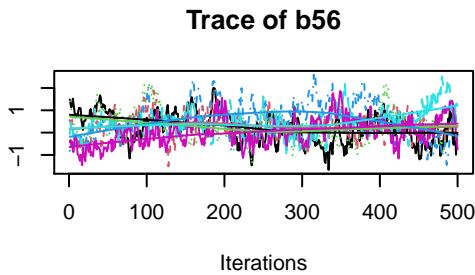
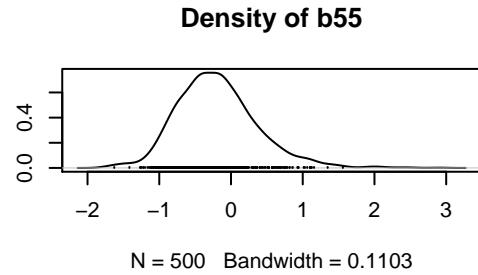
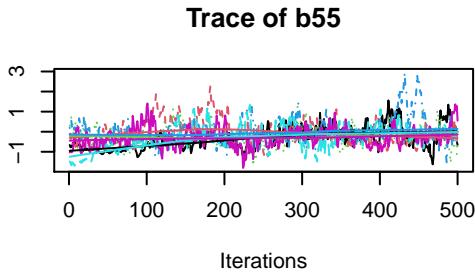


Trace of b54



Density of b54





right_end = 0.25, order = 5

```

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

data_trim025 <- get.trim.data(0.25)

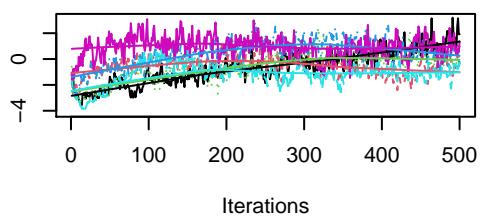
noa_o5_multi_trimr025 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim025$y, x=data_trim025$x, b=b_init[,i], burn=0, nsamp=500,
                        thin=1, order = order, right_end = 0.25)

load("./report/report16/noa_o5_multi_trimr025.RData")

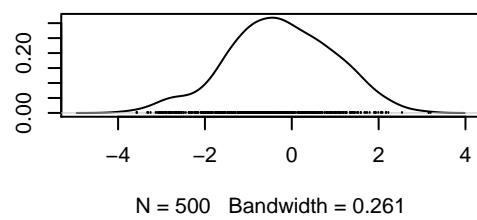
noa_o5_multi_trimr025_coda <- multi_chain_coda_noa(noa_o5_multi_trimr025, burn = 0, N_para, p, order = order)
plot(noa_o5_multi_trimr025_coda)

