

JOINT ANALYSES SLE PI-LowC3 AND OUTCOME

JOIN ANALYSES WITH R RANDOM COEFFICIENT - JMBayes2 R package

```
rm( list=ls() )
setwd("C:/Documenti/Manenti/LES/JOHNS HOPKINS")
library(haven)
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.1 --
## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble   3.1.6     v dplyr    1.0.7
## v tidyr    1.1.4     v stringr  1.4.0
## v readr    2.1.1     vforcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()   masks stats::lag()

sle_status_cross_sectional <- read_dta("sle_status_cross_sectional.dta")
sle_05_long <- read_dta("sle_05_long.dta")
sle_05_time_varying <- read_dta("sle_05_time_varying.dta")
```

JMbayes2 require that all datset are sorted by id

```
sle_status_cross_sectional <- sle_status_cross_sectional %>%
  mutate(id = as.numeric(id)) %>%
  arrange(id)
sle_05_long <- sle_05_long %>%
  mutate(id = as.numeric(id)) %>%
  arrange(id)
sle_05_time_varying <- sle_05_time_varying %>%
  mutate(id = as.numeric(id)) %>%
  arrange(id)
sle_05_long$LOWC3 <- as.factor(sle_05_long$LOWC3)
sle_status_cross_sectional$LOWC3 <- as.factor(sle_status_cross_sectional$LOWC3)
sle_05_time_varying$LOWC3 <- as.factor(sle_05_time_varying$LOWC3)
```

ANALYSES WITH JMbayes2

```
options(scipen=999)
library(JMbayes2)

## Loading required package: survival
## Loading required package: nlme
##
## Attaching package: 'nlme'
```

```

## The following object is masked from 'package:dplyr':
##
##      collapse

## Loading required package: GLMMadaptive

## Loading required package: splines

```

ADJUSTED ANALYSES

ADJUSTED COX WITH TIME-VARYING PH REGRESSION ANALYSIS INCLUDING eGFR

```

Stand.TV.CoxFit <- coxph(Surv(tstart, tstop, status) ~ LOWC3 + eGFR +
  ageatbiopsy + sex + black + hypertension + mmf + cyc,
  data = sle_05_time_varying, cluster = id)
summary(Stand.TV.CoxFit)

## Call:
## coxph(formula = Surv(tstart, tstop, status) ~ LOWC3 + eGFR +
##   ageatbiopsy + sex + black + hypertension + mmf + cyc, data = sle_05_time_varying,
##   cluster = id)
##
##   n= 4656, number of events= 32
##
##              coef exp(coef)  se(coef) robust se      z Pr(>|z|)
## LOWC31      1.055897  2.874551  0.390509  0.394121  2.679  0.00738 **
## eGFR        -0.015474  0.984645  0.005327  0.005157 -3.001  0.00269 **
## ageatbiopsy  0.005516  1.005531  0.016391  0.018655  0.296  0.76747
## sex          0.146607  1.157899  0.408872  0.438065  0.335  0.73787
## black         -0.024690  0.975613  0.381183  0.389015 -0.063  0.94939
## hypertension -0.233997  0.791364  0.404162  0.450298 -0.520  0.60331
## mmf          -1.329326  0.264656  0.407895  0.425602 -3.123  0.00179 **
## cyc          -0.930466  0.394370  0.527699  0.558778 -1.665  0.09588 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##              exp(coef) exp(-coef) lower .95 upper .95
## LOWC31       2.8746     0.3479    1.3277    6.2237
## eGFR         0.9846     1.0156    0.9747    0.9946
## ageatbiopsy  1.0055     0.9945    0.9694    1.0430
## sex          1.1579     0.8636    0.4907    2.7325
## black         0.9756     1.0250    0.4551    2.0913
## hypertension  0.7914     1.2636    0.3274    1.9128
## mmf          0.2647     3.7785    0.1149    0.6095
## cyc          0.3944     2.5357    0.1319    1.1791
##
## Concordance= 0.811  (se = 0.035 )
## Likelihood ratio test= 31.1  on 8 df,  p=0.0001
## Wald test          = 37.08  on 8 df,  p=0.00001
## Score (logrank) test = 36.21  on 8 df,  p=0.00002,  Robust = 21.32  p=0.006
##
##   (Note: the likelihood ratio and score tests assume independence of
##   observations within a cluster, the Wald and robust score tests do not).

```

ADJUSTED LONGITUDINAL ANALYSIS - random slope regression

```

lmeFit.rs.sle <- lme(eGFR ~ LOWC3 + time +
  ageatbiopsy + sex + black + hypertension + mmf + cyc,
  random = ~ 1 + time | id, control = lmeControl(opt = 'optim'), data = sle_05_long)
summary(lmeFit.rs.sle)

## Linear mixed-effects model fit by REML
##   Data: sle_05_long
##   AIC      BIC logLik
## -19945.2 -19861.43 9985.6
##
## Random effects:
##   Formula: ~1 + time | id
##   Structure: General positive-definite, Log-Cholesky parametrization
##             StdDev     Corr
## (Intercept) 38.9143827 (Intr)
## time        0.2631476 -0.999
## Residual    0.0187060
##
## Fixed effects: eGFR ~ LOWC3 + time + ageatbiopsy + sex + black + hypertension + mmf + cyc
##                  Value Std.Error DF t-value p-value
## (Intercept) 83.00888 2.8205210 4459 29.430335 0.0000
## LOWC31      0.01111 0.2842077 188  0.039078 0.9689
## time       -0.56171 0.0188034 4459 -29.872524 0.0000
## ageatbiopsy -0.00762 0.0100528 188 -0.757971 0.4494
## sex         0.45479 0.2816942 188  1.614465 0.1081
## black       -0.40954 0.2455788 188 -1.667671 0.0970
## hypertension -0.60135 0.2501843 188 -2.403613 0.0172
## mmf         0.11525 0.3189839 188  0.361314 0.7183
## cyc        -0.08133 0.3886464 188 -0.209274 0.8345
##
## Correlation:
##              (Intr) LOWC31 time  agtbps sex    black  hyprtn mmf
## LOWC31      -0.028
## time        -0.985  0.002
## ageatbiopsy -0.132  0.048  0.001
## sex         -0.016  0.022 -0.003 -0.044
## black       -0.032 -0.156 -0.001  0.026  0.054
## hypertension -0.030 -0.028  0.000  0.038  0.000 -0.086
## mmf         -0.083  0.061  0.000 -0.032  0.022 -0.089 -0.040
## cyc        -0.080 -0.058  0.002  0.092 -0.209  0.043  0.039  0.574
##
## Standardized Within-Group Residuals:
##   Min      Q1      Med      Q3      Max
## -5.51890641 -0.36779475 -0.01947392  0.23949399  8.66689044
##
## Number of Observations: 4656
## Number of Groups: 196

```

ADJUSTED COX WITH TIME-VARYING PH REGRESSION ANALYSIS NOT INCLUDING eGFR

```

CoxFit <- coxph(Surv(tstart, tstop, status) ~ LOWC3 +
  ageatbiopsy + sex + black + hypertension + mmf + cyc,

```

```

  data = sle_05_time_varying, cluster = id)
summary(CoxFit)

## Call:
## coxph(formula = Surv(tstart, tstop, status) ~ LOWC3 + ageatbiopsy +
##       sex + black + hypertension + mmf + cyc, data = sle_05_time_varying,
##       cluster = id)
##
##   n= 4656, number of events= 32
##
##           coef exp(coef)  se(coef) robust se      z Pr(>|z|)
## LOWC31     0.965686  2.626590  0.377160  0.399286  2.419 0.015583 *
## ageatbiopsy 0.008459  1.008495  0.015529  0.016483  0.513 0.607831
## sex        0.183785  1.201757  0.397462  0.380348  0.483 0.628952
## black      0.082132  1.085599  0.370238  0.379317  0.217 0.828578
## hypertension 0.043705  1.044674  0.390165  0.430385  0.102 0.919116
## mmf        -1.503452  0.222361  0.394777  0.399534 -3.763 0.000168 ***
## cyc        -1.211051  0.297884  0.520627  0.536632 -2.257 0.024023 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##           exp(coef) exp(-coef) lower .95 upper .95
## LOWC31     2.6266    0.3807    1.2009    5.7447
## ageatbiopsy 1.0085    0.9916    0.9764    1.0416
## sex        1.2018    0.8321    0.5702    2.5326
## black      1.0856    0.9212    0.5162    2.2832
## hypertension 1.0447    0.9572    0.4494    2.4284
## mmf        0.2224    4.4972    0.1016    0.4866
## cyc        0.2979    3.3570    0.1041    0.8528
##
## Concordance= 0.779  (se = 0.033 )
## Likelihood ratio test= 21.65  on 7 df,  p=0.003
## Wald test            = 42.68  on 7 df,  p=0.0000004
## Score (logrank) test = 27.28  on 7 df,  p=0.0003,  Robust = 18.04  p=0.01
##
##   (Note: the likelihood ratio and score tests assume independence of
##   observations within a cluster, the Wald and robust score tests do not).

```

with eGFR current value

```
jointFit <- jm(CoxFit, lmeFit.rs.sle, time_var = "time", n_chains = 4L, n_thin = 50, n_iter = 10000, da
```

with eGFR slope

```
fForms <- list(
  "eGFR" = ~ slope(eGFR)
)
jointFit1 <- update(jointFit, functional_forms = fForms)
```

with eGFR AUC

```

fForms <- list(
  "eGFR" = ~ area(eGFR)
)
jointFit2 <- update(jointFit, functional_forms = fForms)

```

ADJUSTED JOINT LONGITUDINAL SURVIVAL ANALYSIS - current eGFR value

```

summary(jointFit)

##
## Call:
## jm(Surv_object = CoxFit, Mixed_objects = lmeFit.rs.sle, time_var = "time",
##      data_Surv = sle_05_time_varying, n_chains = 4L, n_thin = 50,
##      n_iter = 10000)
##
## Data Descriptives:
## Number of Groups: 196           Number of events: 32 (0.7%)
## Number of Observations:
##   eGFR: 4656
##
##          DIC      WAIC      LPML
## marginal 35762.47 598344.1 -48394.1
## conditional 43655.15 1032323.3 -118122.9
##
## Random-effects covariance matrix:
##
##          StdDev     Corr
## (Intr) 38.2722 (Intr)
## time   1.5519 -0.2080
##
## Survival Outcome:
##          Mean   StDev    2.5%   97.5%      P   Rhat
## LOWC31    1.0240 0.5073  0.0314  1.9902 0.0447 1.0062
## ageatbiopsy 0.0066 0.0168 -0.0283  0.0366 0.6658 1.0024
## sex       0.0579 0.4130 -0.7565  0.8539 0.8816 1.0001
## black     -0.0326 0.3888 -0.8304  0.7230 0.9395 1.0093
## hypertension -0.2054 0.3798 -0.9817  0.5223 0.5553 1.0053
## mmf       -1.4207 0.4141 -2.2315 -0.6227 0.0000 1.0088
## cyc       -1.0736 0.5209 -2.1261 -0.0540 0.0474 1.0023
## value(eGFR) -0.0152 0.0053 -0.0257 -0.0054 0.0079 1.0026
##
## Longitudinal Outcome: eGFR (family = gaussian, link = identity)
##          Mean   StDev    2.5%   97.5%      P   Rhat
## (Intercept) 83.8879 2.6411 78.5300 88.7060 0.0000 0.9957
## LOWC31     -0.9666 2.6389 -5.8838  4.1157 0.7474 1.0042
## time      -0.5791 0.3811 -1.2827  0.1783 0.1289 1.0129
## ageatbiopsy -0.0701 0.0777 -0.2207  0.0899 0.3763 0.9987
## sex        3.4558 2.6192 -1.6494  8.3565 0.1842 0.9984
## black     -0.0594 2.2536 -4.4180  4.1845 0.9737 1.0007
## hypertension -3.8975 2.3568 -8.3459  1.0057 0.0947 0.9989
## mmf       1.5003 2.7515 -3.6868  6.6214 0.5842 1.0021

```

```

## cyc           1.3206 2.8139 -4.1780  7.0064 0.6237 0.9987
## sigma        3.8556 0.6875  2.7714  5.5193 0.0000 1.0175
##
## MCMC summary:
## chains: 4
## iterations per chain: 10000
## burn-in per chain: 500
## thinning: 50
## time: 9.5 min

```

ADJUSTED JOINT LONGITUDINAL SURVIVAL ANALYSIS - slope eGFR

```
summary(jointFit1)
```

```

##
## Call:
## jm(Surv_object = CoxFit, Mixed_objects = lmeFit.rs.sle, time_var = "time",
##      functional_forms = fForms, data_Surv = sle_05_time_varying,
##      n_chains = 4L, n_thin = 50, n_iter = 10000)
##
## Data Descriptives:
## Number of Groups: 196          Number of events: 32 (0.7%)
## Number of Observations:
##   eGFR: 4656
##
##             DIC       WAIC       LPML
## marginal    35882.60  625279.5 -49971.82
## conditional 43645.21 1018776.3 -118511.09
##
## Random-effects covariance matrix:
##
##             StdDev     Corr
## (Intr) 38.3489 (Intr)
## time   1.5558 -0.2298
##
## Survival Outcome:
##             Mean   StDev   2.5%   97.5%     P   Rhat
## LOWC31      0.9740 0.5184 -0.0254  1.9870 0.0553 1.0049
## ageatbiopsy 0.0078 0.0170 -0.0269  0.0414 0.6526 1.0007
## sex         0.1270 0.4087 -0.7305  0.8956 0.7526 1.0042
## black        0.0702 0.3769 -0.6939  0.7659 0.8842 1.0215
## hypertension 0.0112 0.4209 -0.8114  0.7750 0.9737 1.0156
## mmf         -1.6291 0.4296 -2.4646 -0.8719 0.0000 1.0054
## cyc         -1.3947 0.5255 -2.4338 -0.3891 0.0105 1.0064
## slope(eGFR) 0.2345 0.3257 -0.4127  0.8025 0.4395 1.0161
##
## Longitudinal Outcome: eGFR (family = gaussian, link = identity)
##             Mean   StDev   2.5%   97.5%     P   Rhat
## (Intercept) 83.8933 2.6403 78.6263 88.8041 0.0000 0.9956
## LOWC31      -0.9274 2.6365 -5.7323  4.1125 0.7579 1.0040
## time        -0.5552 0.3832 -1.2726  0.1980 0.1395 1.0063
## ageatbiopsy -0.0699 0.0775 -0.2228  0.0945 0.3763 0.9980
## sex          3.4730 2.6346 -1.6991  8.5215 0.1816 0.9985
## black        -0.0872 2.2476 -4.4973  4.1922 0.9368 1.0007

