

# report21

Haoliang Zheng

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## data

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

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

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

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

```

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

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

data_trim05 <- get.trim.data(0.5)

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

data_trim05 <- get.trim.data(0.5)

load("./report/report21/multi_adapt_poly_trim05_o2_3.RData")
load("./report/report21/multi_adapt_poly_trim05_o2_alphaPG3.RData")
load("./report/report21/multi_adapt_poly_trim05_o2_allnoPG3.RData")

```

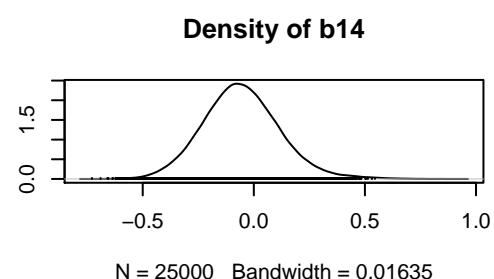
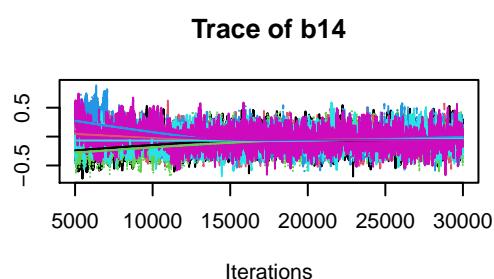
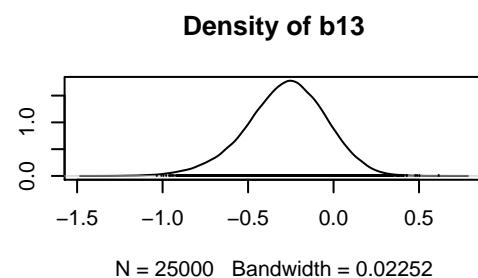
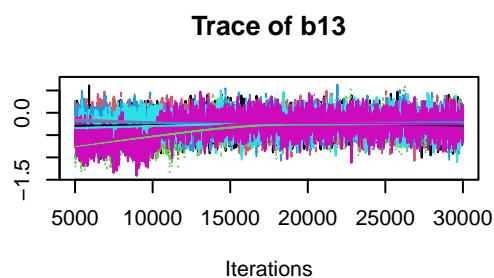
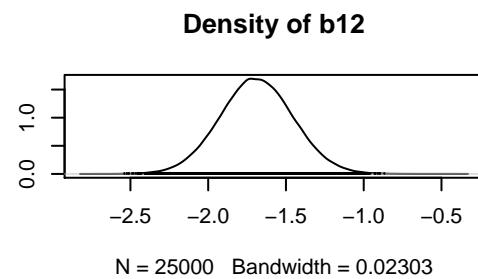
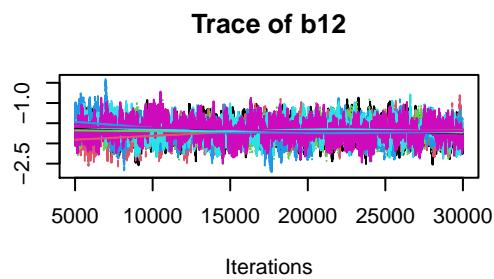
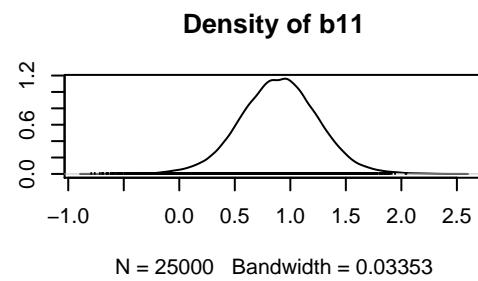
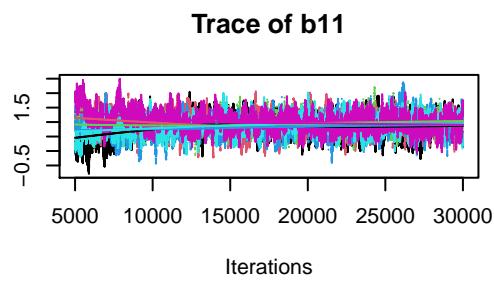
## traceplot

### all\_PG

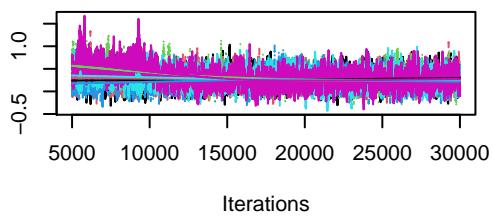
```

multi_adapt_poly_trim05_o2_3_coda <- multi_chain_coda(multi_adapt_poly_trim05_o2_3,
                                                       burn = 5000, N_para, p, order = 2)
plot(multi_adapt_poly_trim05_o2_3_coda)

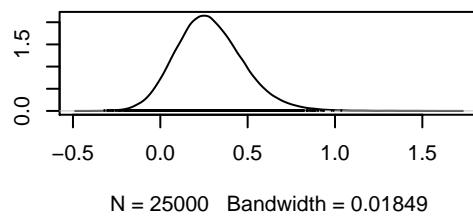
```