```

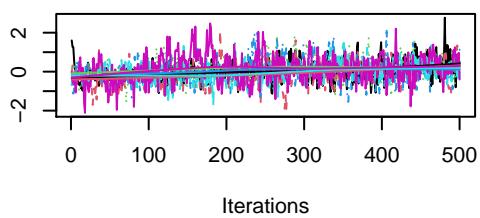
Trace of b_{11}



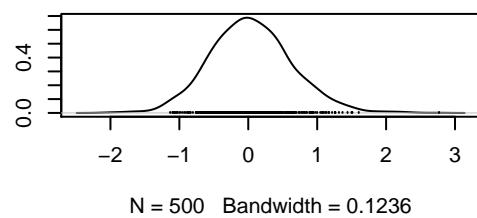
Density of b_{11}



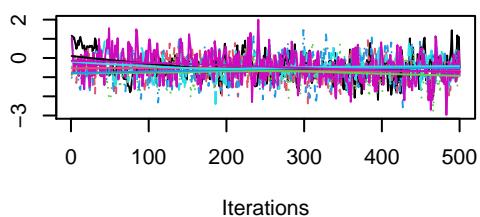
Trace of b_{12}



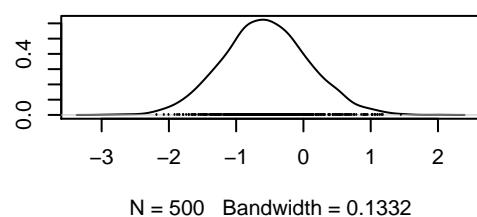
Density of b_{12}



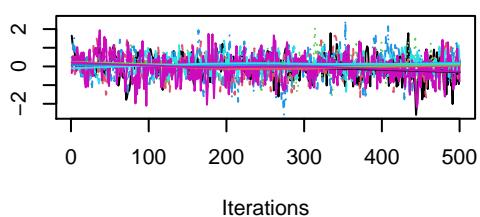
Trace of b_{13}



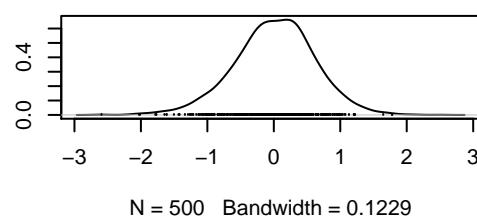
Density of b_{13}



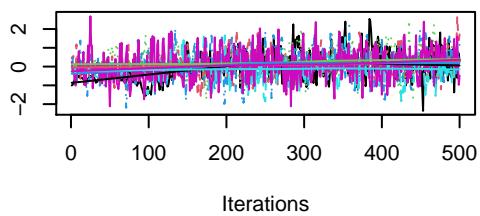
Trace of b_{14}



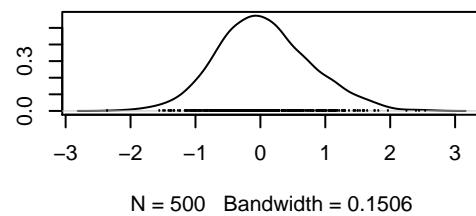
Density of b_{14}



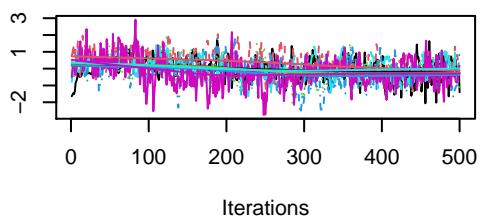
Trace of b15



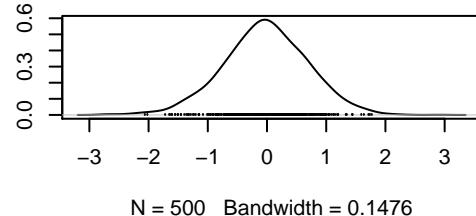
Density of b15



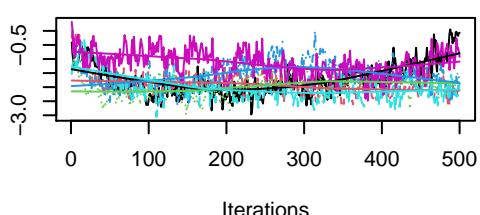
Trace of b16



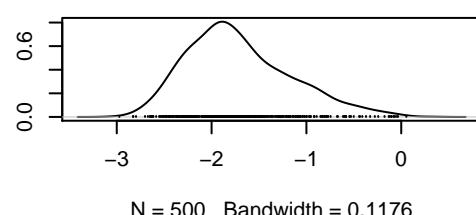
Density of b16



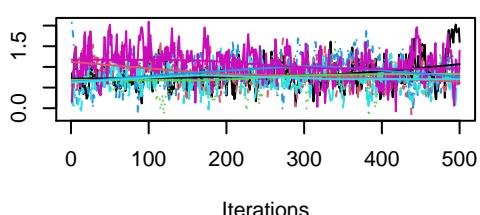
Trace of b21



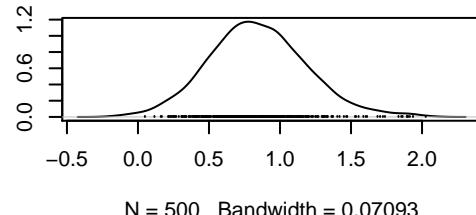
Density of b21



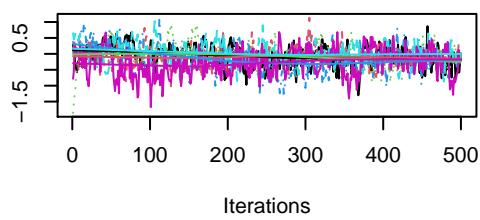
Trace of b22



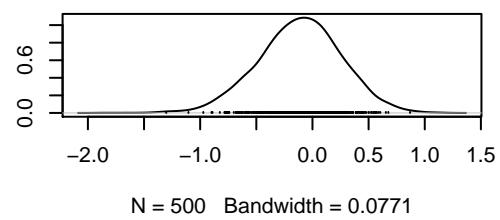
Density of b22



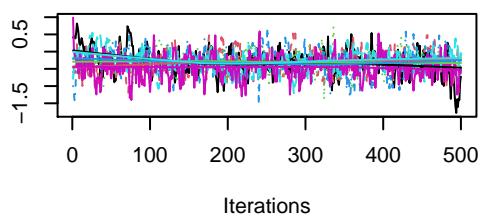
Trace of b23



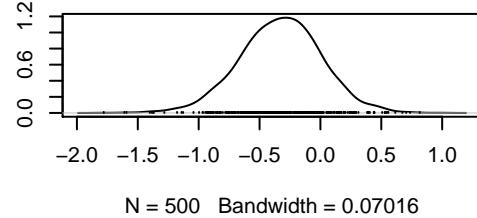
Density of b23



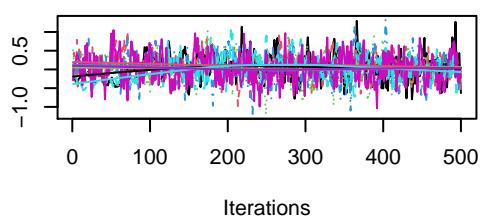
Trace of b24



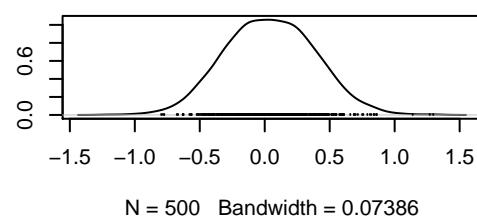