```

```

## hypertension -3.8841 2.3571 -8.3717 0.8785 0.1053 0.9988
## mmf 1.4767 2.7673 -3.6409 6.7329 0.6079 1.0030
## cyc 1.3165 2.8172 -4.1075 6.9944 0.6211 0.9983
## sigma 3.8519 0.6891 2.8487 5.5577 0.0000 1.0085
##
## MCMC summary:
## chains: 4
## iterations per chain: 10000
## burn-in per chain: 500
## thinning: 50
## time: 8 min

```

ADJUSTED JOINT LONGITUDINAL SURVIVAL ANALYSIS - normalized area/cumulative-effect eGFR

```

summary(jointFit2)

```

```

##
## Call:
## jm(Surv_object = CoxFit, Mixed_objects = lmeFit.rs.sle, time_var = "time",
##      functional_forms = fForms, data_Surv = sle_05_time_varying,
##      n_chains = 4L, n_thin = 50, n_iter = 10000)
##
## Data Descriptives:
## Number of Groups: 196 Number of events: 32 (0.7%)
## Number of Observations:
## eGFR: 4656
##
## DIC WAIC LPML
## marginal 35880.48 611327.1 -49985.83
## conditional 43629.45 1026878.5 -120011.17
##
## Random-effects covariance matrix:
##
## StdDev Corr
## (Intr) 38.2695 (Intr)
## time 1.5494 -0.2104
##
## Survival Outcome:
## Mean StDev 2.5% 97.5% P Rhat
## LOWC31 1.0041 0.4976 0.0265 1.9720 0.0447 1.0025
## ageatbiopsy 0.0064 0.0175 -0.0300 0.0378 0.7053 1.0051
## sex 0.0686 0.4090 -0.7600 0.8648 0.8316 0.9989
## black -0.0306 0.3775 -0.7645 0.7497 0.9026 1.0301
## hypertension -0.1977 0.3827 -0.9608 0.5349 0.6184 0.9993
## mmf -1.4171 0.4014 -2.1735 -0.6492 0.0026 1.0035
## cyc -1.0660 0.5254 -2.1363 -0.0744 0.0395 0.9962
## area(eGFR) -0.0150 0.0053 -0.0254 -0.0048 0.0000 1.0038
##
## Longitudinal Outcome: eGFR (family = gaussian, link = identity)
## Mean StDev 2.5% 97.5% P Rhat
## (Intercept) 83.8867 2.6407 78.5437 88.7820 0.0000 0.9956
## LOWC31 -0.9626 2.6389 -5.9538 4.1431 0.7368 1.0036
## time -0.5767 0.3838 -1.3019 0.1764 0.1316 1.0143

```

```

## ageatbiopsy -0.0703 0.0777 -0.2229 0.0886 0.3868 0.9991
## sex 3.4615 2.6287 -1.7786 8.4736 0.1816 0.9979
## black -0.0652 2.2474 -4.4358 4.1999 0.9553 1.0003
## hypertension -3.9043 2.3584 -8.3778 0.9508 0.0947 0.9987
## mmf 1.5029 2.7658 -3.5099 6.7184 0.5921 1.0020
## cyc 1.3160 2.8275 -4.3294 7.1144 0.6237 0.9983
## sigma 3.8442 0.6557 2.8281 5.2884 0.0000 1.0106
##
## MCMC summary:
## chains: 4
## iterations per chain: 10000
## burn-in per chain: 500
## thinning: 50
## time: 7.7 min

```

COMPARE MODELS - ADJUSTED

```
compare_jm(jointFit, jointFit1, jointFit2)
```

```

##
## DIC WAIC LPML
## jointFit 35762.47 598344.1 -48394.10
## jointFit2 35880.48 611327.1 -49985.83
## jointFit1 35882.60 625279.5 -49971.82
##
## The criteria are calculated based on the marginal log-likelihood.

```

CALCULATE P values and 95% credible intervals

```
jmb2.ci.p <- function(x, times = 1) {
  b.m <- mean(c.all)
  b.sd <- sd(c.all)
  b.ci <- quantile(c.all, probs = c(0.025, 0.975))
  tw <- c(mean(c.all <= 0), mean(c.all >= 0))
  prob.not = min(tw)
  p <- 2 * prob.not
  hr <- exp(mean(c.all) * times)
  ci <- exp(quantile(c.all, probs = c(0.025, 0.975)) * times)
  if (ci[2] < ci[1]) {
    cat("HR: ", round(hr, 2), "(95%CI: ", round(ci[2], 2), " to ", round(ci[1], 2), "; P= ", round(p, 4))
  } else {
    cat("HR: ", round(hr, 2), "(95%CI: ", round(ci[1], 2), " to ", round(ci[2], 2), "; P= ", round(p, 4))
  }
}
```

ESTIMATES FROM THE MODELS - current value - adjusted

```
b <- coef(jointFit)
b$gammas["LOWC31"]

## LLOWC31
## 1.023958
```

```
b$association
```

```
##      Mean  
## -0.01515129
```

reproducing JMbayes2 output - current value - adjusted

```
c.1 <- jointFit$mcmc[[3]][[1]][,1]  
c.2 <- jointFit$mcmc[[3]][[2]][,1]  
c.3 <- jointFit$mcmc[[3]][[3]][,1]  
c.4 <- jointFit$mcmc[[3]][[4]][,1]  
c.all <- c(c.1,c.2,c.3,c.4)  
jmb2.ci.p(c.all)
```

```
## HR: 2.78 (95%CI: 1.03 to 7.32 ; P= 0.0447 )
```

calculation association parameter (per 10mL/min/1.73m² decrease) - current value -adjusted

```
c.1 <- jointFit$mcmc[[4]][[1]]  
c.2 <- jointFit$mcmc[[4]][[2]]  
c.3 <- jointFit$mcmc[[4]][[3]]  
c.4 <- jointFit$mcmc[[4]][[4]]  
c.all <- c(c.1,c.2,c.3,c.4)  
jmb2.ci.p(c.all, times = -10)
```

```
## HR: 1.16 (95%CI: 1.06 to 1.29 ; P= 0.0079 )
```

ESTIMATES FROM THE MODELS - slope eGFR - adjusted

```
b <- coef(jointFit1)  
b$gammas["LOWC31"]
```

```
## LLOWC31  
## 0.9740477
```

```
b$association
```

```
##      Mean  
## 0.2344569
```

calculations: reproducing JMbayes2 output - slope eGFR - adjusted

```
c.1 <- jointFit1$mcmc[[3]][[1]][,1]  
c.2 <- jointFit1$mcmc[[3]][[2]][,1]  
c.3 <- jointFit1$mcmc[[3]][[3]][,1]  
c.4 <- jointFit1$mcmc[[3]][[4]][,1]  
c.all <- c(c.1,c.2,c.3,c.4)  
jmb2.ci.p(c.all)
```

```
## HR: 2.65 (95%CI: 0.97 to 7.29 ; P= 0.0553 )
```

calculation association parameter (per 10mL/min/1.73m² decrease)

- slope eGFR - adjusted

```
c.1 <- jointFit1$mcmc[[4]][[1]]
c.2 <- jointFit1$mcmc[[4]][[2]]
c.3 <- jointFit1$mcmc[[4]][[3]]
c.4 <- jointFit1$mcmc[[4]][[4]]
c.all <- c(c.1,c.2,c.3,c.4)
jmb2.ci.p(c.all, times = 1)

## HR: 1.26 (95%CI: 0.66 to 2.23 ; P= 0.4395 )
```

ESTIMATES FROM THE MODELS - normalized area/cumulative-effect eGFR

- adjusted

```
b <- coef(jointFit2)
b$gammas["LOWC31"]
```

```
## LOWC31
## 1.0041
```

```
b$association
```

```
##          Mean
## -0.01498253
```

calculations: reproducing JMbayes2 output - normalized area/cumulative-effect eGFR -adjusted

```
c.1 <- jointFit2$mcmc[[3]][[1]][,1]
c.2 <- jointFit2$mcmc[[3]][[2]][,1]
c.3 <- jointFit2$mcmc[[3]][[3]][,1]
c.4 <- jointFit2$mcmc[[3]][[4]][,1]
c.all <- c(c.1,c.2,c.3,c.4)
jmb2.ci.p(c.all)

## HR: 2.73 (95%CI: 1.03 to 7.19 ; P= 0.0447 )
```

calculation association parameter (per 10mL/min/1.73m² decrease)

- normalized area/cumulative-effect eGFR - adjusted

```
c.1 <- jointFit2$mcmc[[4]][[1]]
c.2 <- jointFit2$mcmc[[4]][[2]]
c.3 <- jointFit2$mcmc[[4]][[3]]
c.4 <- jointFit2$mcmc[[4]][[4]]
c.all <- c(c.1,c.2,c.3,c.4)
jmb2.ci.p(c.all, times = -10)

## HR: 1.16 (95%CI: 1.05 to 1.29 ; P= 0 )
```

CRUDE ANALYSES

CRUDE LONGITUDINAL ANALYSIS - random slope regression

```
lmeFit.rs.sle <- lme(eGFR ~ LOWC3 + time,  
random = ~ 1 + time | id, data = sle_05_long)
```

CRUDE COX WITH TIME-VARYING PH REGRESSION ANALYSIS

```
CoxFit <- coxph(Surv(tstart, tstop, status) ~ LOWC3,  
data = sle_05_time_varying, cluster = id)
```

CRUDE COX WITH TIME-VARYING PH REGRESSION ANALYSIS INCLUDING eGFR

```
Stand.TV.CoxFit <- coxph(Surv(tstart, tstop, status) ~ LOWC3 + eGFR,  
data = sle_05_time_varying, cluster = id)
```

ADJUSTED COX WITH TIME-VARYING PH REGRESSION ANALYSIS NOT INCLUDING eGFR

```
CoxAFit <- coxph(Surv(tstart, tstop, status) ~ LOWC3 + mmf + ageatbiopsy + sex + black + hypertension,  
data = sle_05_time_varying, cluster = id)
```

standard Cox PH model crude

```
summary(CoxFit)  
  
## Call:  
## coxph(formula = Surv(tstart, tstop, status) ~ LOWC3, data = sle_05_time_varying,  
##       cluster = id)  
##  
##      n= 4656, number of events= 32  
##  
##            coef exp(coef) se(coef) robust se      z Pr(>|z|)  
## LOWC31 1.0177    2.7667   0.3575   0.3570 2.851  0.00436 **  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
##            exp(coef) exp(-coef) lower .95 upper .95  
## LOWC31     2.767     0.3614     1.374      5.57  
##  
## Concordance= 0.625  (se = 0.047 )  
## Likelihood ratio test= 7.49  on 1 df,  p=0.006  
## Wald test          = 8.13  on 1 df,  p=0.004  
## Score (logrank) test = 8.82  on 1 df,  p=0.003,  Robust = 5.76  p=0.02  
##  
##  (Note: the likelihood ratio and score tests assume independence of  
##  observations within a cluster, the Wald and robust score tests do not).
```

standard Cox PH model adjusted

```
summary(CoxAFit)

## Call:
## coxph(formula = Surv(tstart, tstop, status) ~ LOWC3 + mmf + ageatbiopsy +
##       sex + black + hypertension, data = sle_05_time_varying, cluster = id)
##
## n= 4656, number of events= 32
##
##              coef exp(coef) se(coef) robust se      z Pr(>|z|)
## LOWC31      0.91568  2.49848  0.38042   0.39588  2.313 0.02072 *
## mmf        -1.02581  0.35851  0.37207   0.37269 -2.752 0.00592 **
## ageatbiopsy  0.01554  1.01566  0.01530   0.01575  0.987 0.32380
## sex        -0.01647  0.98367  0.39399   0.39855 -0.041 0.96704
## black       0.14626  1.15750  0.37136   0.38567  0.379 0.70451
## hypertension 0.17953  1.19665  0.38421   0.39446  0.455 0.64902
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##              exp(coef) exp(-coef) lower .95 upper .95
## LOWC31      2.4985    0.4002    1.1500    5.4281
## mmf        0.3585    2.7893    0.1727    0.7443
## ageatbiopsy 1.0157    0.9846    0.9848    1.0475
## sex        0.9837    1.0166    0.4504    2.1483
## black       1.1575    0.8639    0.5435    2.4649
## hypertension 1.1967    0.8357    0.5523    2.5926
##
## Concordance= 0.713 (se = 0.04 )
## Likelihood ratio test= 15.75 on 6 df,  p=0.02
## Wald test          = 24.9 on 6 df,  p=0.0004
## Score (logrank) test = 17.53 on 6 df,  p=0.008,  Robust = 15.65 p=0.02
##
## (Note: the likelihood ratio and score tests assume independence of
## observations within a cluster, the Wald and robust score tests do not).
```

with eGFR current value - crude

```
jointCFit <- jm(CoxFit, lmeFit.rs.sle, time_var = "time", n_chains = 4L, n_thin = 50, n_iter = 10000, d...
```

with eGFR slope - crude

```
fForms <- list(
  "eGFR" = ~ slope(eGFR)
)
jointCFit1 <- update(jointCFit, functional_forms = fForms)
```

with eGFR AUC - crude

```
fForms <- list(
  "eGFR" = ~ area(eGFR)
)
jointCFit2 <- update(jointCFit, functional_forms = fForms)
```