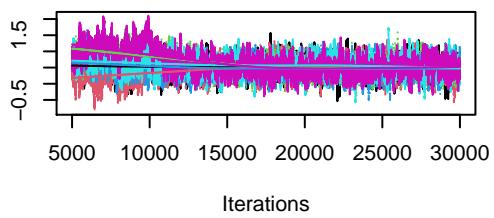
**Trace of b15**



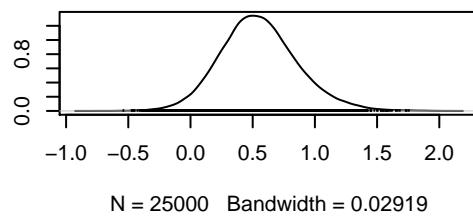
**Density of b15**



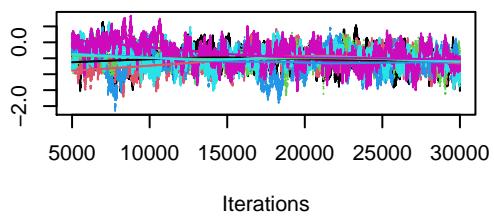
**Trace of b16**



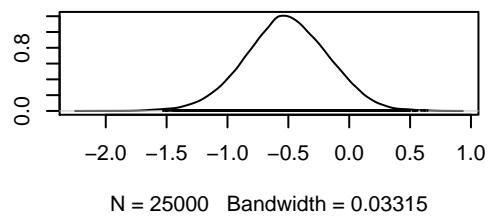
**Density of b16**



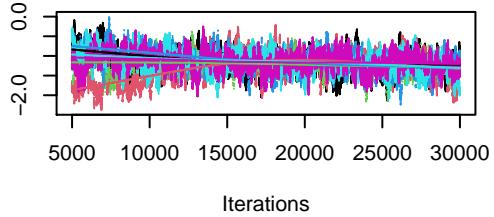
**Trace of b21**



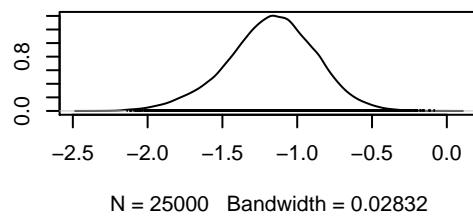
**Density of b21**



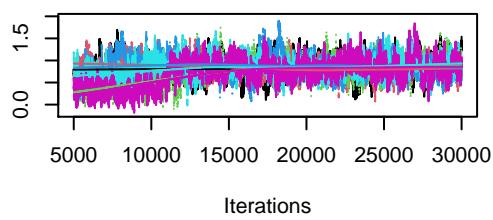
**Trace of b22**



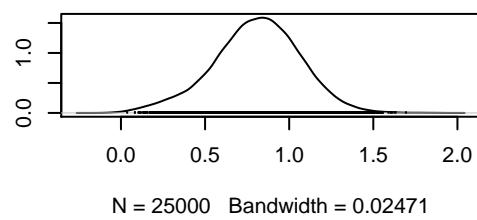
**Density of b22**



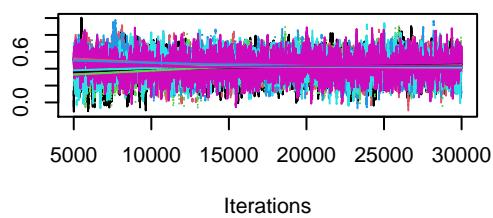
**Trace of b23**



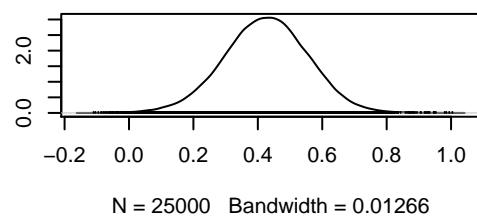
**Density of b23**



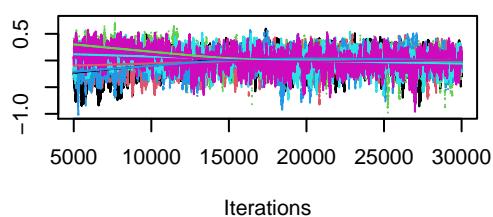
**Trace of b24**



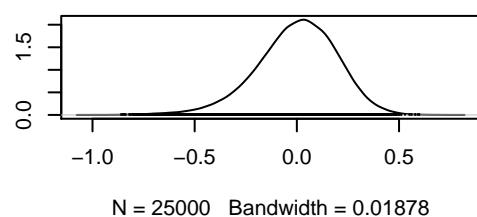
**Density of b24**



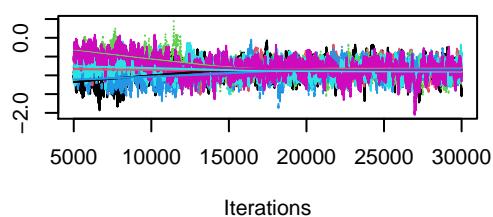
**Trace of b25**



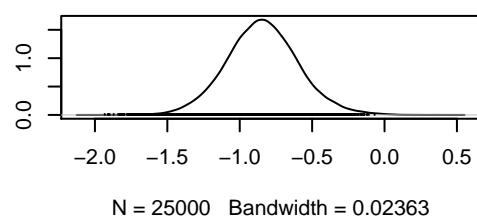
**Density of b25**



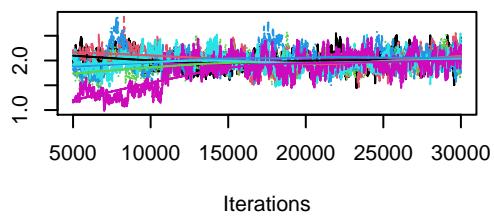
**Trace of b26**



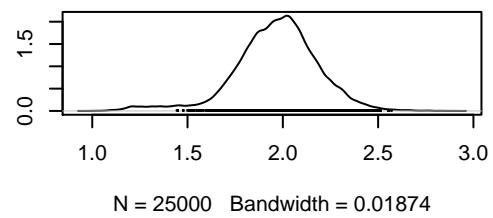