Density of b24



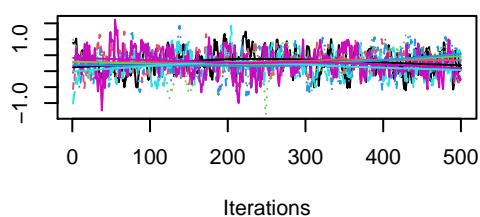
Trace of b25



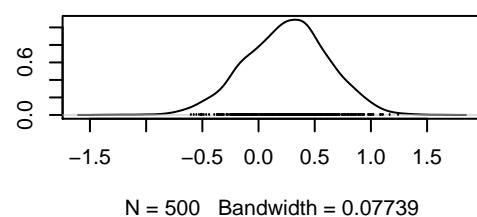
Density of b25



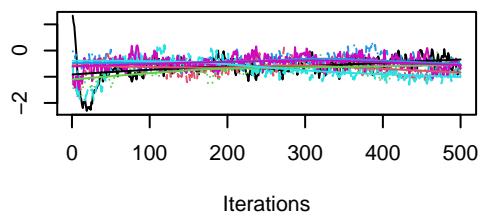
Trace of b26



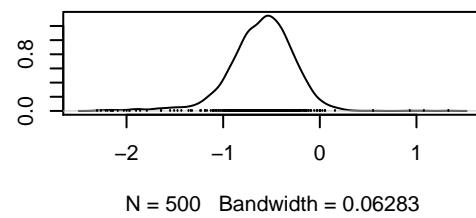
Density of b26



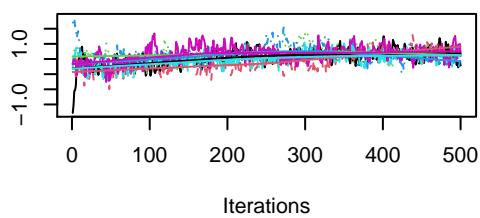
Trace of b31



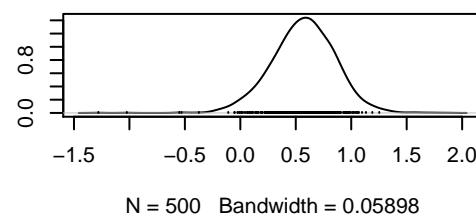
Density of b31



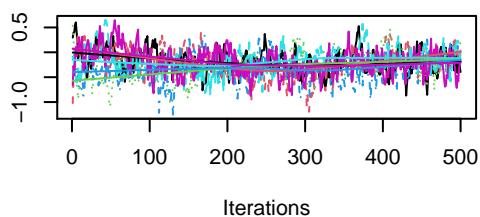
Trace of b32



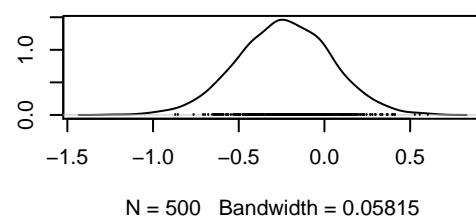
Density of b32



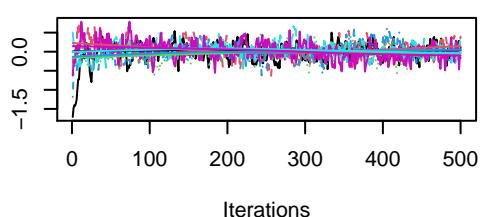
Trace of b33



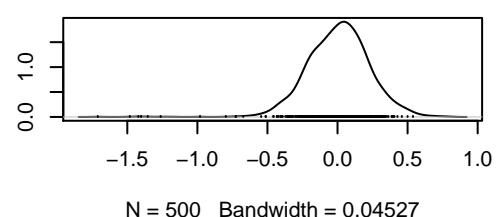
Density of b33

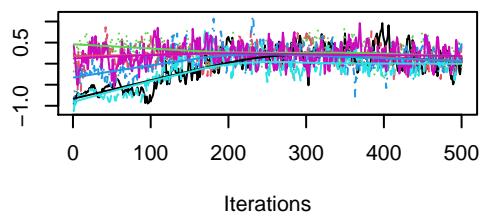
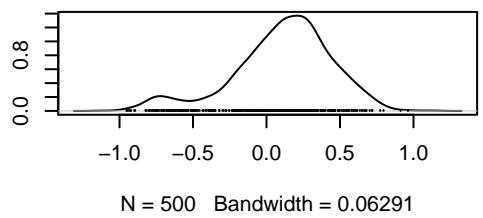
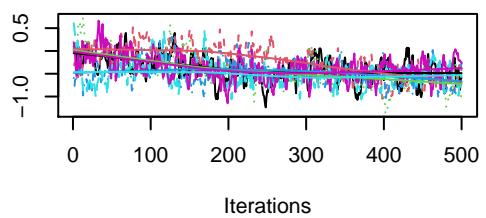
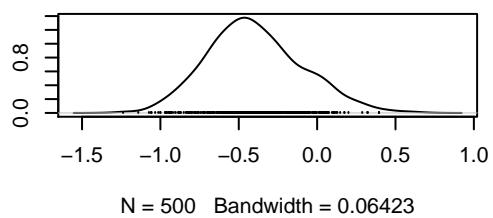
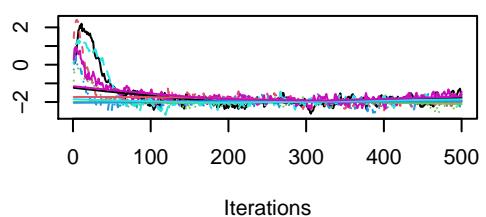
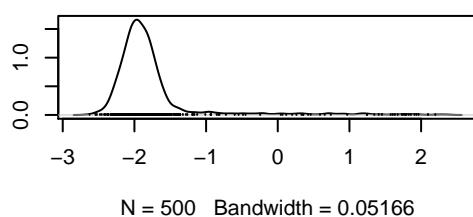
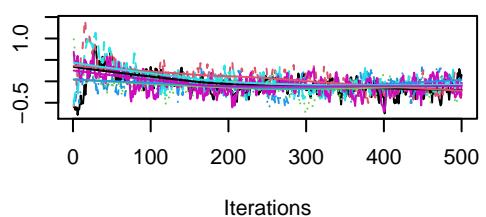
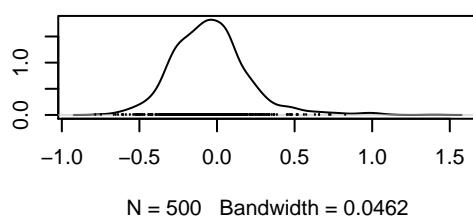


Trace of b34

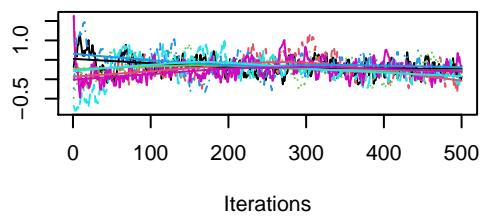


Density of b34

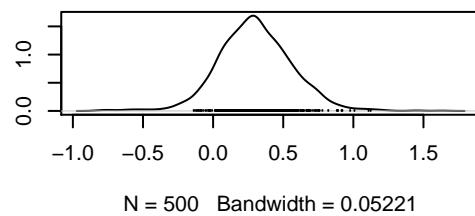


Trace of b35**Density of b35****Trace of b36****Density of b36****Trace of b41****Density of b41****Trace of b42****Density of b42**