CRUDE JOINT LONGITUDINAL SURVIVAL ANALYSIS - current eGFR value

```
summary(jointCFit)

##
## Call:
## jm(Surv_object = CoxFit, Mixed_objects = lmeFit.rs.sle, time_var = "time",
##      data_Surv = sle_05_time_varying, n_chains = 4L, n_thin = 50,
##      n_iter = 10000)
##
## Data Descriptives:
## Number of Groups: 196           Number of events: 32 (0.7%)
## Number of Observations:
##   eGFR: 4656
##
##          DIC      WAIC      LPML
## marginal 33332.51 720753.1 -48570.77
## conditional 42119.75 1461850.2 -142059.65
##
## Random-effects covariance matrix:
##
##          StdDev     Corr
## (Intr) 39.2436 (Intr)
## time   1.1030 -0.2500
##
## Survival Outcome:
##          Mean  StDev    2.5%   97.5%      P     Rhat
## LOWC31    0.9678 0.4805 -0.0167  1.8267 0.0526 1.0086
## value(eGFR) -0.0177 0.0053 -0.0285 -0.0078 0.0000 0.9995
##
## Longitudinal Outcome: eGFR (family = gaussian, link = identity)
##          Mean  StDev    2.5%   97.5%      P     Rhat
## (Intercept) 82.5758 2.2759 77.9953 86.8364 0.0000 0.9989
## LOWC31     -1.0145 2.6792 -6.2621  4.1255 0.7158 0.9988
## time       -0.5521 0.3367 -1.2154  0.0910 0.0974 1.0005
## sigma      2.5066 0.5433  1.6839  3.8149 0.0000 1.0074
##
## MCMC summary:
## chains: 4
## iterations per chain: 10000
## burn-in per chain: 500
## thinning: 50
## time: 5.9 min
```

CRUDE JOINT LONGITUDINAL SURVIVAL ANALYSIS - slope eGFR

```
summary(jointCFit1)

##
## Call:
## jm(Surv_object = CoxFit, Mixed_objects = lmeFit.rs.sle, time_var = "time",
##      functional_forms = fForms, data_Surv = sle_05_time_varying,
```

```

##      n_chains = 4L, n_thin = 50, n_iter = 10000)
##
## Data Descriptives:
## Number of Groups: 196           Number of events: 32 (0.7%)
## Number of Observations:
##   eGFR: 4656
##
##          DIC      WAIC      LPML
## marginal 33631.78 766826.8 -51810.44
## conditional 42308.30 1521938.7 -169366.01
##
## Random-effects covariance matrix:
##
##          StdDev     Corr
## (Intr) 39.2343 (Intr)
## time   1.1169 -0.2634
##
## Survival Outcome:
##          Mean   StDev    2.5%  97.5%      P     Rhat
## LOWC31 0.9665 0.5118 -0.0955 1.9341 0.0632 1.0172
## slope(eGFR) 0.3296 0.3882 -0.4404 1.0650 0.3842 1.0026
##
## Longitudinal Outcome: eGFR (family = gaussian, link = identity)
##          Mean   StDev    2.5%  97.5%      P     Rhat
## (Intercept) 82.5663 2.2700 77.9819 86.7739 0.0000 0.9991
## LOWC31     -0.9951 2.6750 -6.2066  4.1025 0.7158 0.9992
## time       -0.5375 0.3389 -1.1868  0.1130 0.1079 1.0003
## sigma      2.4983 0.5680  1.6803  3.7992 0.0000 1.0133
##
## MCMC summary:
## chains: 4
## iterations per chain: 10000
## burn-in per chain: 500
## thinning: 50
## time: 6 min

```

CRUDE JOINT LONGITUDINAL SURVIVAL ANALYSIS - normalized

area/cumulative-effect eGFR

```
summary(jointCFit2)
```

```

##
## Call:
## jm(Surv_object = CoxFit, Mixed_objects = lmeFit.rs.sle, time_var = "time",
##     functional_forms = fForms, data_Surv = sle_05_time_varying,
##     n_chains = 4L, n_thin = 50, n_iter = 10000)
##
## Data Descriptives:
## Number of Groups: 196           Number of events: 32 (0.7%)
## Number of Observations:
##   eGFR: 4656
##
##          DIC      WAIC      LPML
## marginal 33378.51 760320.4 -53796.1

```

```

## conditional 42329.67 1530227.8 -168851.1
##
## Random-effects covariance matrix:
##
##          StdDev     Corr
## (Intr) 39.1723 (Intr)
## time   1.1090 -0.2495
##
## Survival Outcome:
##          Mean  StDev    2.5%  97.5%      P    Rhat
## LOWC31    0.9750 0.4869  0.0609  1.9732 0.0342 1.0003
## area(eGFR) -0.0176 0.0051 -0.0279 -0.0080 0.0000 1.0016
##
## Longitudinal Outcome: eGFR (family = gaussian, link = identity)
##          Mean  StDev    2.5%  97.5%      P    Rhat
## (Intercept) 82.5640 2.2748 77.9538 86.7425 0.0000 0.9994
## LOWC31      -1.0099 2.6774 -6.3219  4.0563 0.6947 0.9981
## time        -0.5517 0.3363 -1.2405  0.0835 0.0974 1.0004
## sigma       2.4908 0.5486  1.6238  3.8855 0.0000 1.0086
##
## MCMC summary:
## chains: 4
## iterations per chain: 10000
## burn-in per chain: 500
## thinning: 50
## time: 6.2 min

```

CALCULATE P values and 95% credible intervals

```

jmb2.ci.p <- function(x, times = 1) {
  b.m <- mean(c.all)
  b.sd <- sd(c.all)
  b.ci <- quantile(c.all, probs = c(0.025, 0.975))
  tw <- c(mean(c.all <= 0), mean(c.all >= 0))
  prob.not = min(tw)
  p <- 2 * prob.not
  hr <- exp(mean(c.all) * times)
  ci <- exp(quantile(c.all, probs = c(0.025, 0.975)) * times)
  if (ci[2] < ci[1]) {
    cat("HR: ", round(hr,2), "(95%CI: ", round(ci[2],2), " to ", round(ci[1],2), "; P= ", round(p, 4))
  } else {
    cat("HR: ", round(hr,2), "(95%CI: ", round(ci[1],2), " to ", round(ci[2],2), "; P= ", round(p, 4))
  }
}

```

ESTIMATES FROM THE MODELS - current value - crude

```

b <- coef(jointCFit)
b$gammas["LOWC31"]

## <NA>
##    NA

```

```
b$association
```

```
##          Mean  
## -0.01773441
```

calculations: reproducing JMbayes2 output - current value - crude

```
c.1 <- jointCFit$mcmc[[3]][[1]][,1]  
c.2 <- jointCFit$mcmc[[3]][[2]][,1]  
c.3 <- jointCFit$mcmc[[3]][[3]][,1]  
c.4 <- jointCFit$mcmc[[3]][[4]][,1]  
c.all <- c(c.1,c.2,c.3,c.4)  
jmb2.ci.p(c.all)
```

```
## HR: 2.63 (95%CI: 0.98 to 6.21 ; P= 0.0526 )
```

calculation association parameter (per 10mL/min/1.73m² decrease) - current value - crude

```
c.1 <- jointCFit$mcmc[[4]][[1]]  
c.2 <- jointCFit$mcmc[[4]][[2]]  
c.3 <- jointCFit$mcmc[[4]][[3]]  
c.4 <- jointCFit$mcmc[[4]][[4]]  
c.all <- c(c.1,c.2,c.3,c.4)  
jmb2.ci.p(c.all, times = -10)
```

```
## HR: 1.19 (95%CI: 1.08 to 1.33 ; P= 0 )
```

ESTIMATES FROM THE MODELS - slope eGFR - crude

```
b <- coef(jointCFit1)  
b$gammas["LOWC31"]
```

```
## <NA>  
## NA
```

```
b$association
```

```
##          Mean  
## 0.3295705
```

calculations: reproducing JMbayes2 output - slope eGFR - crude

```
c.1 <- jointCFit1$mcmc[[3]][[1]][,1]  
c.2 <- jointCFit1$mcmc[[3]][[2]][,1]  
c.3 <- jointCFit1$mcmc[[3]][[3]][,1]  
c.4 <- jointCFit1$mcmc[[3]][[4]][,1]  
c.all <- c(c.1,c.2,c.3,c.4)  
jmb2.ci.p(c.all)
```

```
## HR: 2.63 (95%CI: 0.91 to 6.92 ; P= 0.0632 )
```

calculation association parameter (per 10mL/min/1.73m² decrease)

- slope eGFR - crude

```
c.1 <- jointCFit1$mcmc[[4]][[1]]
c.2 <- jointCFit1$mcmc[[4]][[2]]
c.3 <- jointCFit1$mcmc[[4]][[3]]
c.4 <- jointCFit1$mcmc[[4]][[4]]
c.all <- c(c.1,c.2,c.3,c.4)
jmb2.ci.p(c.all, times = 1)

## HR: 1.39 (95%CI: 0.64 to 2.9 ; P= 0.3842 )
```

ESTIMATES FROM THE MODELS - normalized area/cumulative-effect eGFR

- crude

```
b <- coef(jointCFit2)
b$gammas["LOWC31"]
```

```
## <NA>
##   NA
b$association

##           Mean
## -0.01764902
```

calculations: reproducing JMbayes2 output - normalized area/cumulative-effect eGFR

```
c.1 <- jointCFit2$mcmc[[3]][[1]][,1]
c.2 <- jointCFit2$mcmc[[3]][[2]][,1]
c.3 <- jointCFit2$mcmc[[3]][[3]][,1]
c.4 <- jointCFit2$mcmc[[3]][[4]][,1]
c.all <- c(c.1,c.2,c.3,c.4)
jmb2.ci.p(c.all)

## HR: 2.65 (95%CI: 1.06 to 7.19 ; P= 0.0342 )
```

calculation association parameter (per 10mL/min/1.73m² decrease)

- normalized area/cumulative-effect eGFR - crude

```
c.1 <- jointCFit2$mcmc[[4]][[1]]
c.2 <- jointCFit2$mcmc[[4]][[2]]
c.3 <- jointCFit2$mcmc[[4]][[3]]
c.4 <- jointCFit2$mcmc[[4]][[4]]
c.all <- c(c.1,c.2,c.3,c.4)
jmb2.ci.p(c.all, times = -10)

## HR: 1.19 (95%CI: 1.08 to 1.32 ; P= 0 )
```

COMPARE MODELS - ADJUSTED AND CRUDE

```
compare_jm(jointFit, jointFit1, jointFit2)

##
##          DIC      WAIC      LPML
##  jointFit 35762.47 598344.1 -48394.10
##  jointFit2 35880.48 611327.1 -49985.83
##  jointFit1 35882.60 625279.5 -49971.82
##
## The criteria are calculated based on the marginal log-likelihood.

compare_jm(jointCFit, jointCFit1, jointCFit2)

##
##          DIC      WAIC      LPML
##  jointCFit 33332.51 720753.1 -48570.77
##  jointCFit2 33378.51 760320.4 -53796.10
##  jointCFit1 33631.78 766826.8 -51810.44
##
## The criteria are calculated based on the marginal log-likelihood.
```

Compare parameters of the longitudinal model

```
long.beta <- fixef(jointFit)
long.beta1 <- fixef(jointFit1)
long.beta2 <- fixef(jointFit2)
long.Cbeta <- fixef(jointCFit)
long.Cbeta1 <- fixef(jointCFit1)
long.Cbeta2 <- fixef(jointCFit2)
long.beta

## $eGFR
## (Intercept)    LOWC31       time ageatbiopsy        sex      black
## 83.88786452 -0.96664668 -0.57907025 -0.07010149 3.45584616 -0.05938407
## hypertension     mmf        cyc
## -3.89745464   1.50030089   1.32062508
long.beta1

## $eGFR
## (Intercept)    LOWC31       time ageatbiopsy        sex      black
## 83.89331370 -0.92738424 -0.55518801 -0.06994764 3.47300257 -0.08715287
## hypertension     mmf        cyc
## -3.88411816   1.47665650   1.31649526
long.beta2

## $eGFR
## (Intercept)    LOWC31       time ageatbiopsy        sex      black
## 83.88673808 -0.96260705 -0.57666080 -0.07029867 3.46153880 -0.06516350
## hypertension     mmf        cyc
## -3.90433720   1.50289486   1.31598565
long.Cbeta

## $eGFR
```

```

## (Intercept)      LOWC31       time
## 82.5757995   -1.0144681   -0.5521035
long.Cbeta1

## $eGFR
## (Intercept)      LOWC31       time
## 82.5663239   -0.9950653   -0.5374919
long.Cbeta2

## $eGFR
## (Intercept)      LOWC31       time
## 82.5640156   -1.0098699   -0.5517391

```

random effects survival model

```

re.surv <- ranef(jointFit)[,1]
re.surv1 <- ranef(jointFit1)[,1]
re.surv2 <- ranef(jointFit2)[,1]
re.Csurv <- ranef(jointCFit)[,1]
re.Csurv1 <- ranef(jointCFit1)[,1]
re.Csurv2 <- ranef(jointCFit2)[,1]

```

random effects longitudinal model

```

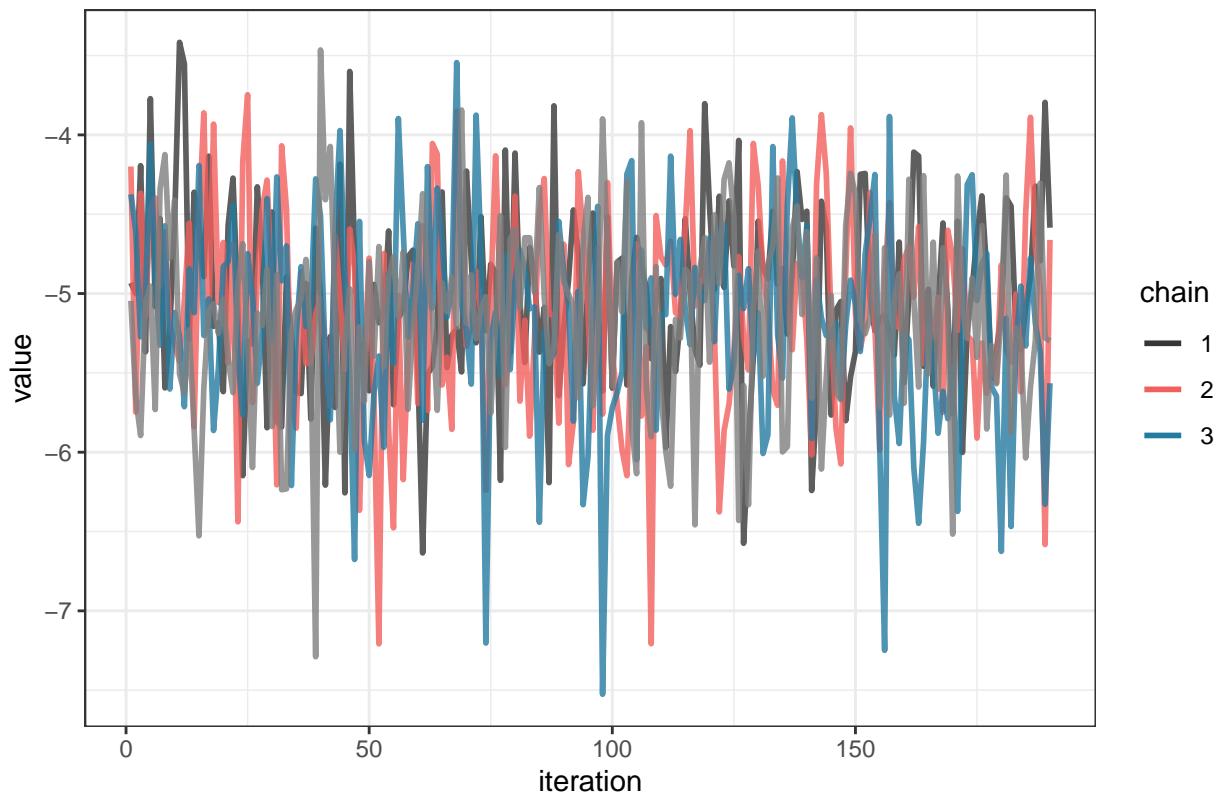
re.long <- ranef(jointFit)[,2]
re.long1 <- ranef(jointFit1)[,2]
re.long2 <- ranef(jointFit2)[,2]
re.Clong <- ranef(jointCFit)[,2]
re.Clong1 <- ranef(jointCFit1)[,2]
re.Clong2 <- ranef(jointCFit2)[,2]