**Density of b26**



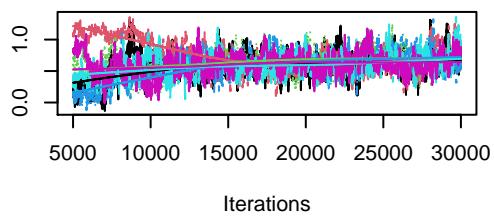
**Trace of a1**



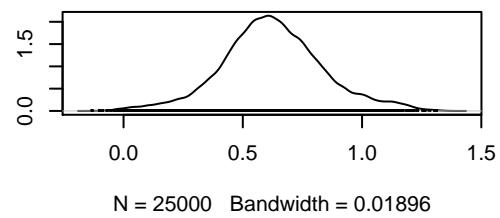
**Density of a1**



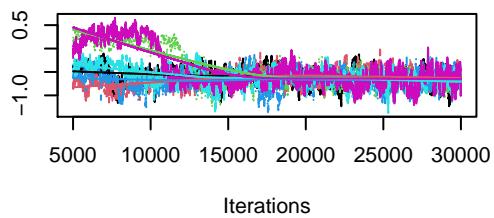
**Trace of a2**



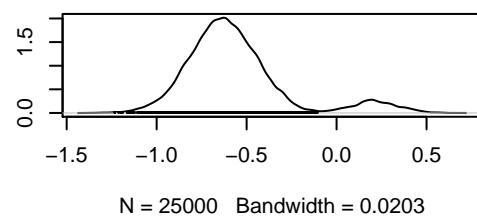
**Density of a2**



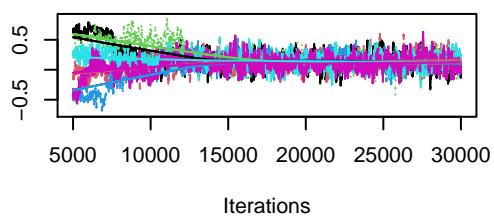
**Trace of a3**



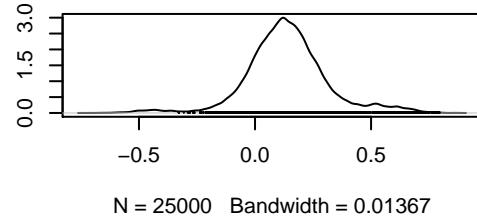
**Density of a3**

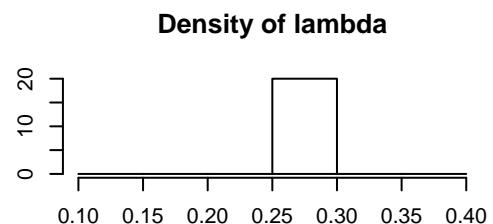
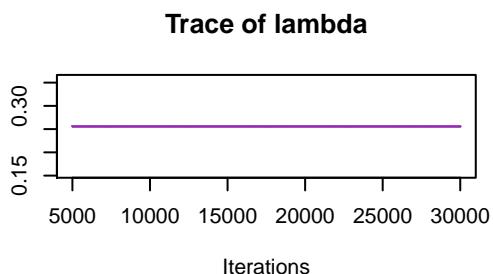
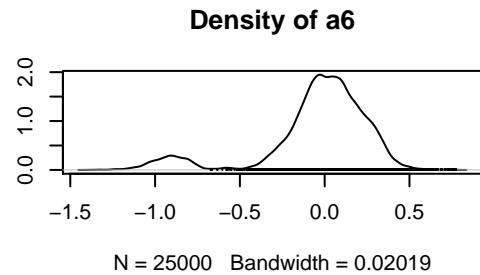
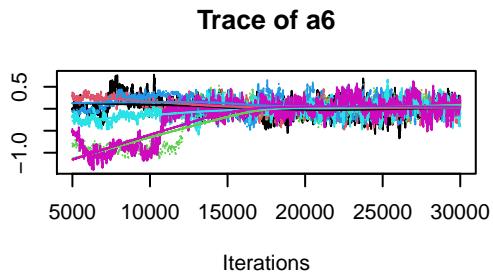
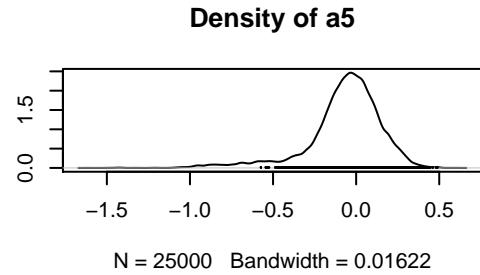
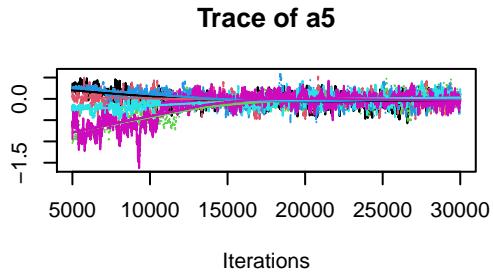


**Trace of a4**



**Density of a4**

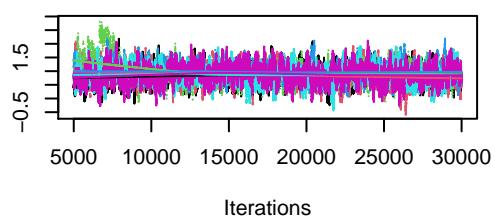




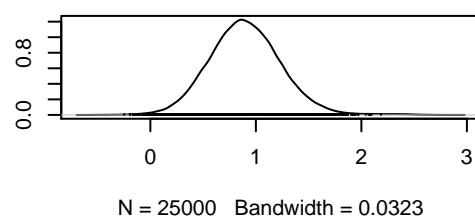
alphano\_PG

```
multi_adapt_poly_trim05_o2_alphaPG3_coda <- multi_chain_coda(multi_adapt_poly_trim05_o2_alphaPG3,
                                                               burn = 5000, N_para, p, order = 2)
plot(multi_adapt_poly_trim05_o2_alphaPG3_coda)
```