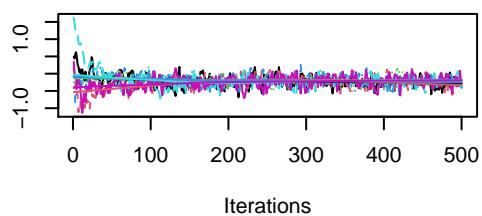
Trace of b43



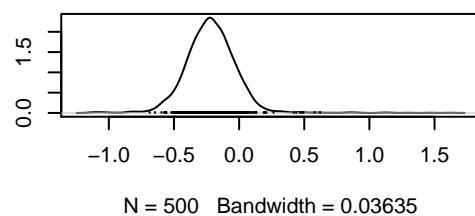
Density of b43



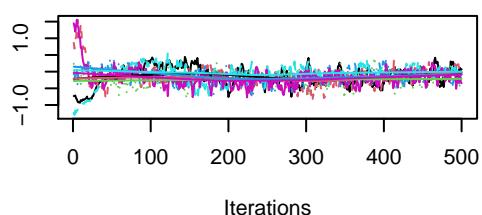
Trace of b44



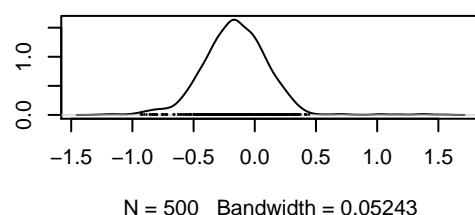
Density of b44



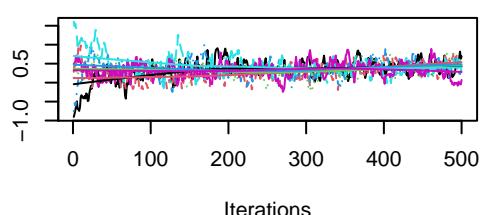
Trace of b45



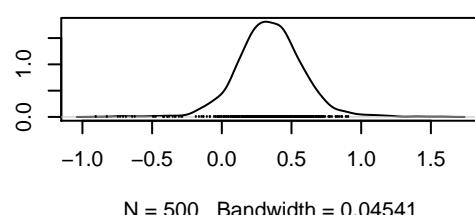
Density of b45



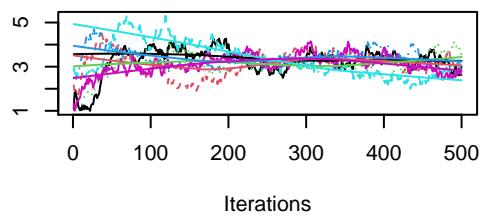
Trace of b46



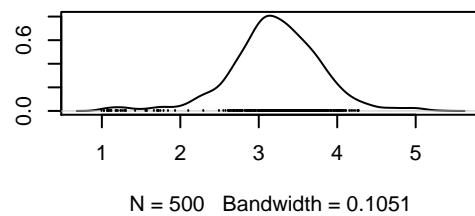
Density of b46



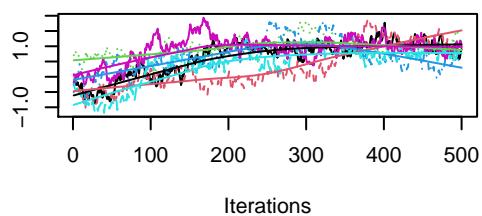
Trace of b51



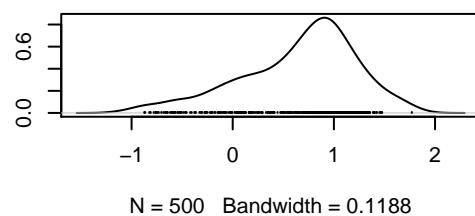
Density of b51



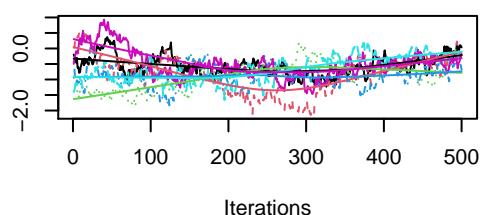
Trace of b52



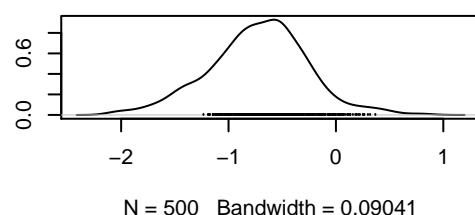
Density of b52



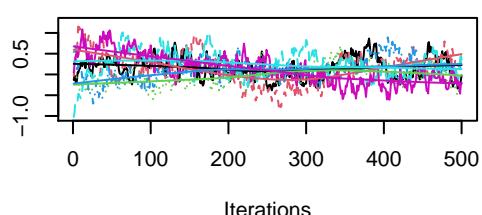
Trace of b53



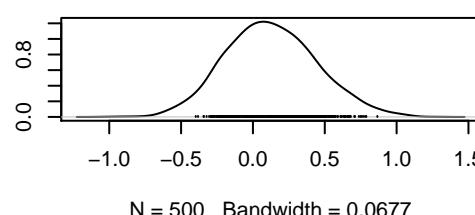
Density of b53

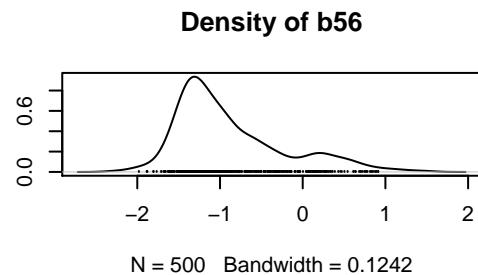
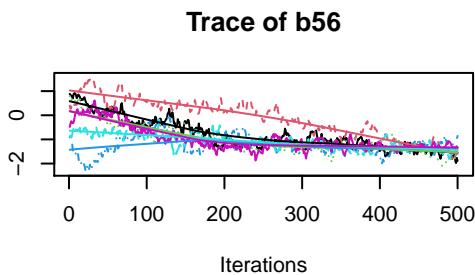
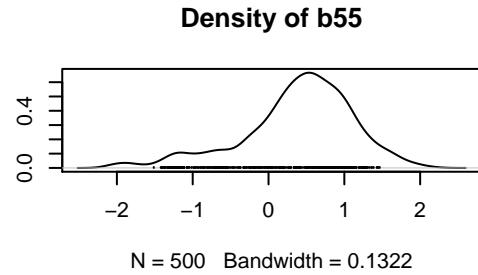
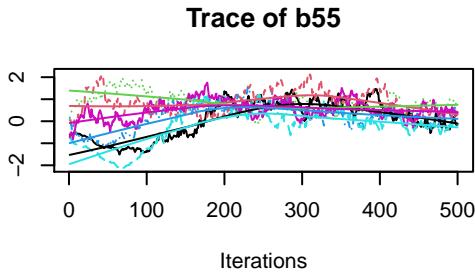