```

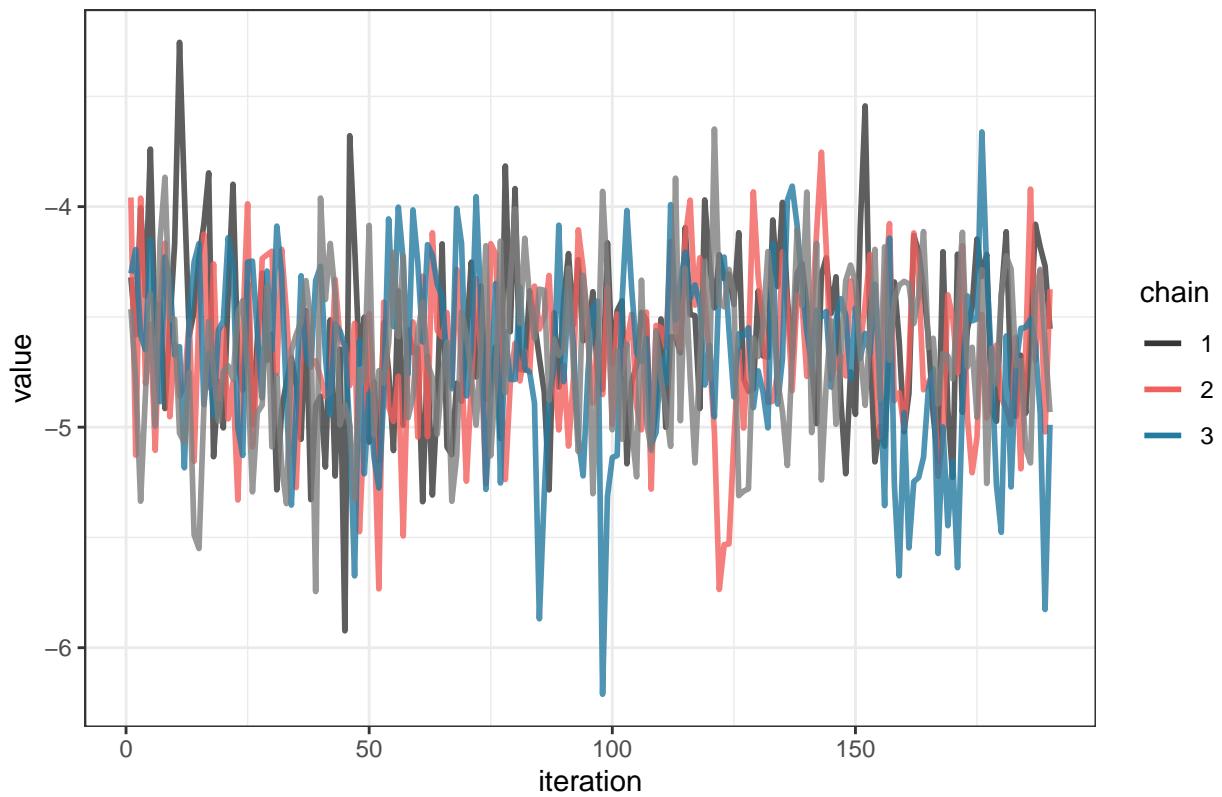
traceplots (scroll with left and right arrow)

```
traceplt <- ggtraceplot(jointFit)
```