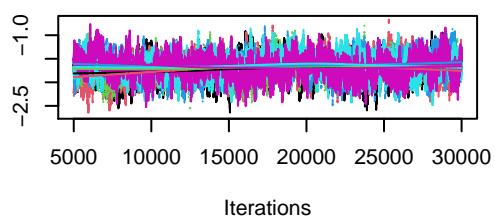
**Trace of  $b_{11}$**



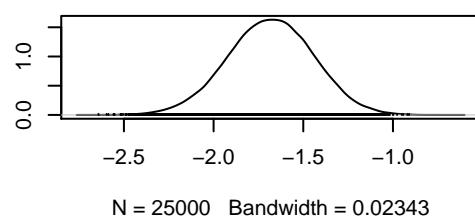
**Density of  $b_{11}$**



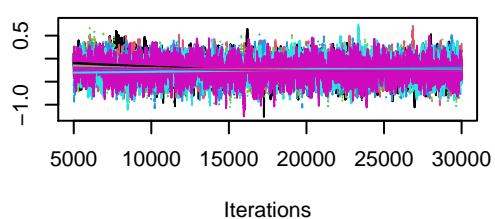
**Trace of  $b_{12}$**



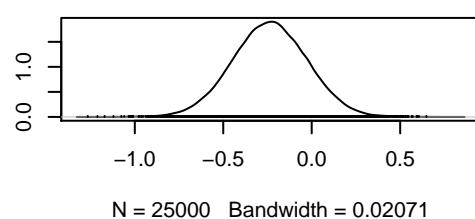
**Density of  $b_{12}$**



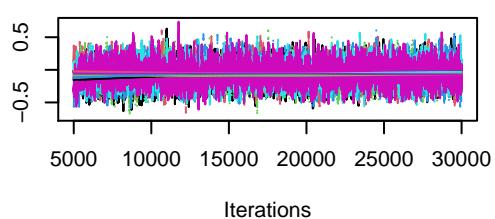
**Trace of  $b_{13}$**



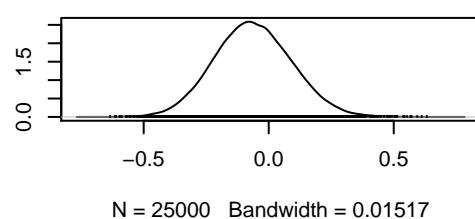
**Density of  $b_{13}$**



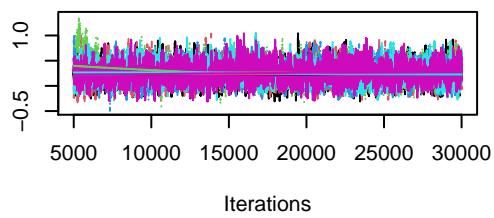
**Trace of  $b_{14}$**



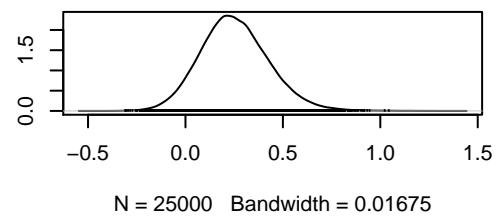
**Density of  $b_{14}$**



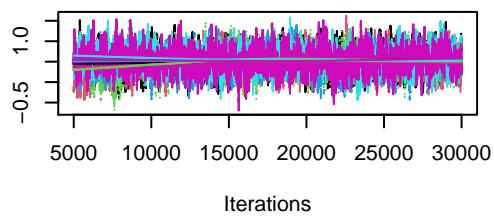
**Trace of b15**



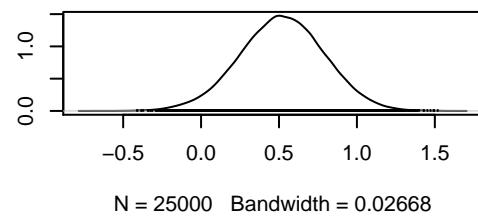
**Density of b15**



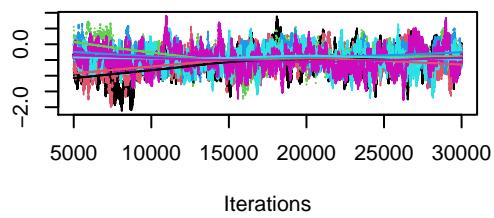
**Trace of b16**



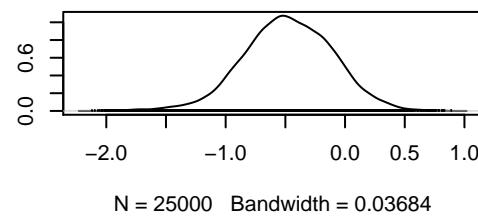
**Density of b16**



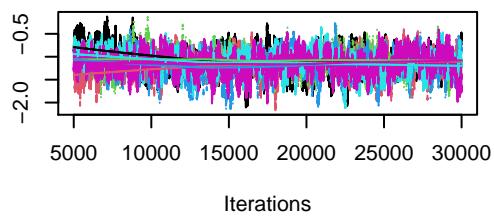
**Trace of b21**



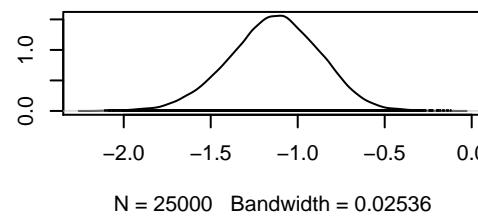
**Density of b21**



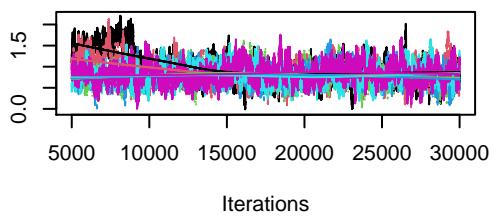
**Trace of b22**



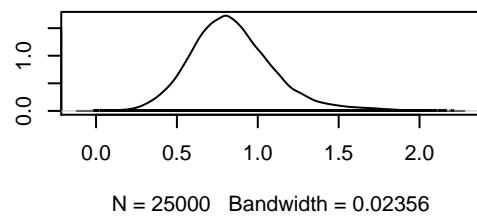
**Density of b22**



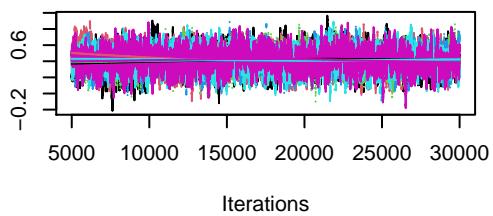