Trace of b54



Density of b54





right_end = 0.35, order = 5

```

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

data_trim035 <- get.trim.data(0.35)

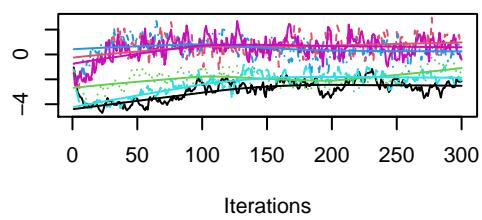
noa_o5_multi_trimr035 <- foreach(i = 1:N_para) %dorng%
  bdregjump_noa_trimr(y=data_trim035$y, x=data_trim035$x, b=b_init[, , i], burn=0, nsamp=300,
                        thin=1, order = order, right_end = 0.35)

load("./report/report16/noa_o5_multi_trimr035.RData")

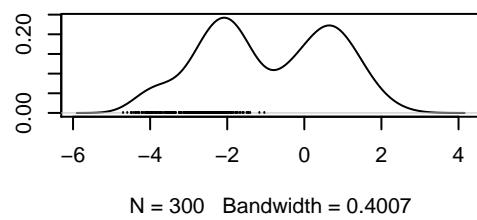
noa_o5_multi_trimr035_coda <- multi_chain_coda_noa(noa_o5_multi_trimr035, burn = 0, N_para, p, order = order)
plot(noa_o5_multi_trimr035_coda)