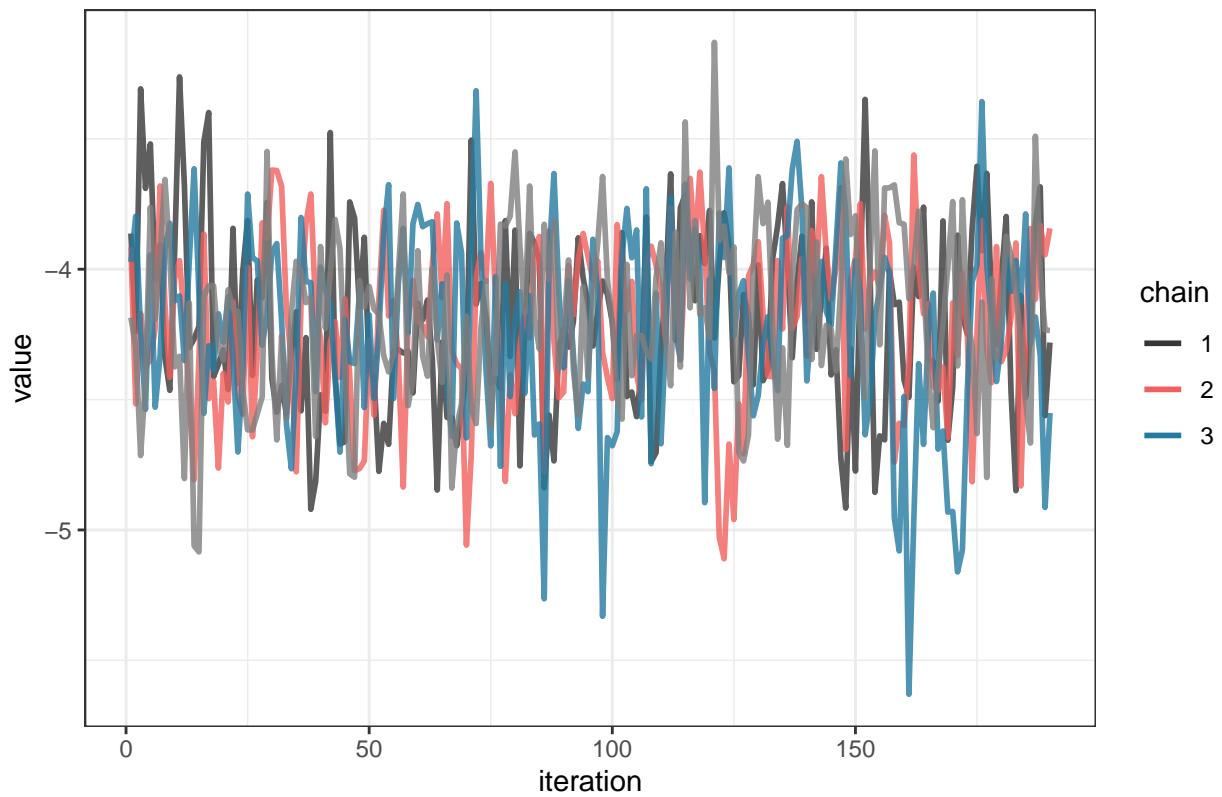
Traceplot of bs_gammas_1



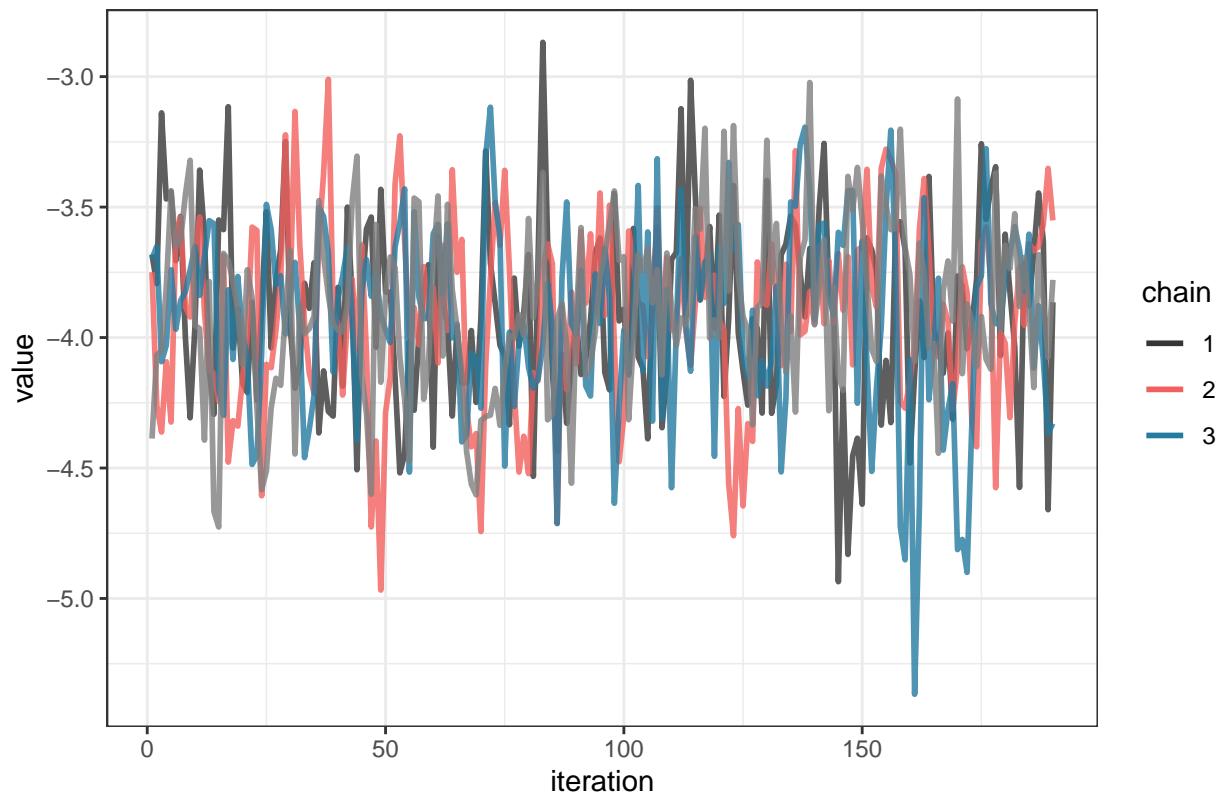
Traceplot of bs_gammas_2



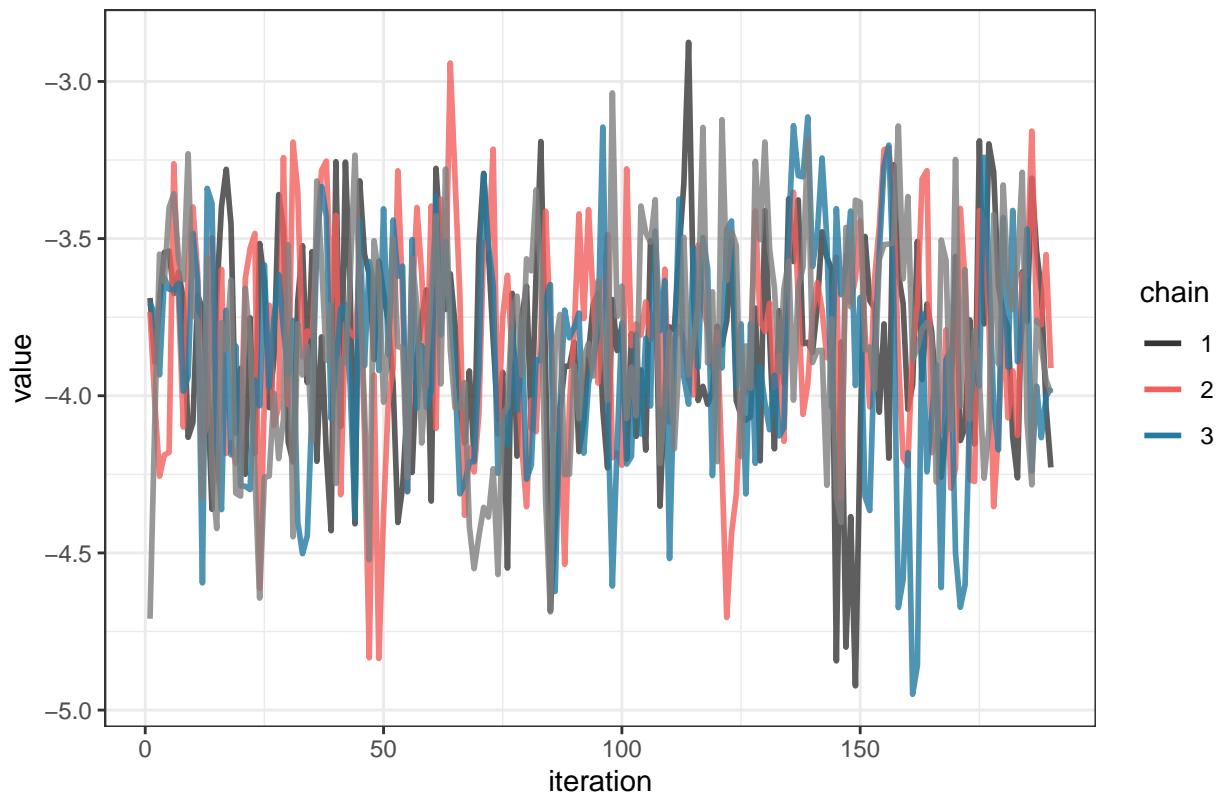
Traceplot of bs_gammas_3



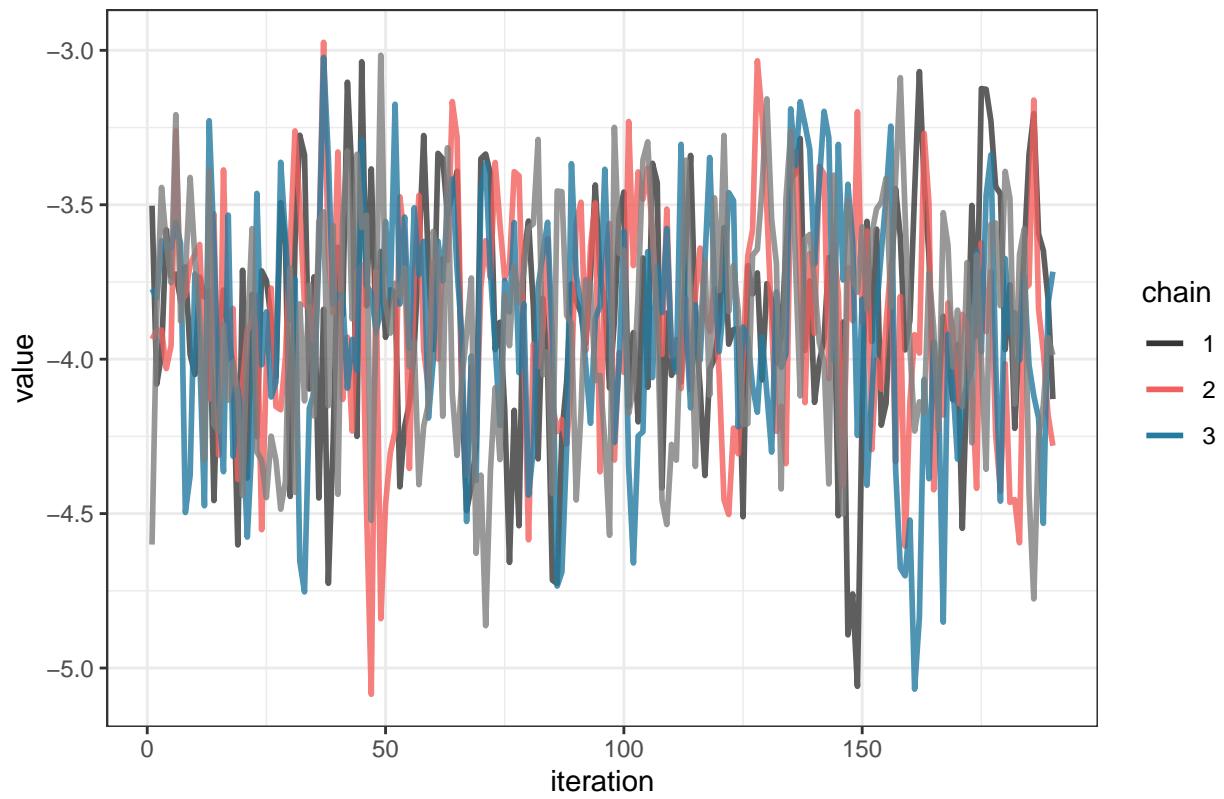
Traceplot of bs_gammas_4



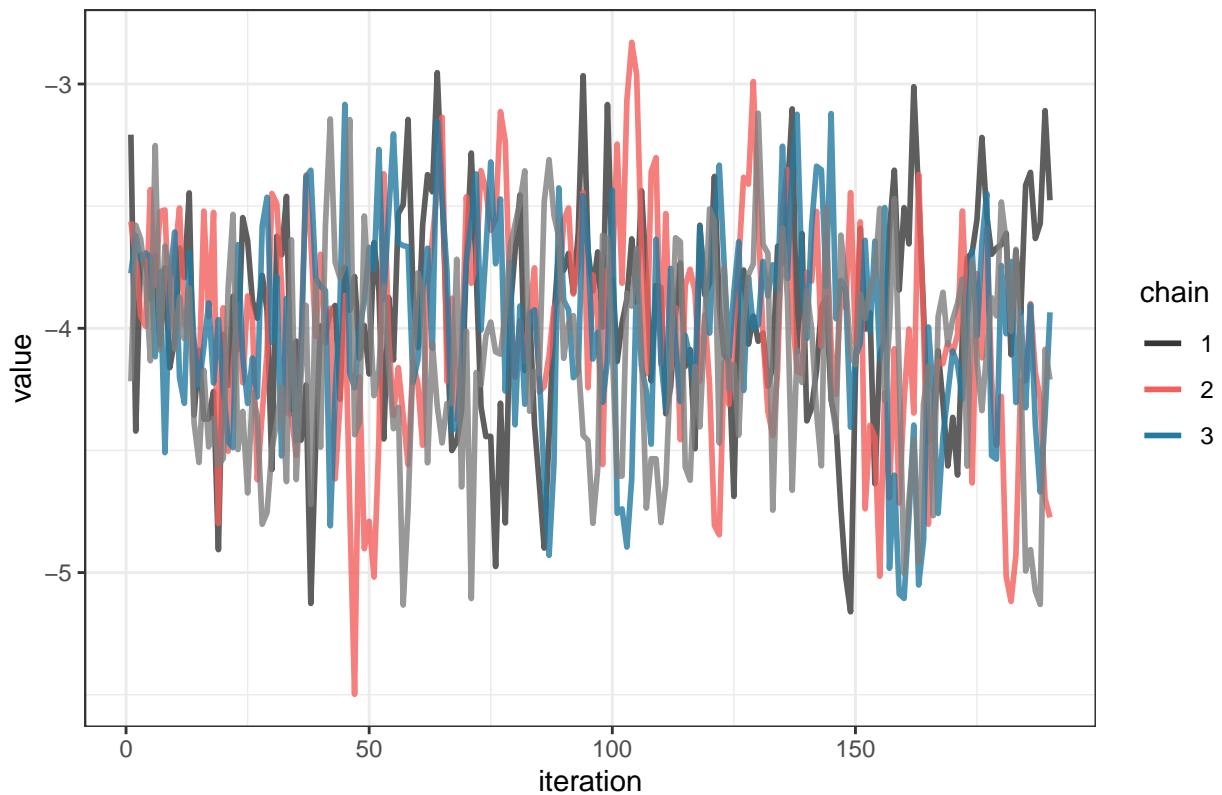
Traceplot of bs_gammas_5