**Trace of b23**



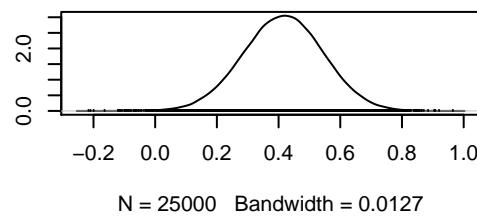
**Density of b23**



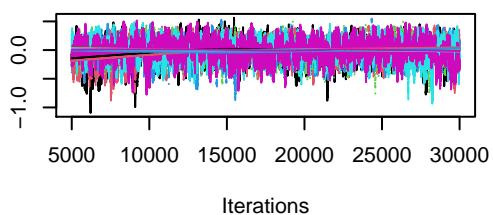
**Trace of b24**



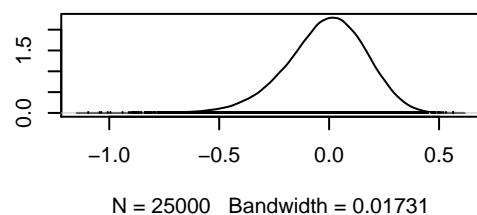
**Density of b24**



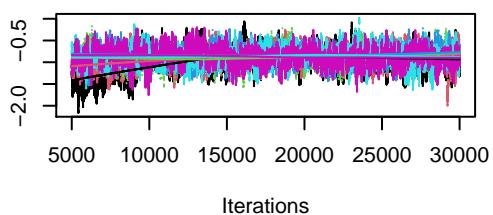
**Trace of b25**



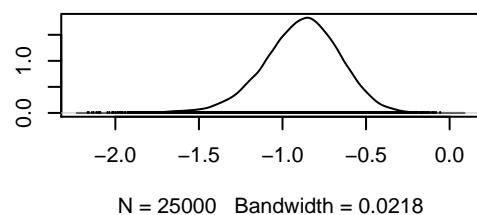
**Density of b25**



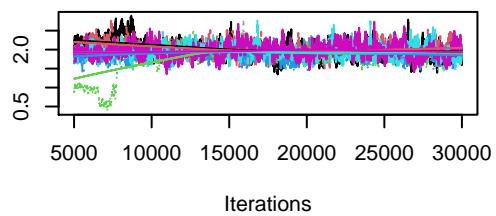
**Trace of b26**



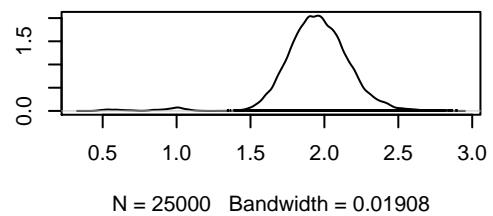
**Density of b26**



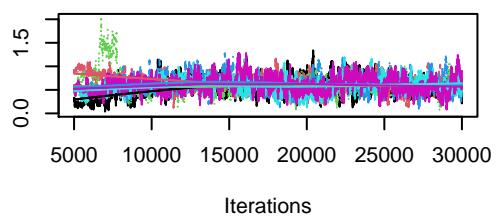
**Trace of a1**



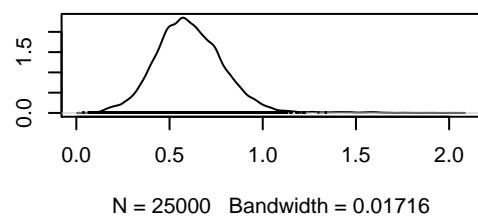
**Density of a1**



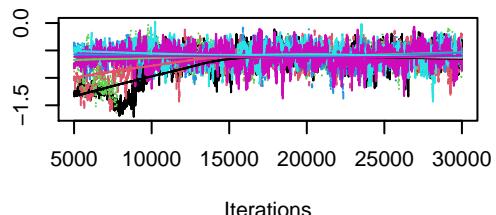
**Trace of a2**



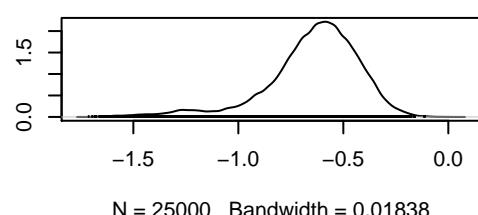
**Density of a2**



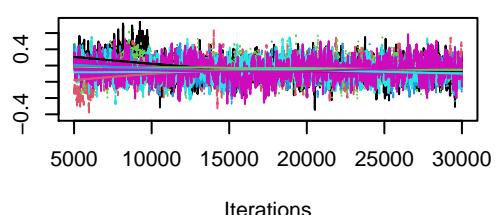
**Trace of a3**



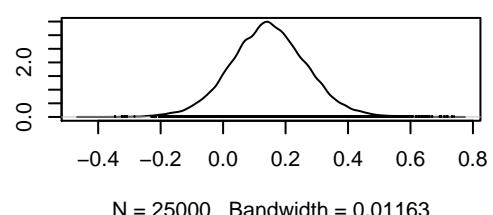
**Density of a3**

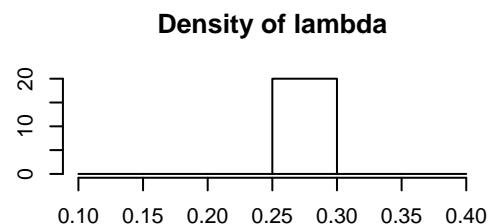
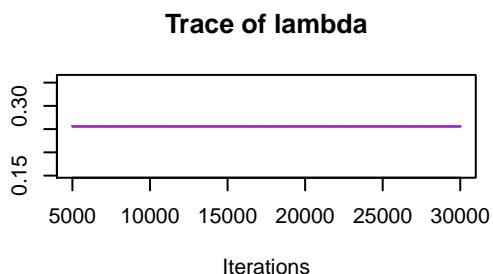
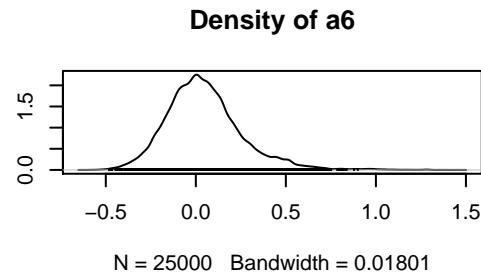
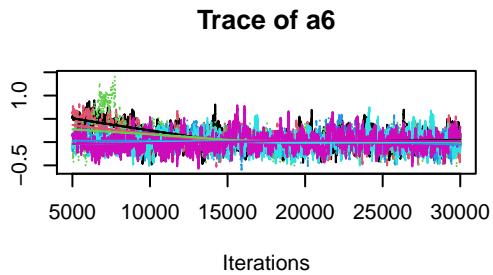
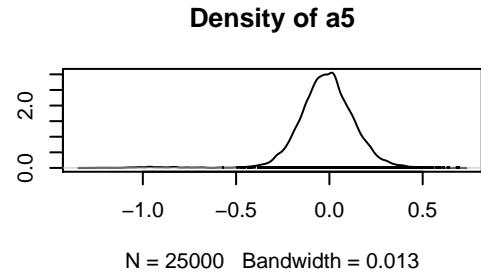
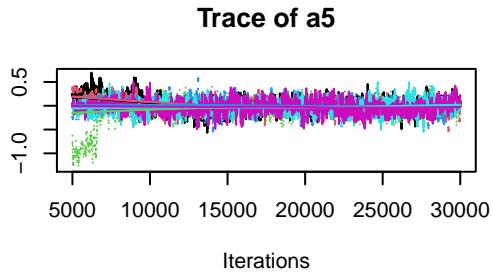