```

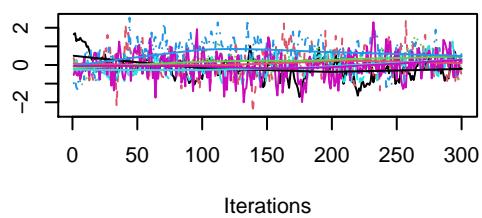
Trace of b_{11}



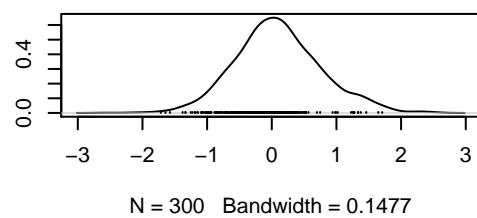
Density of b_{11}



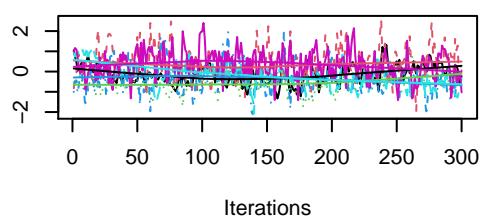
Trace of b_{12}



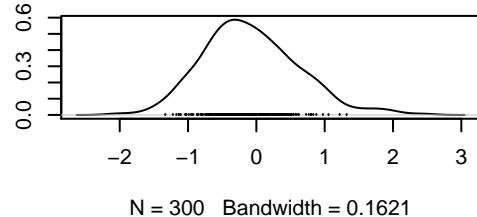
Density of b_{12}



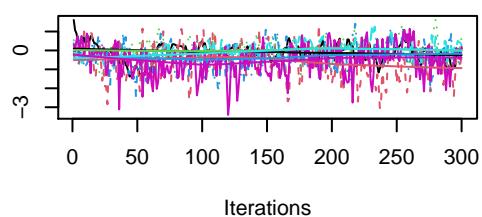
Trace of b_{13}



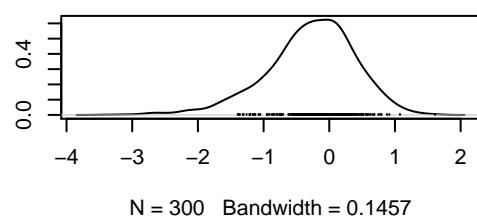
Density of b_{13}



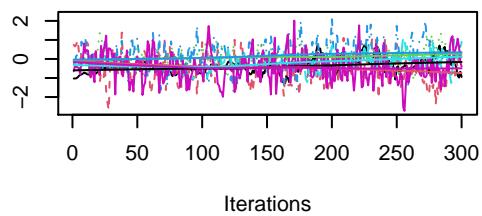
Trace of b_{14}



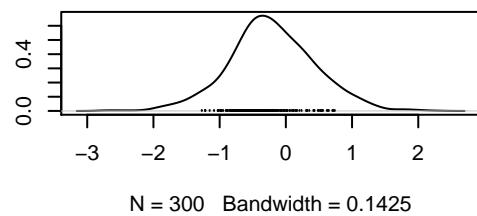
Density of b_{14}



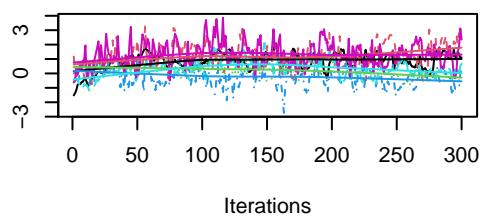
Trace of b15



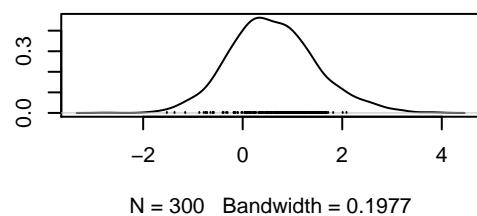
Density of b15



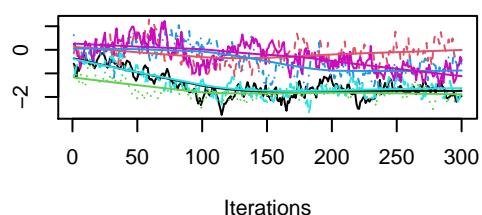
Trace of b16



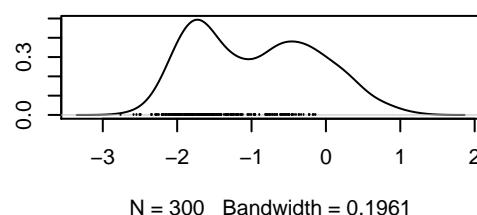
Density of b16



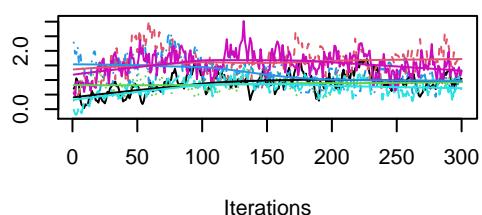
Trace of b21



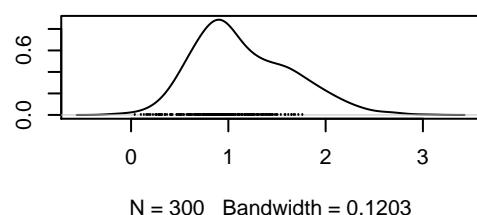
Density of b21



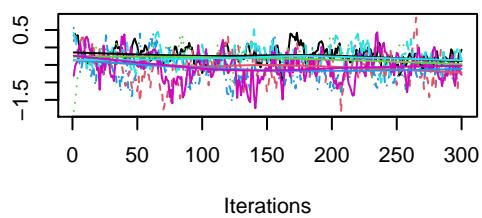
Trace of b22



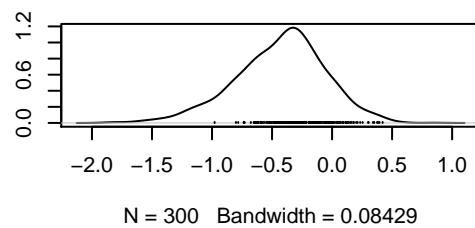
Density of b22



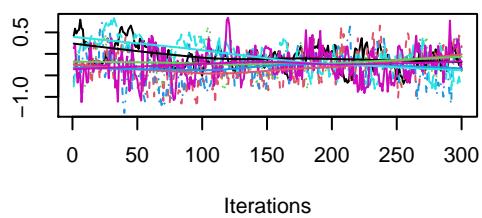
Trace of b23



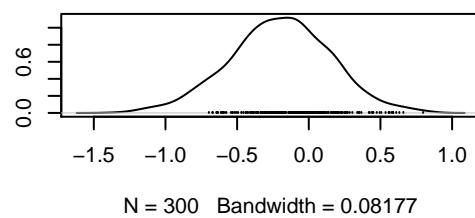
Density of b23



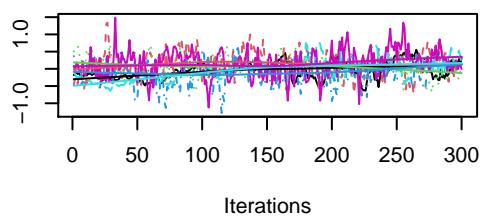
Trace of b24