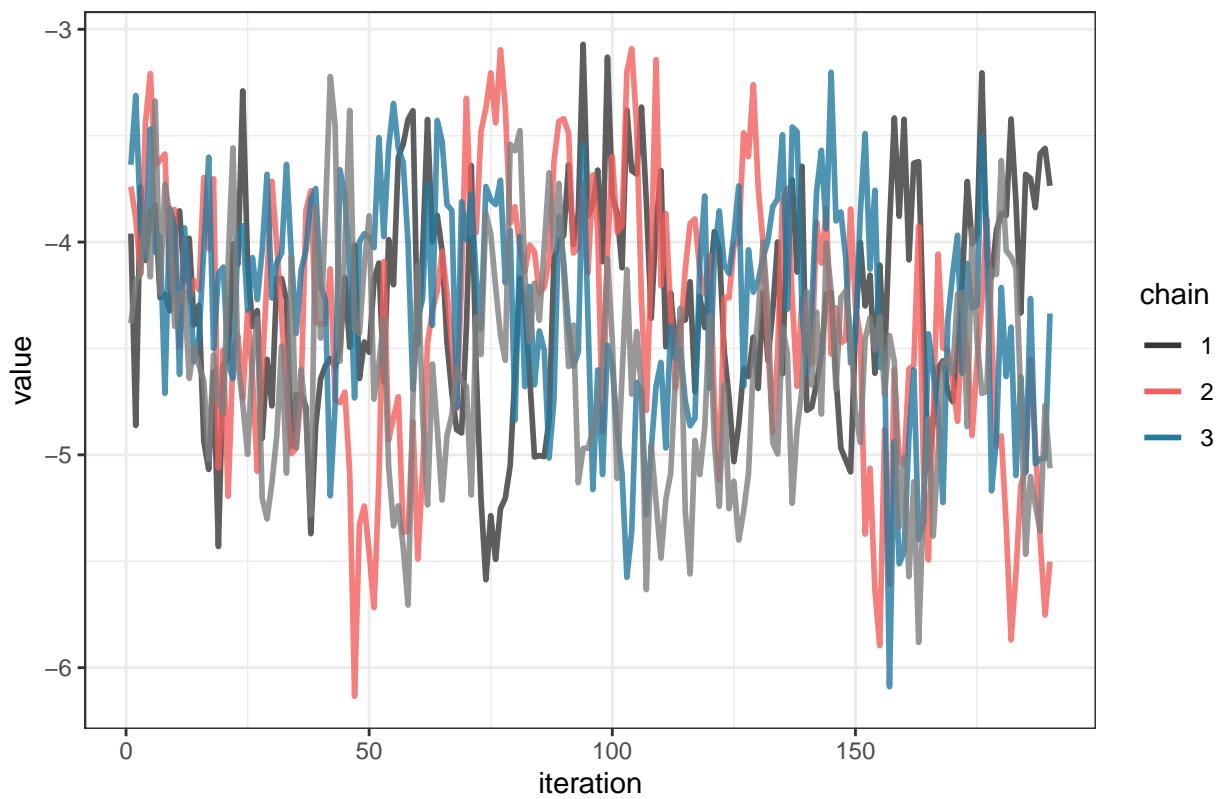
Traceplot of bs_gammas_6



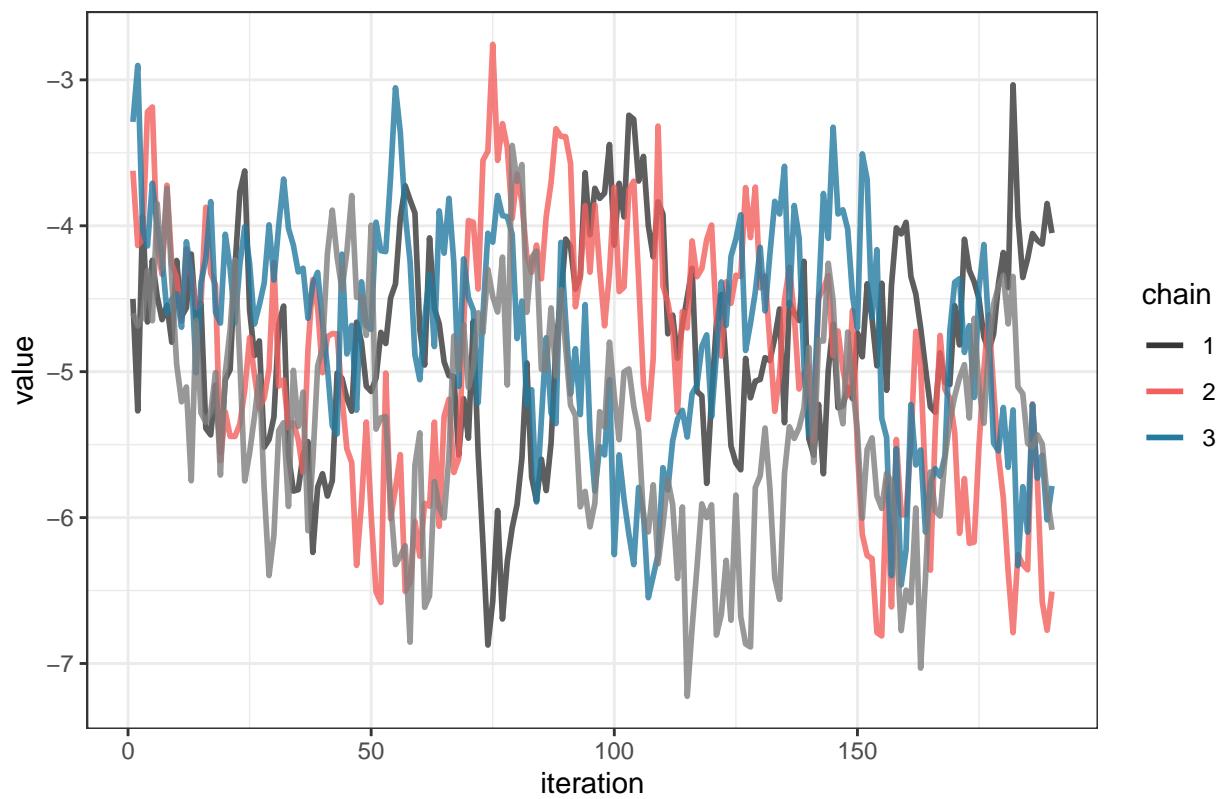
Traceplot of bs_gammas_7



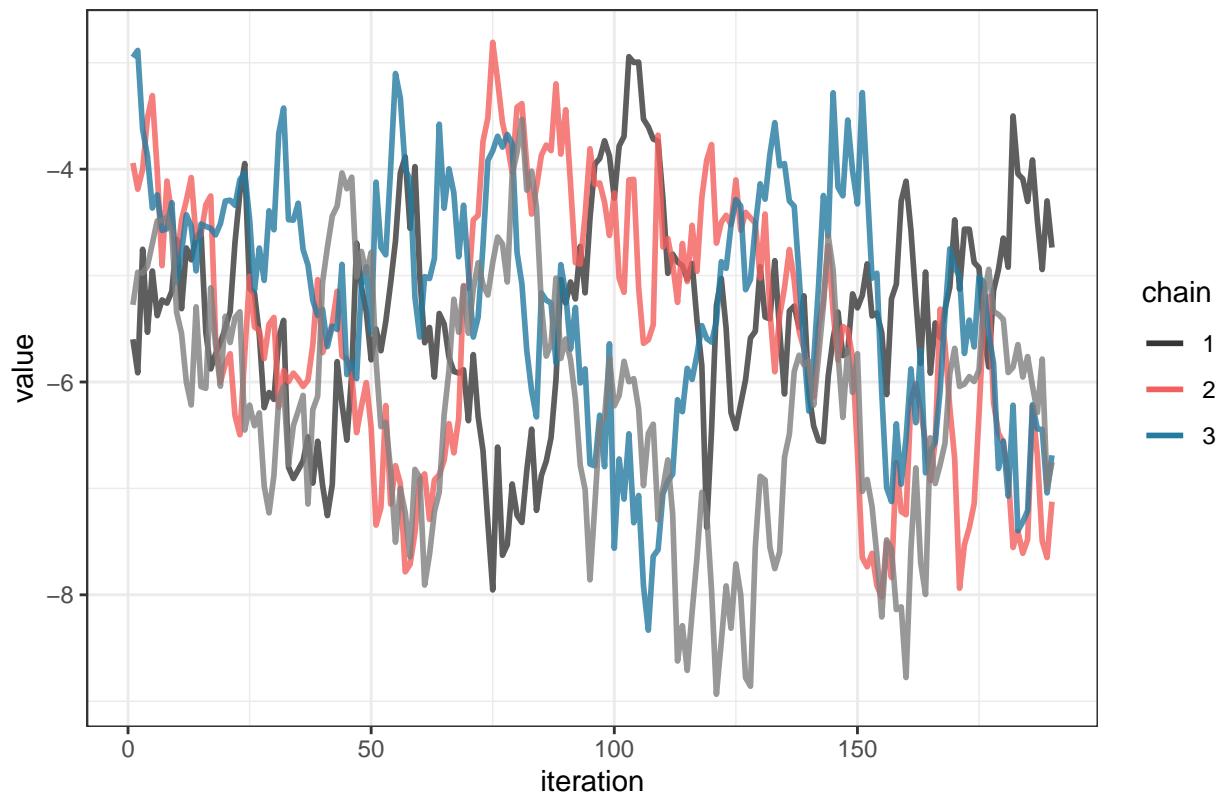
Traceplot of bs_gammas_8



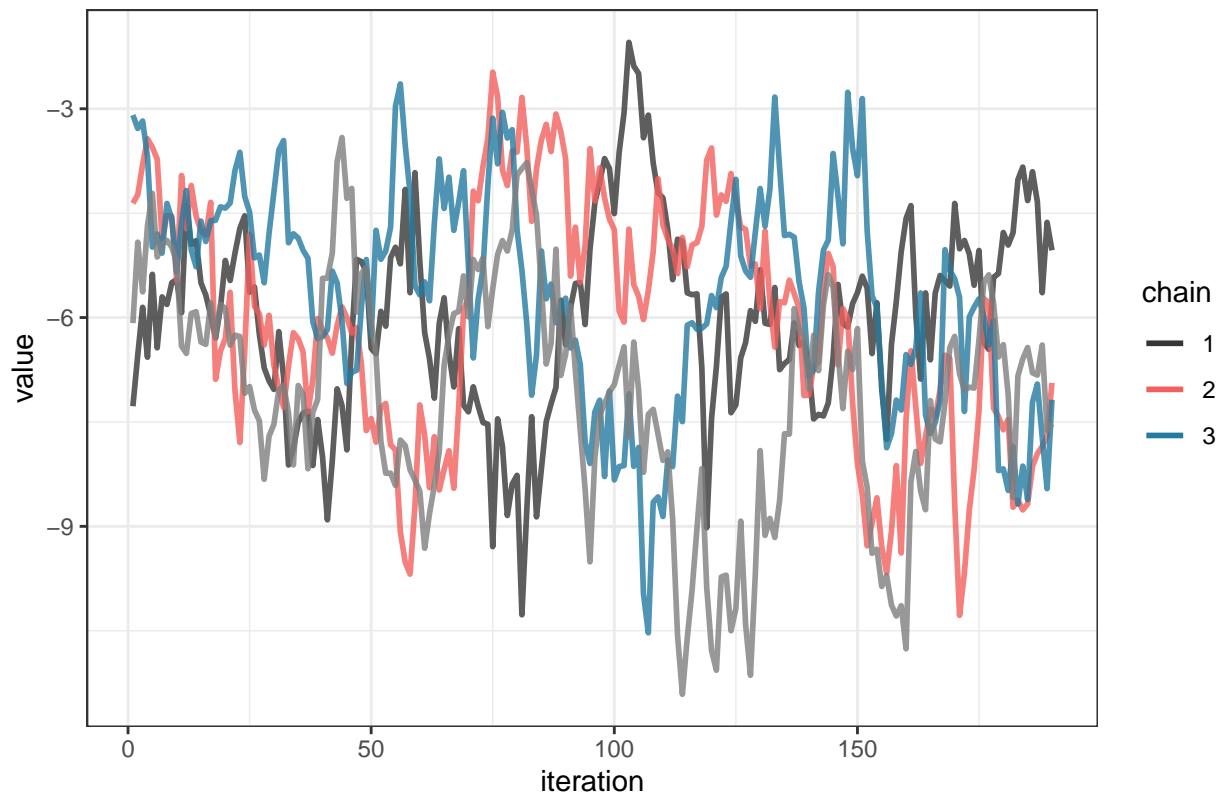
Traceplot of bs_gammas_9



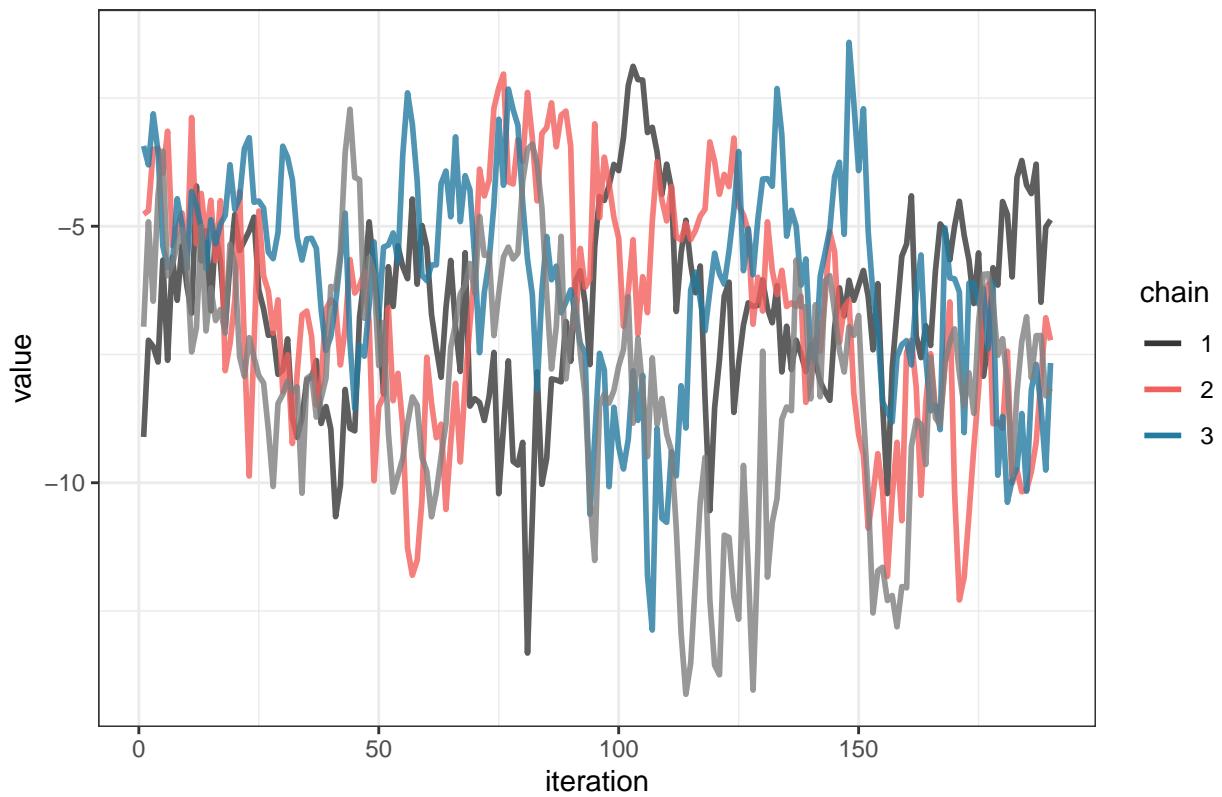
Traceplot of bs_gammas_10