**Trace of a4**



**Density of a4**

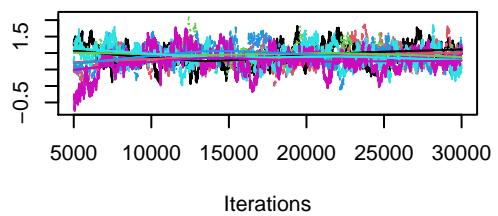




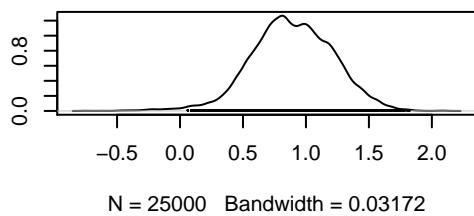
## allno\_PG

```
multi_adapt_poly_trim05_o2_allnoPG3_coda <- multi_chain_coda(multi_adapt_poly_trim05_o2_allnoPG3,
                                                               burn = 5000, N_para, p, order = 2)
plot(multi_adapt_poly_trim05_o2_allnoPG3_coda)
```

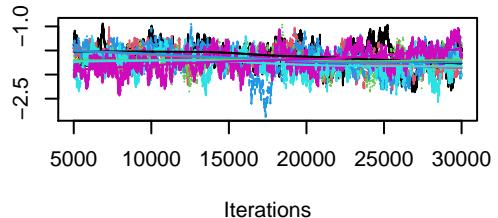
**Trace of  $b_{11}$**



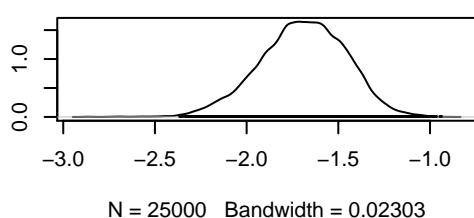
**Density of  $b_{11}$**



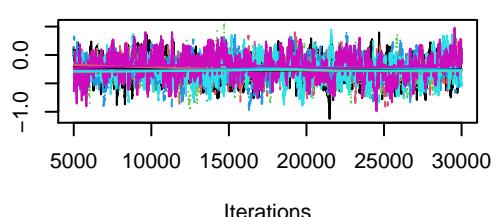
**Trace of  $b_{12}$**



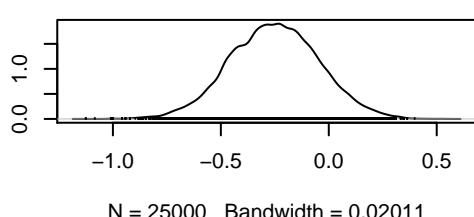
**Density of  $b_{12}$**



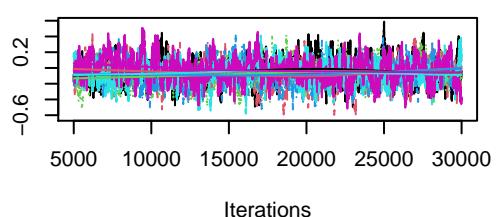
**Trace of  $b_{13}$**



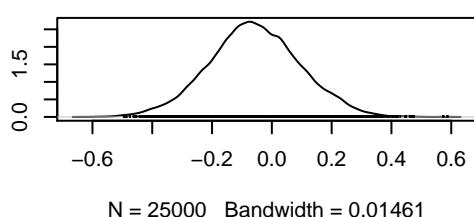
**Density of  $b_{13}$**



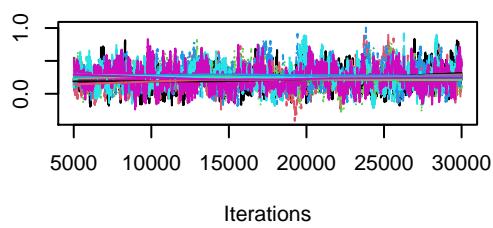
**Trace of  $b_{14}$**



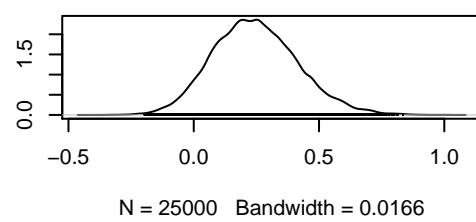
**Density of  $b_{14}$**



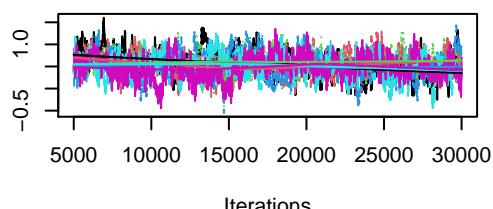
**Trace of b15**



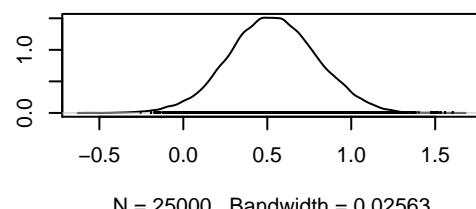