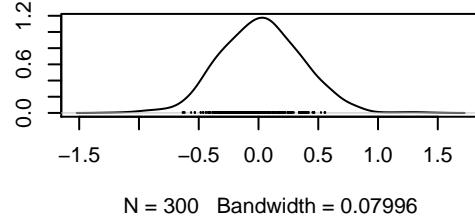
Density of b24



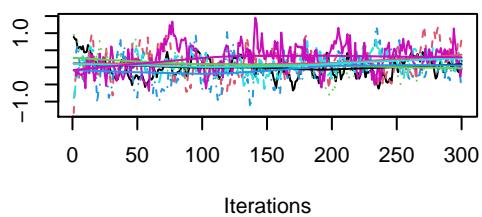
Trace of b25



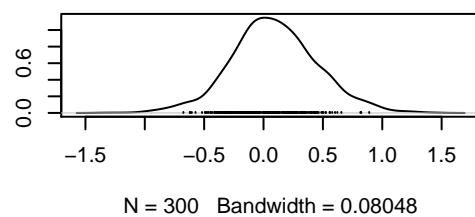
Density of b25



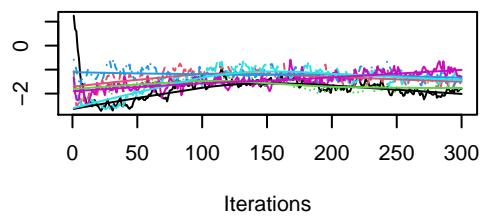
Trace of b26



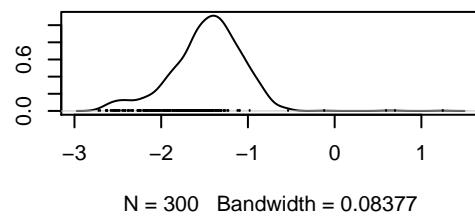
Density of b26



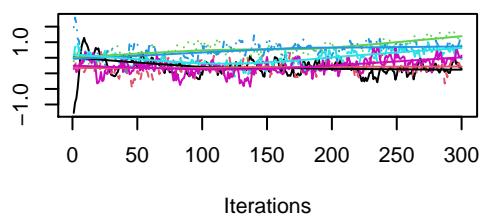
Trace of b31



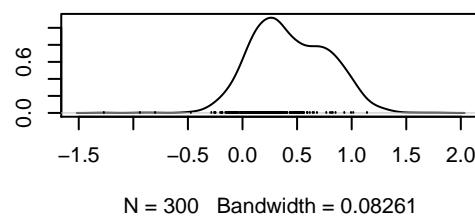
Density of b31



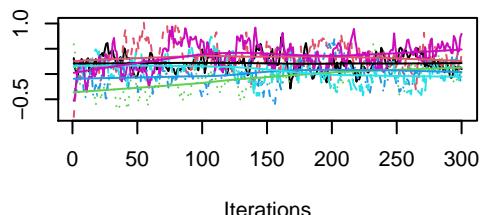
Trace of b32



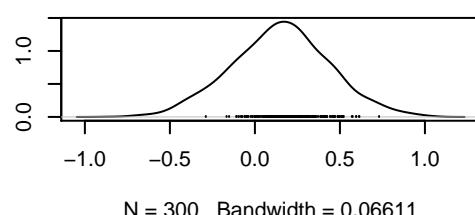
Density of b32



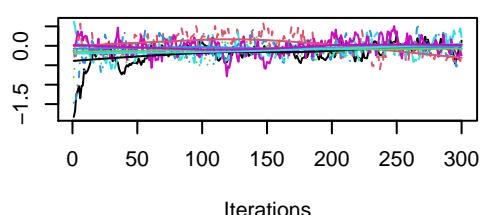
Trace of b33



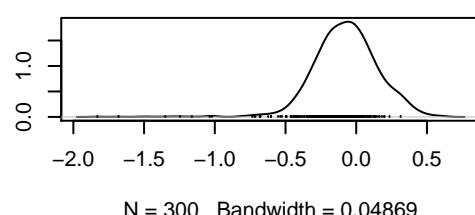
Density of b33



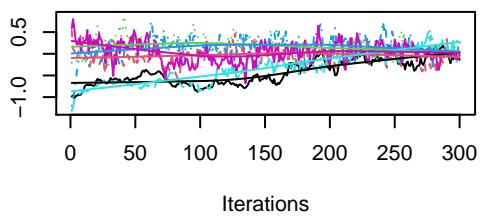
Trace of b34



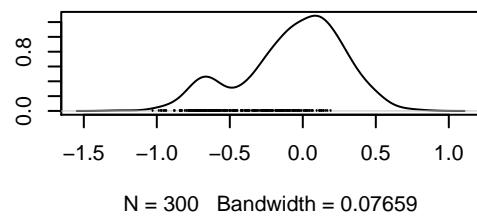
Density of b34



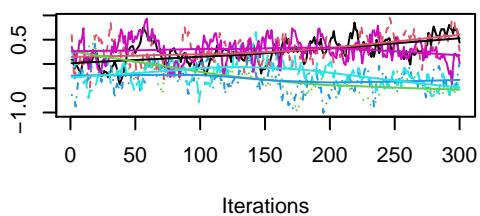
Trace of b35



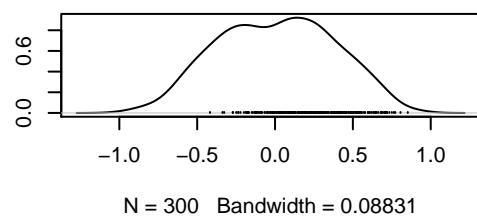
Density of b35



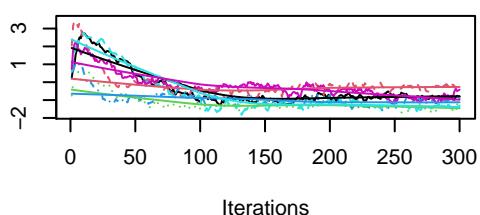
Trace of b36



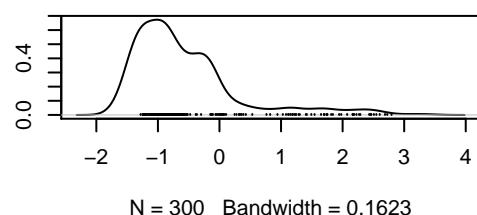
Density of b36



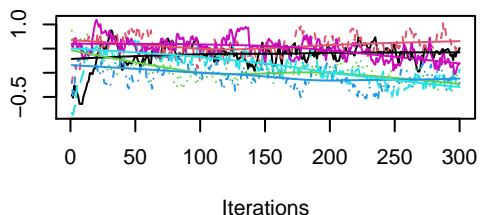
Trace of b41



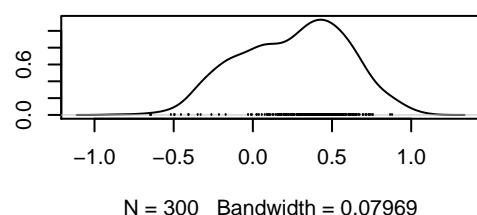
Density of b41



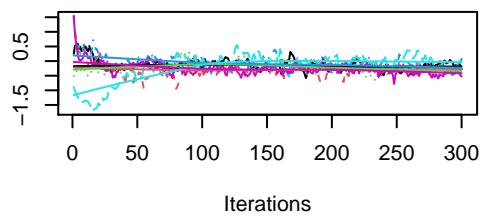