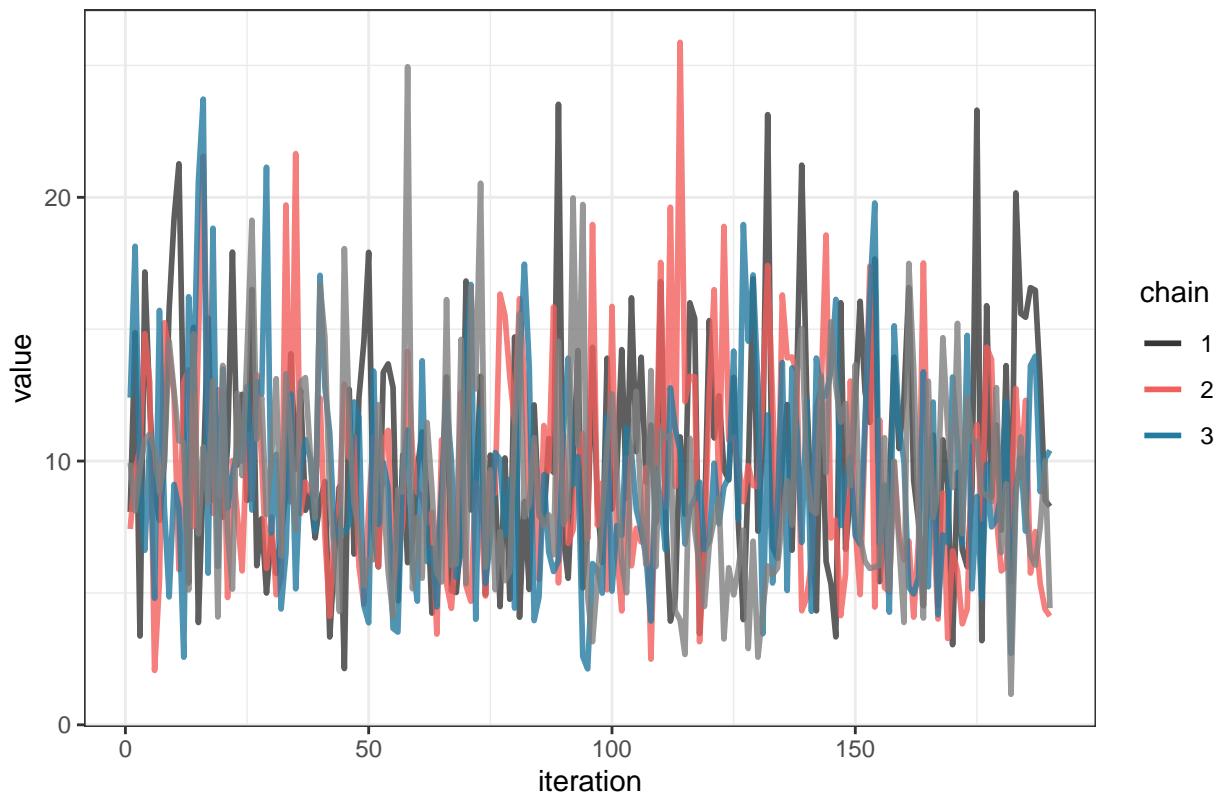
Traceplot of bs_gammas_11



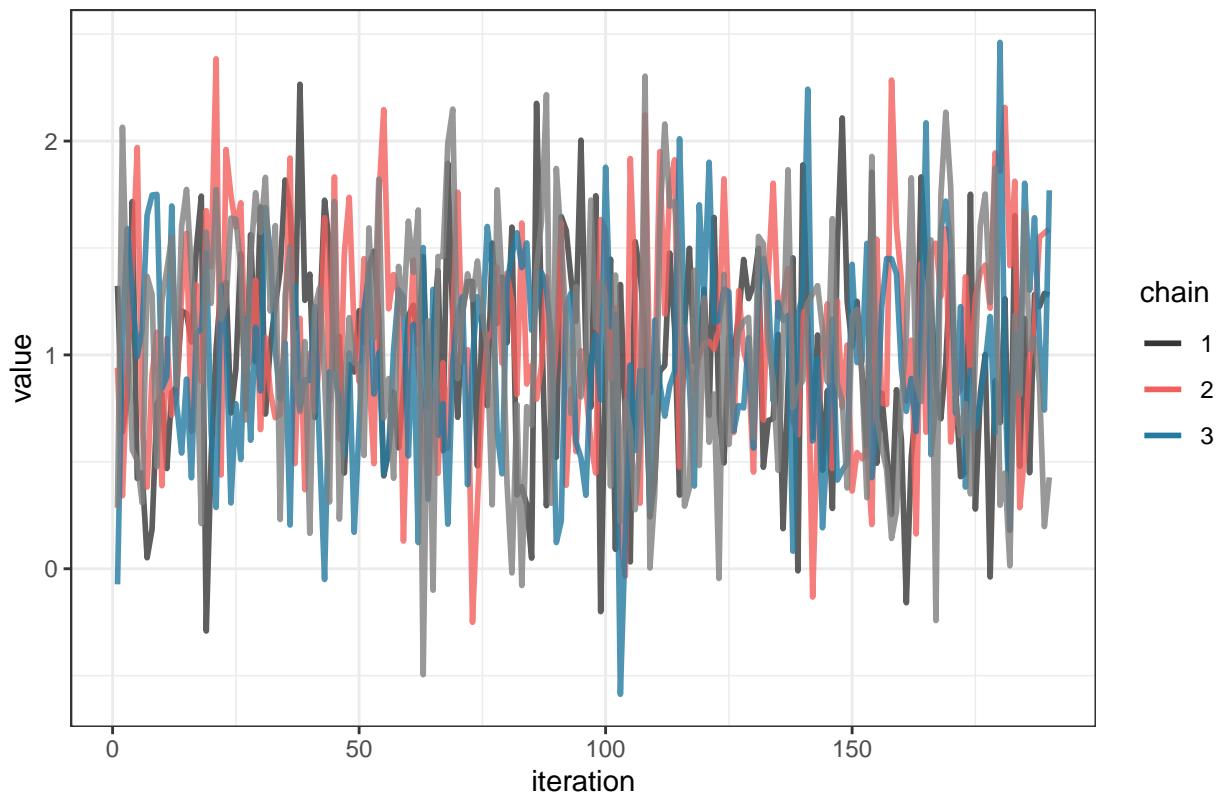
Traceplot of bs_gammas_12



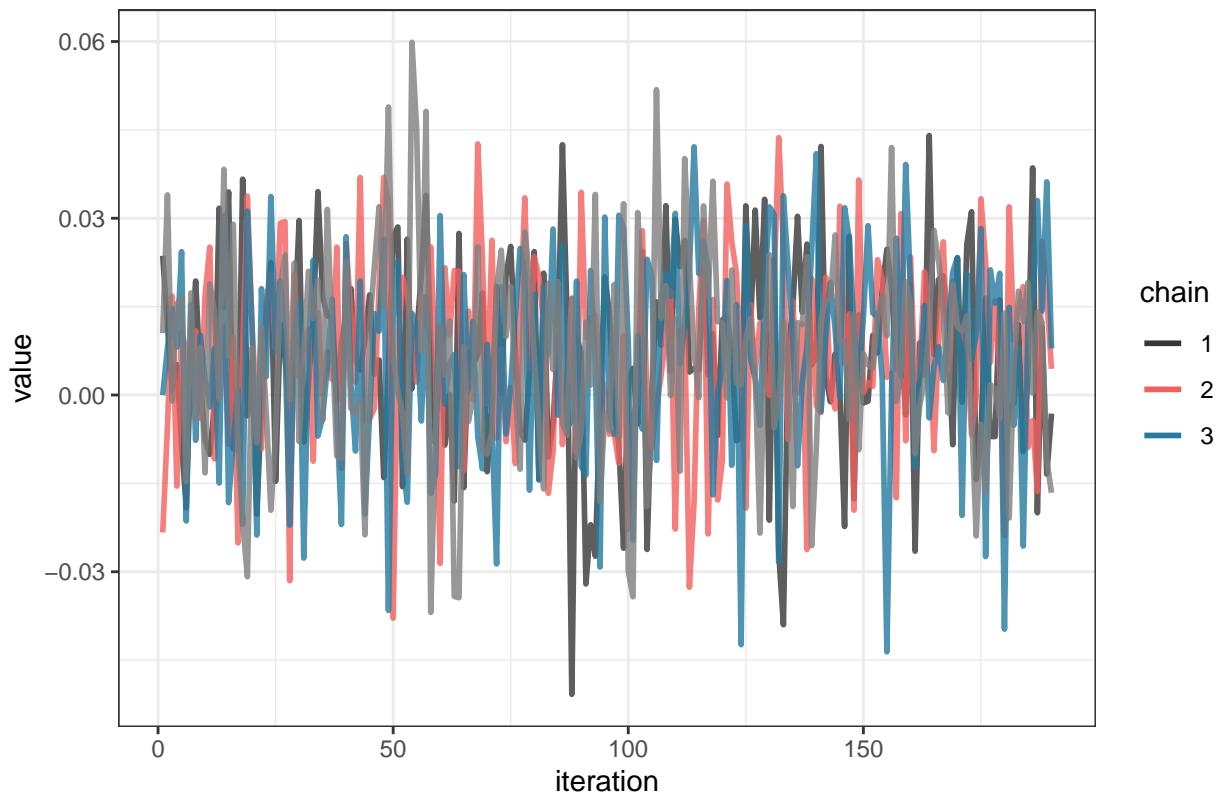
Traceplot of tau_bs_gammas



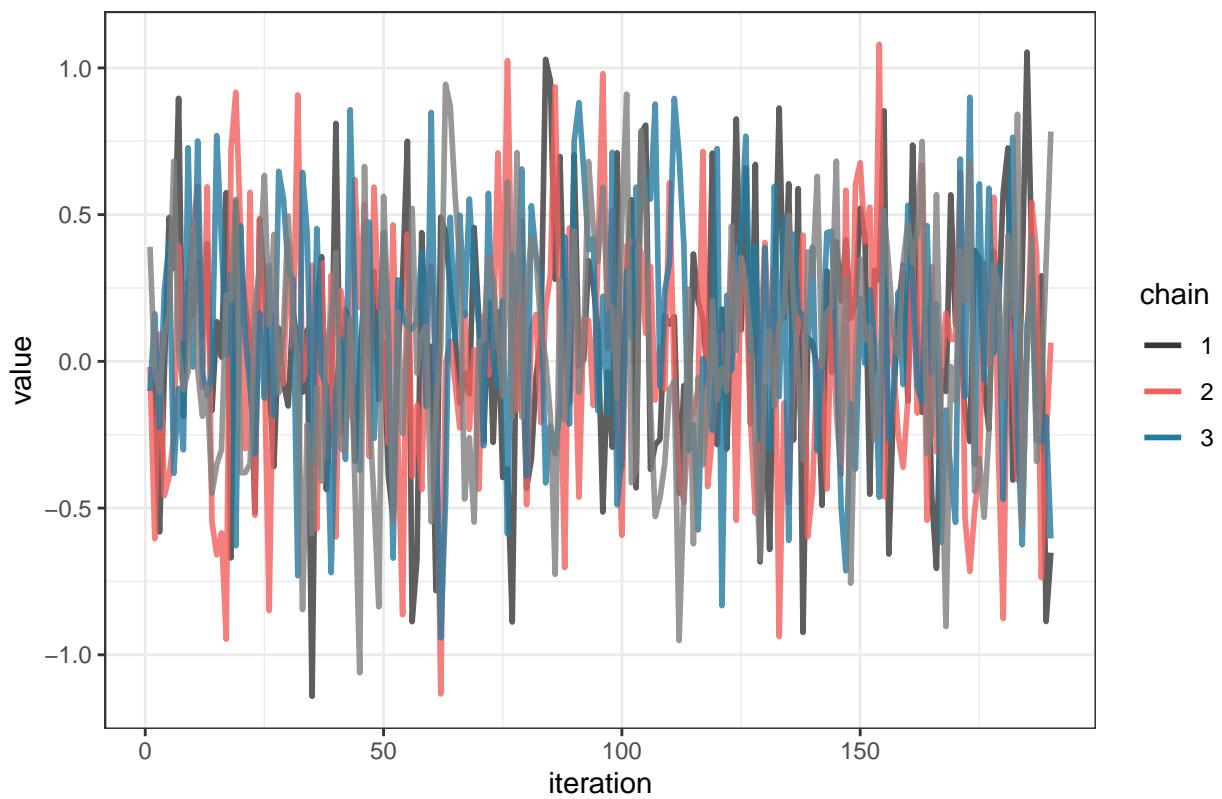
Traceplot of LOWC31



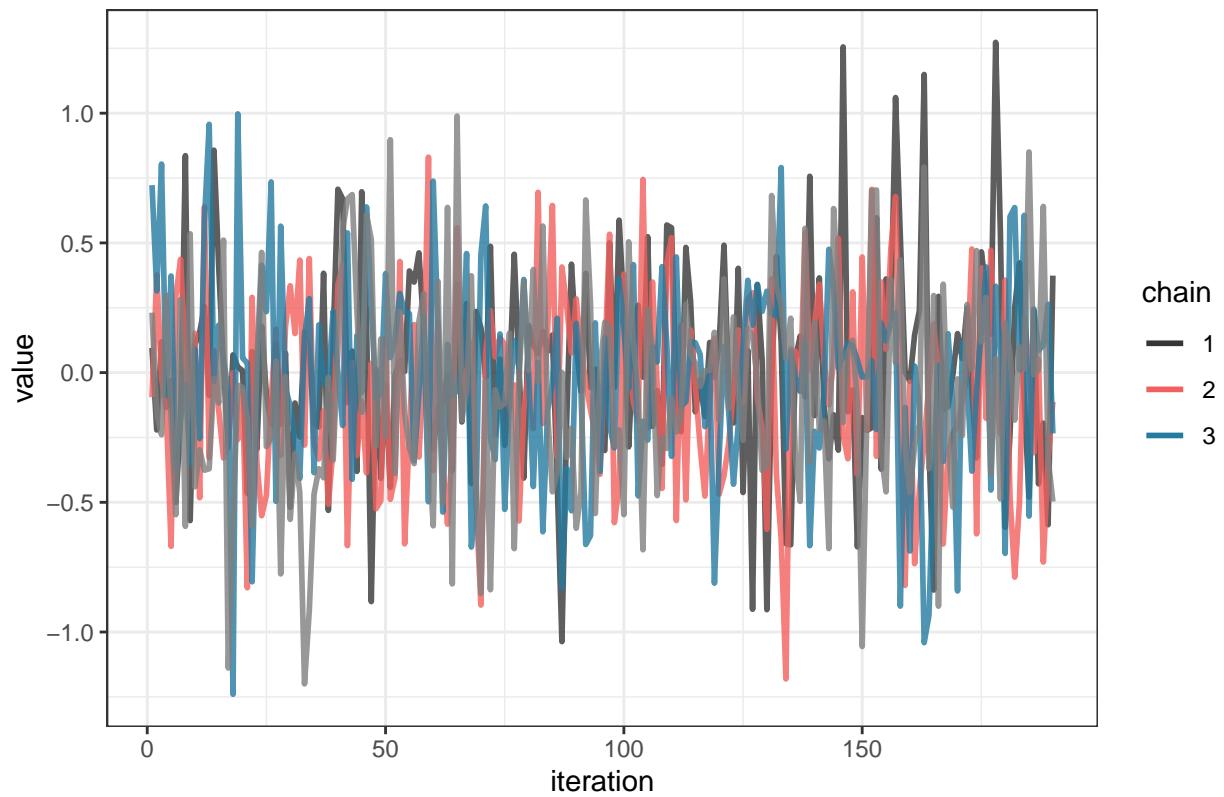
Traceplot of ageatbiopsy



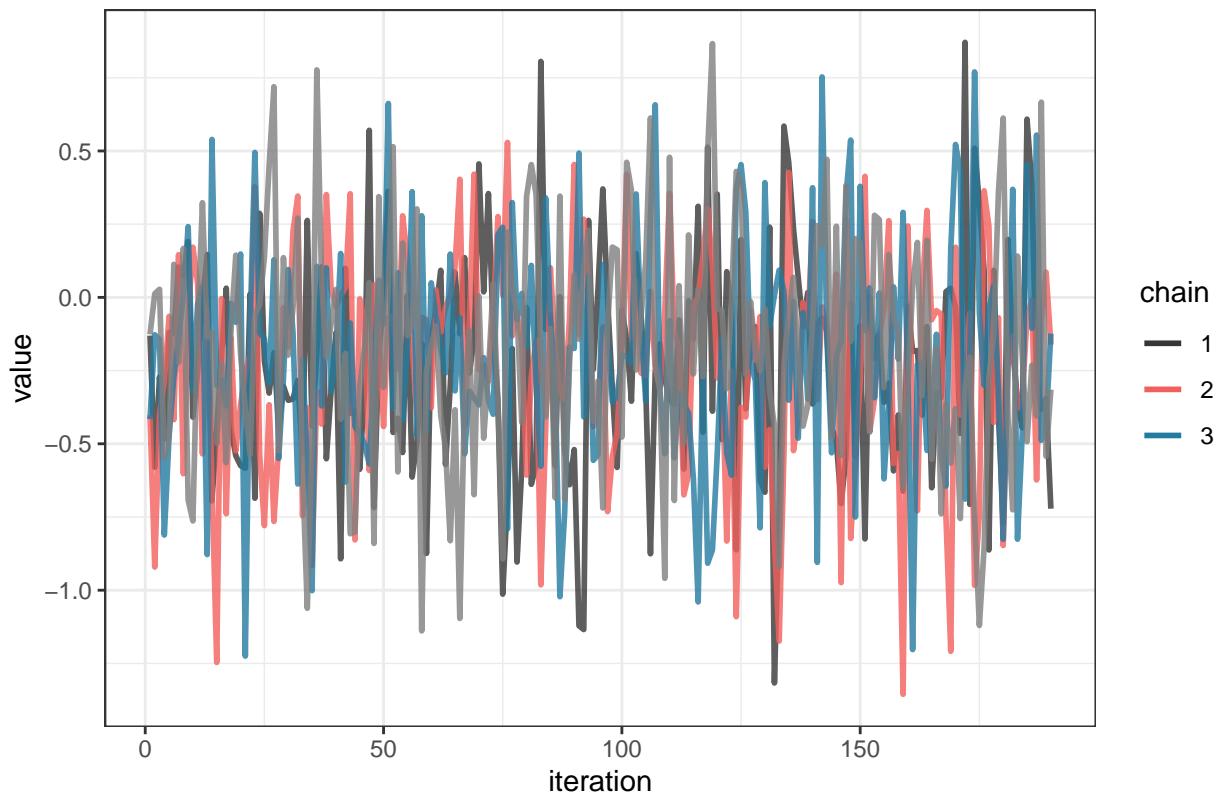