**Density of b15**



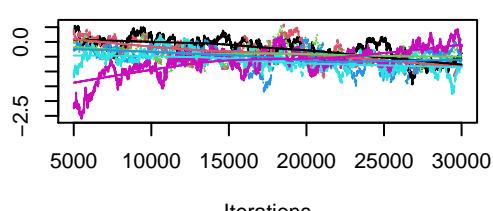
**Trace of b16**



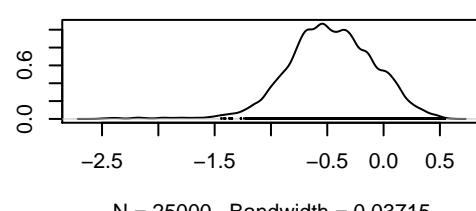
**Density of b16**



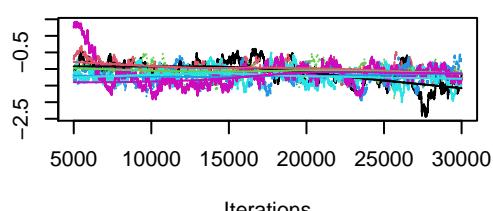
**Trace of b21**



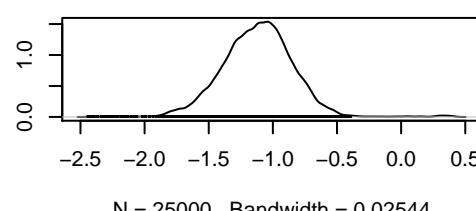
**Density of b21**



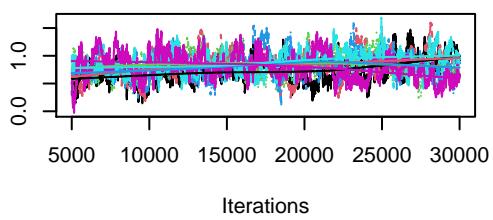
**Trace of b22**



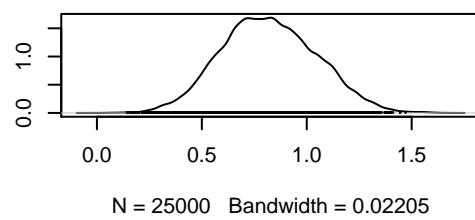
**Density of b22**



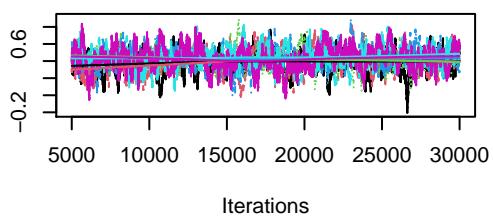
**Trace of b23**



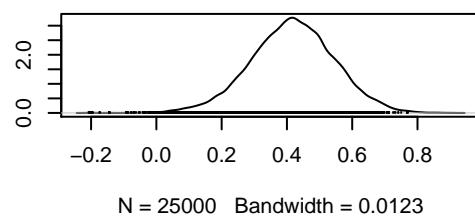
**Density of b23**



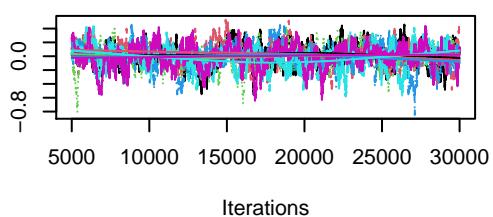
**Trace of b24**



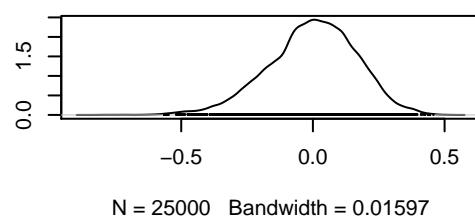
**Density of b24**



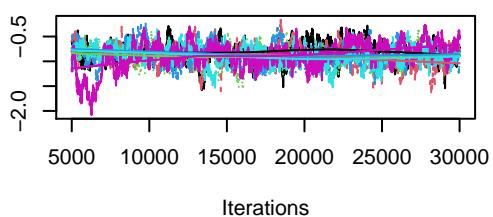
**Trace of b25**



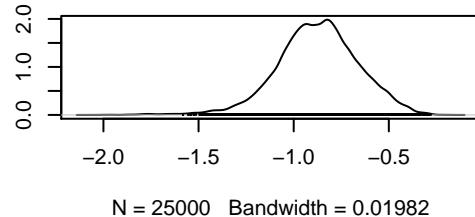
**Density of b25**

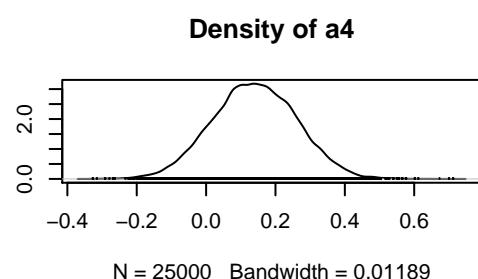
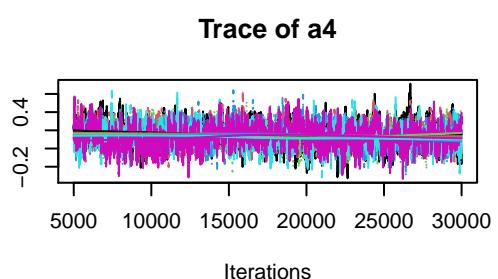
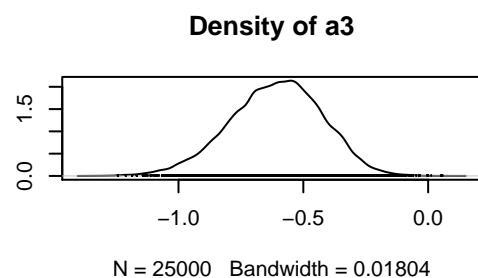
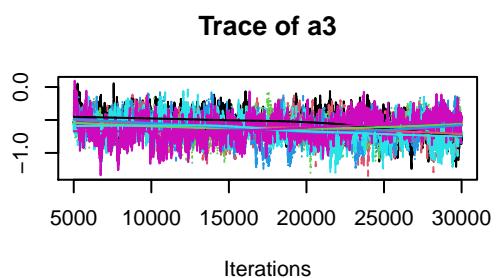
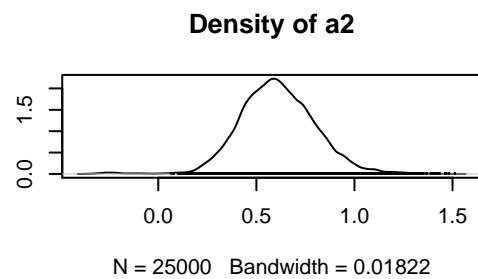
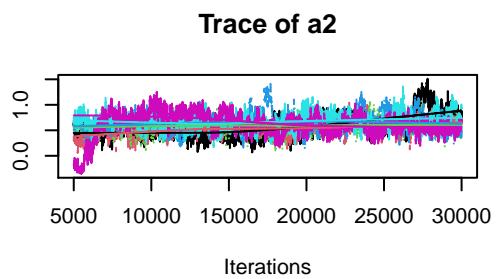
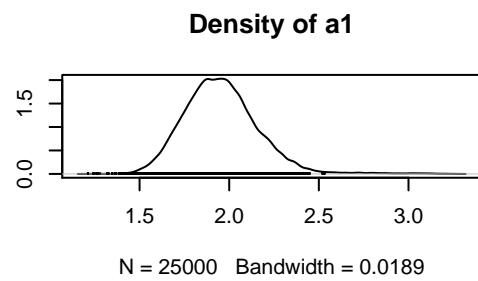
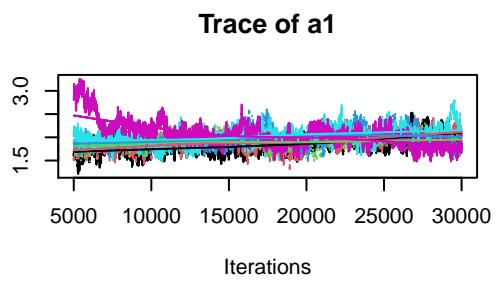