Trace of b42



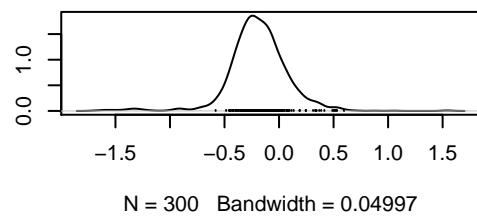
Density of b42



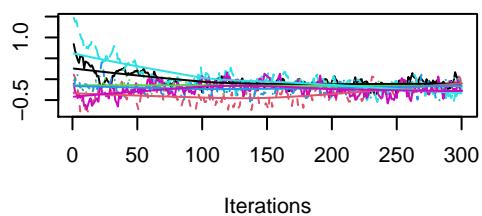
Trace of b43



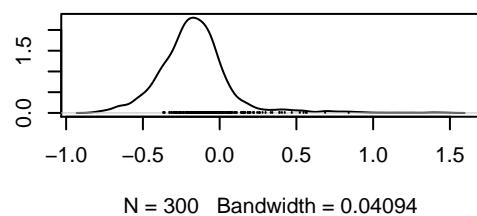
Density of b43



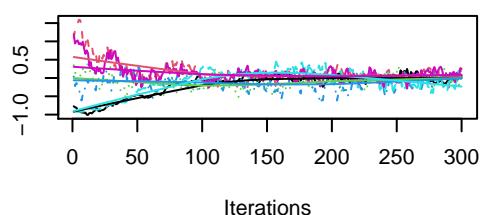
Trace of b44



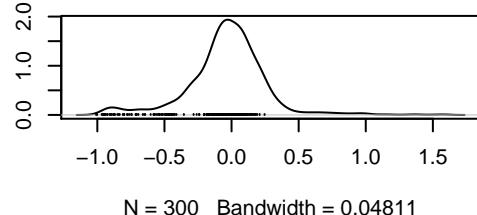
Density of b44



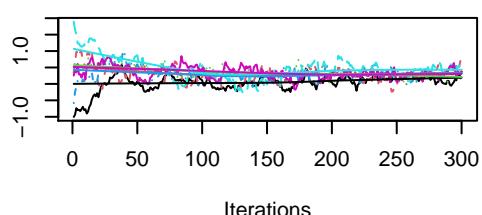
Trace of b45



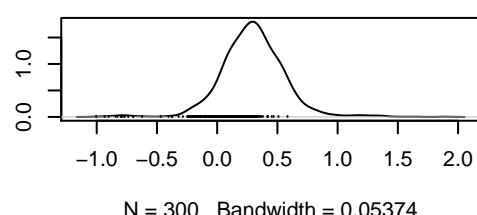
Density of b45



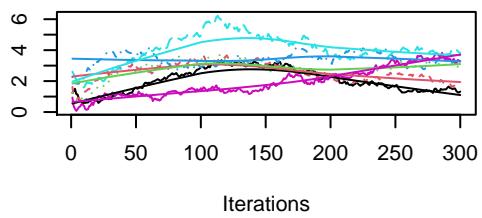
Trace of b46



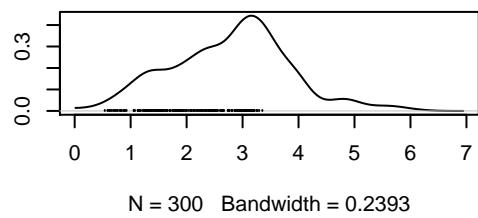
Density of b46



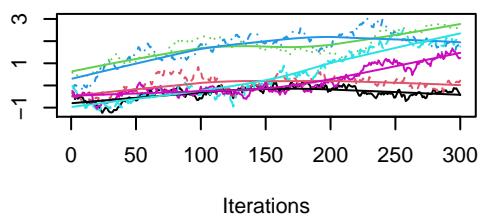
Trace of b51



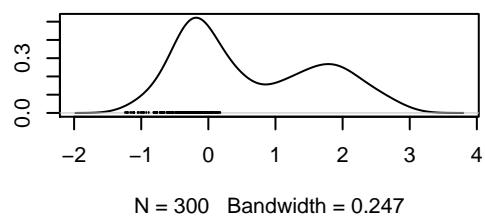
Density of b51



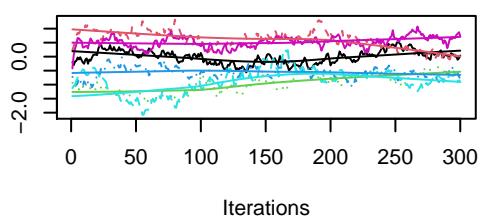
Trace of b52



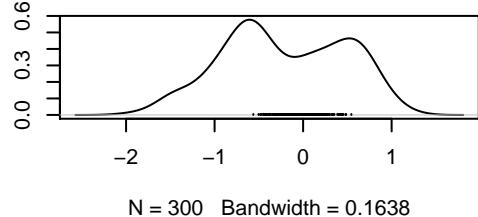
Density of b52



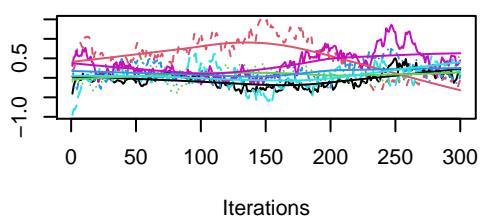
Trace of b53



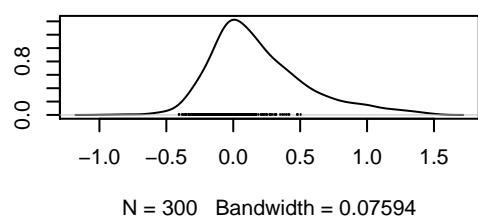
Density of b53



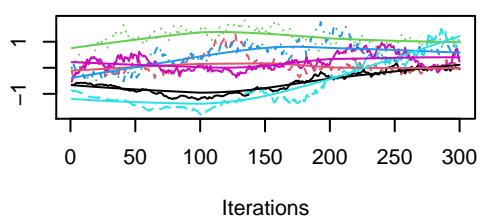
Trace of b54



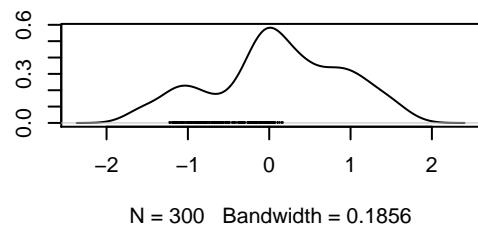
Density of b54



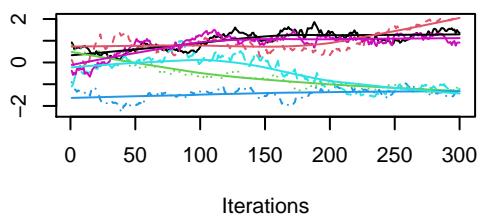
Trace of b55



Density of b55



Trace of b56



Density of b56