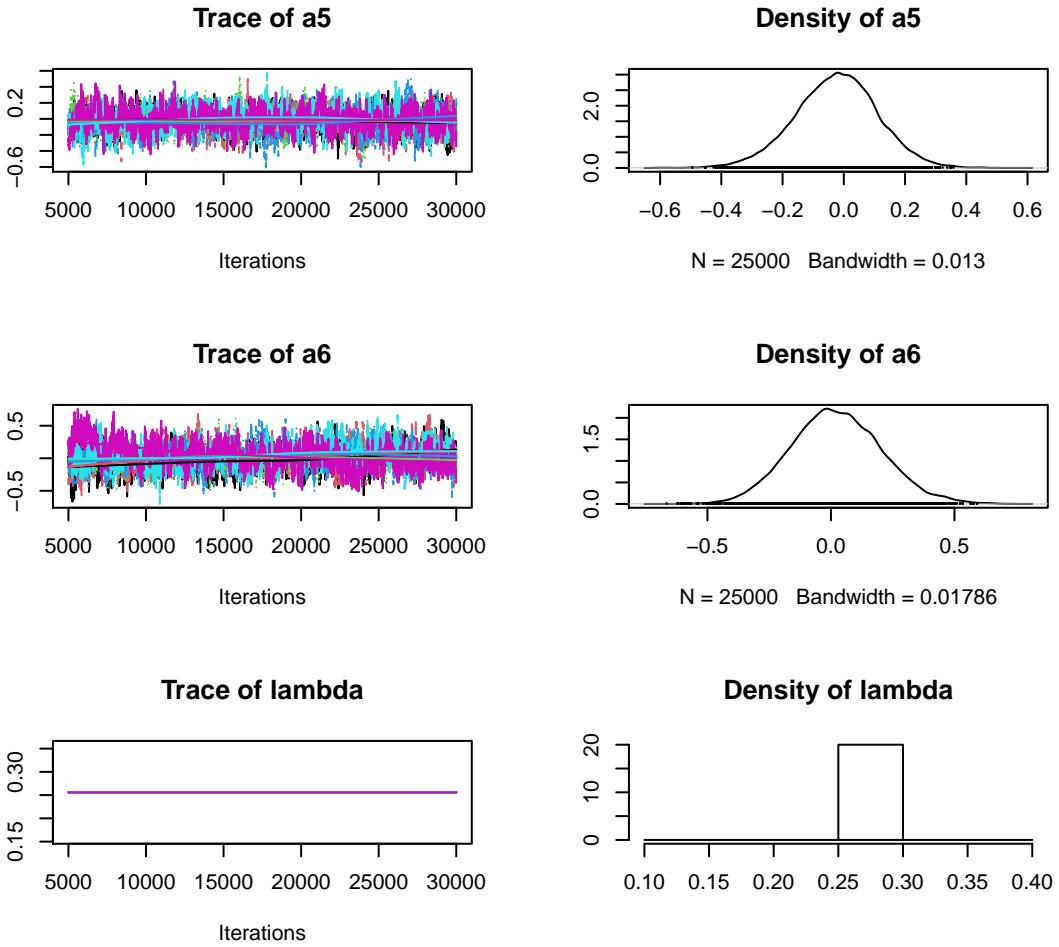
**Trace of b26**



**Density of b26**







psrf

```

n_range <- seq(5000, 25000, 500)
psrf_result <- data.frame()
for(nl in n_range){
  all_PG_coda <- multi_chain_coda_nol(multi_adapt_poly_trim05_o2_3,
                                         burn = 5000, N_para, p, order = 2,
                                         nlast = nl)
  alphano_PG_coda <- multi_chain_coda_nol(multi_adapt_poly_trim05_o2_alphaPG3,
                                             burn = 5000, N_para, p, order = 2,
                                             nlast = nl)
  allno_PG_coda <- multi_chain_coda_nol(multi_adapt_poly_trim05_o2_allnoPG3,
                                            burn = 5000, N_para, p, order = 2,
                                            nlast = nl)

  all_PG_coda_onlya <- multi_chain_coda_nol_onlya(multi_adapt_poly_trim05_o2_3,
                                                       burn = 5000, N_para, p, order = 2,
                                                       nlast = nl)
  alphano_PG_coda_onlya <- multi_chain_coda_nol_onlya(multi_adapt_poly_trim05_o2_alphaPG3,
                                                        burn = 5000, N_para, p, order = 2,
                                                        nlast = nl)
}

```

```

allno_PG_coda_onlya <- multi_chain_coda_nol_onlya(multi_adapt_poly_trim05_o2_allnoPG3,
                                                    burn = 5000, N_para, p, order = 2,
                                                    nlast = nl)

gd_result1 <- gelman.diag(all_PG_coda)
gd_result2 <- gelman.diag(alphano_PG_coda)
gd_result3 <- gelman.diag(allno_PG_coda)

gd_result1_onlya <- gelman.diag(all_PG_coda_onlya)
gd_result2_onlya <- gelman.diag(alphano_PG_coda_onlya)
gd_result3_onlya <- gelman.diag(allno_PG_coda_onlya)

psrf_result1 <- data.frame(value = gd_result1$psrf[,1],
                             variable = rownames(gd_result1$psrf),
                             type = "all_PG", n = nl)

psrf_result2 <- data.frame(value = gd_result2$psrf[,1],
                             variable = rownames(gd_result2$psrf),
                             type = "alphano_PG", n = nl)

psrf_result3 <- data.frame(value = gd_result3$psrf[,1],
                             variable = rownames(gd_result3$psrf),
                             type = "allno_PG", n = nl)

mpsrf_all_result <- data.frame(value = c(gd_result1$mpsrf, gd_result2$mpsrf, gd_result3$mpsrf),
                                 variable = "mpsrf_all", type = c("all_PG", "alphano_PG", "allno_PG"),
                                 n = nl)

mpsrf_a_result <- data.frame(value = c(gd_result1_onlya$mpsrf,
                                         gd_result2_onlya$mpsrf, gd_result3_onlya$mpsrf),
                               variable = "mpsrf_a", type = c("all_PG", "alphano_PG", "allno_PG"),
                               n = nl)

psrf_result <- rbind(psrf_result, psrf_result1, psrf_result2, psrf_result3,
                      mpsrf_all_result, mpsrf_a_result)
}

rownames(psrf_result) <- NULL

ggplot(data = psrf_result) +
  geom_line(aes(x = n, y = value, color = type)) +
  facet_wrap(~variable, scales = "free_y")

```