Traceplot of sex



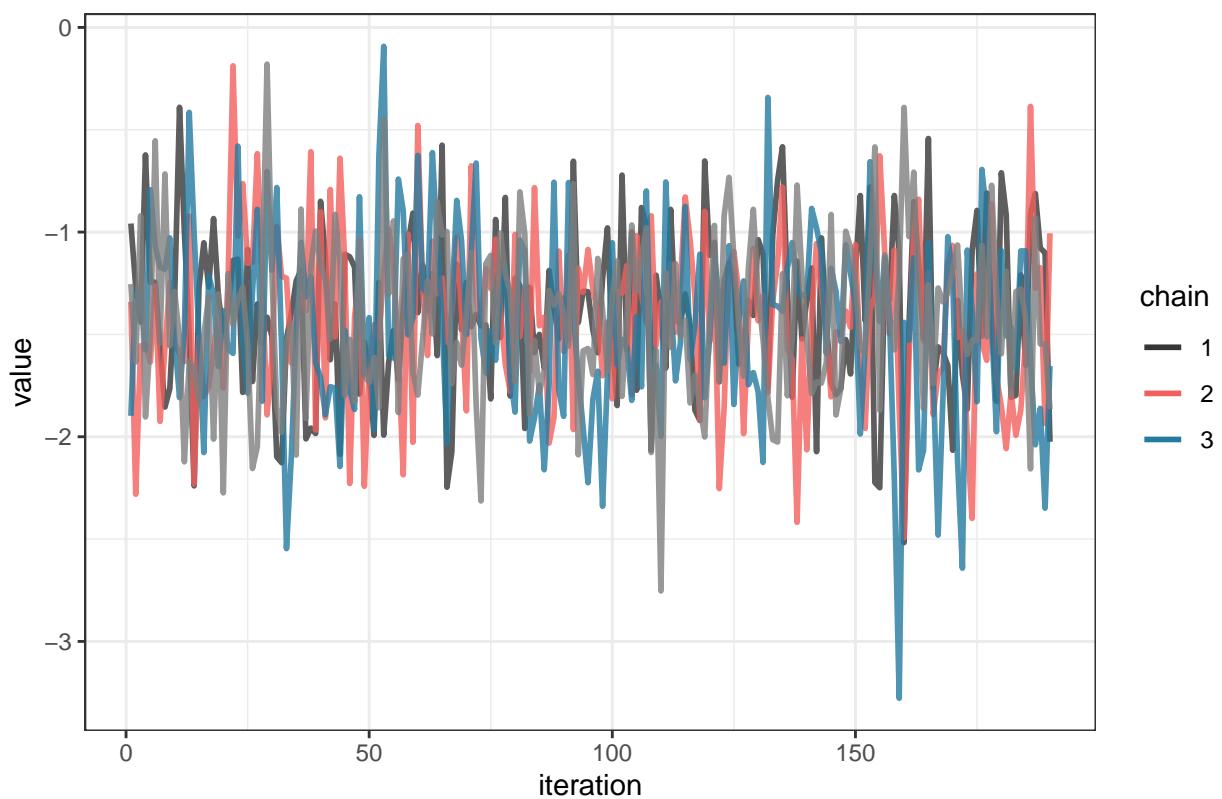
Traceplot of black



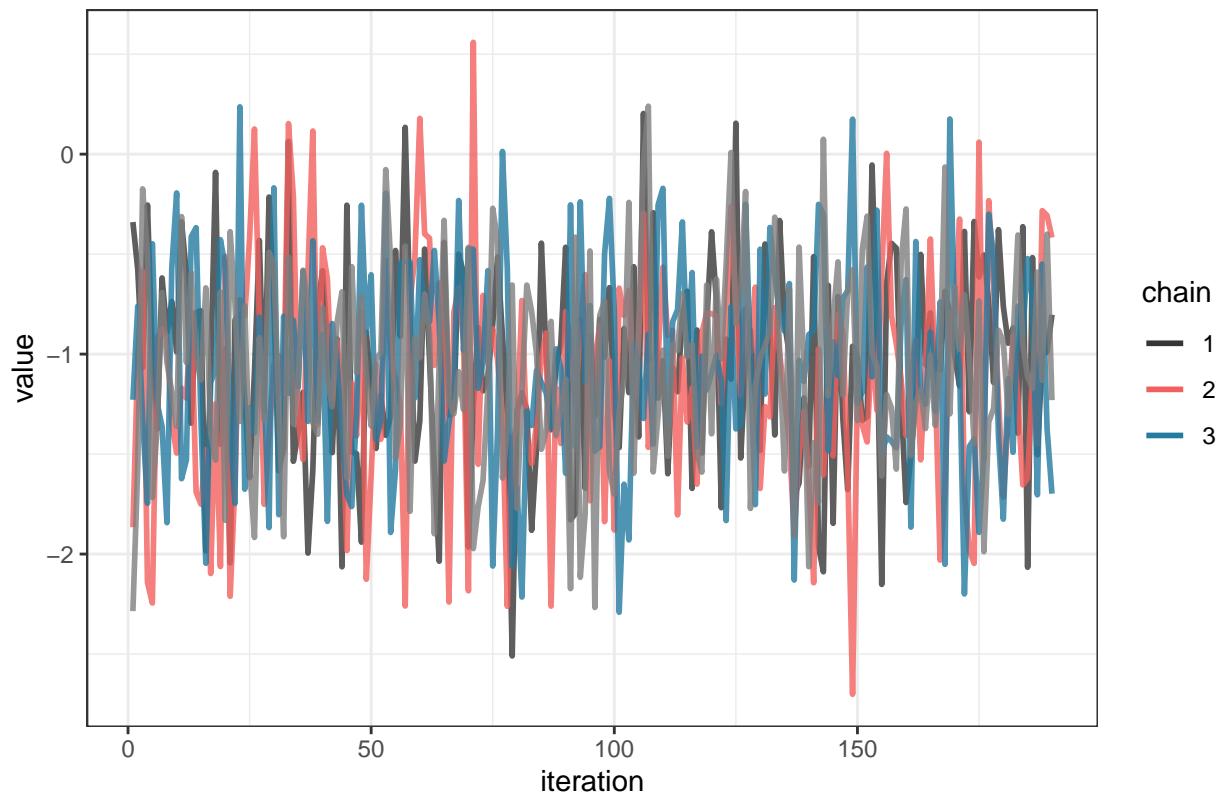
Traceplot of hypertension



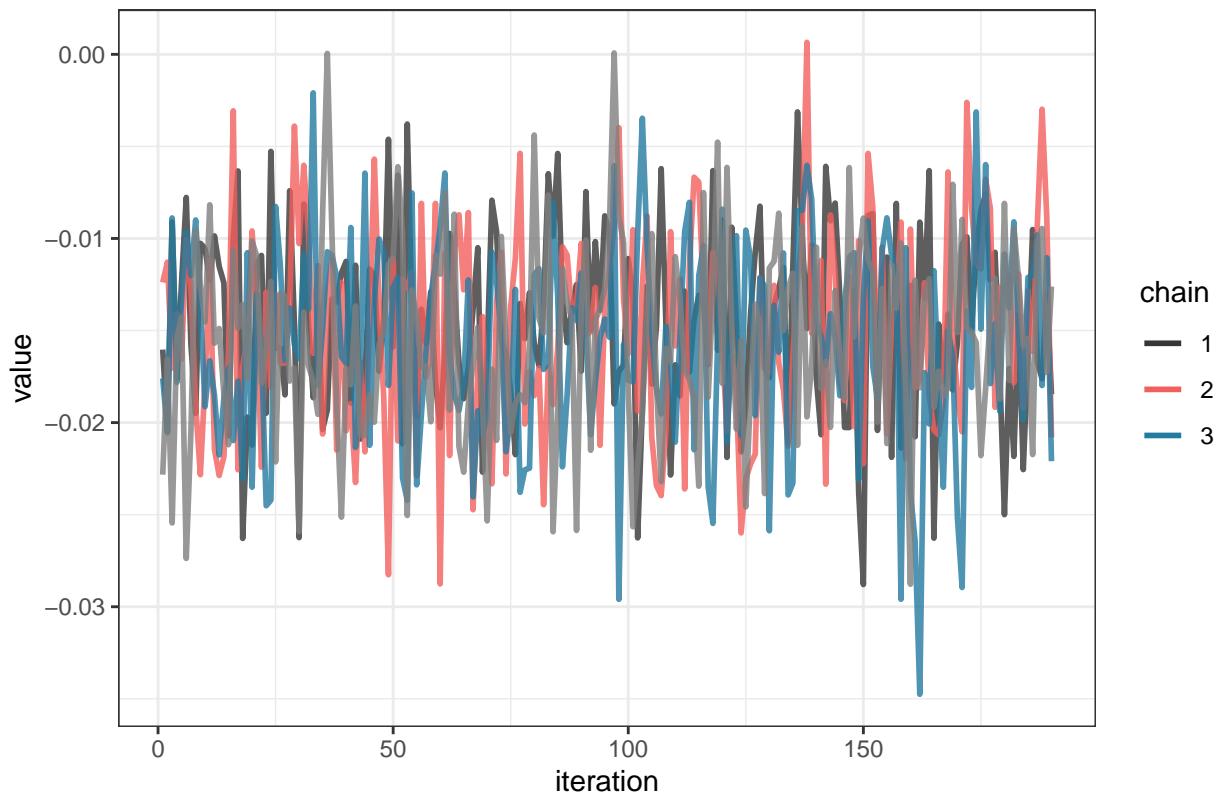
Traceplot of mmf



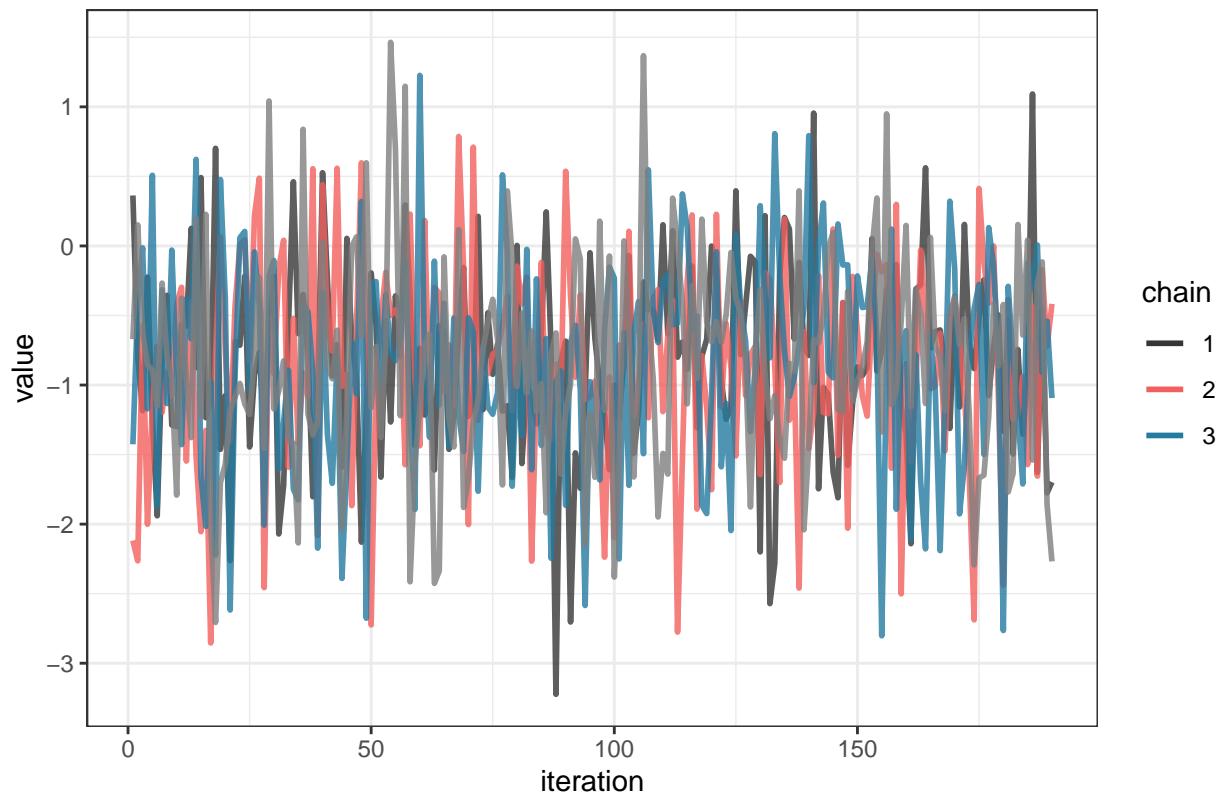
Traceplot of cyc



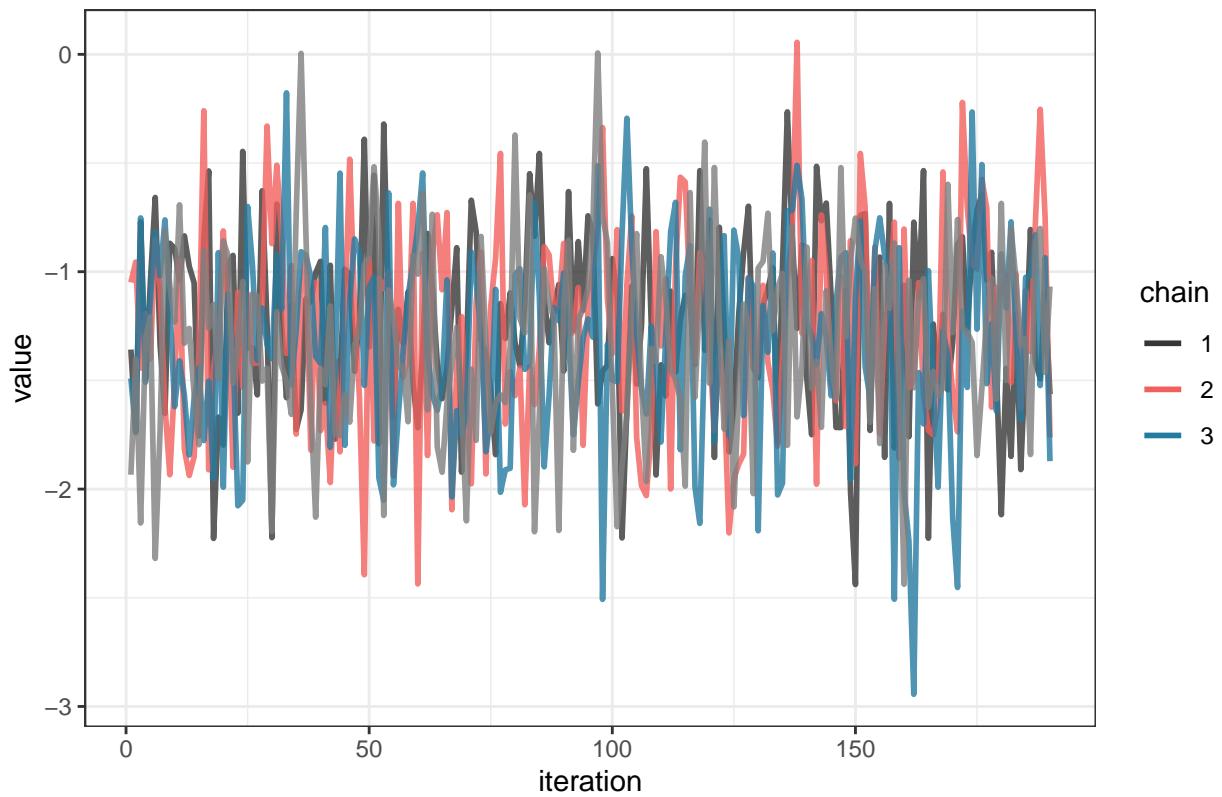
Traceplot of value(eGFR)



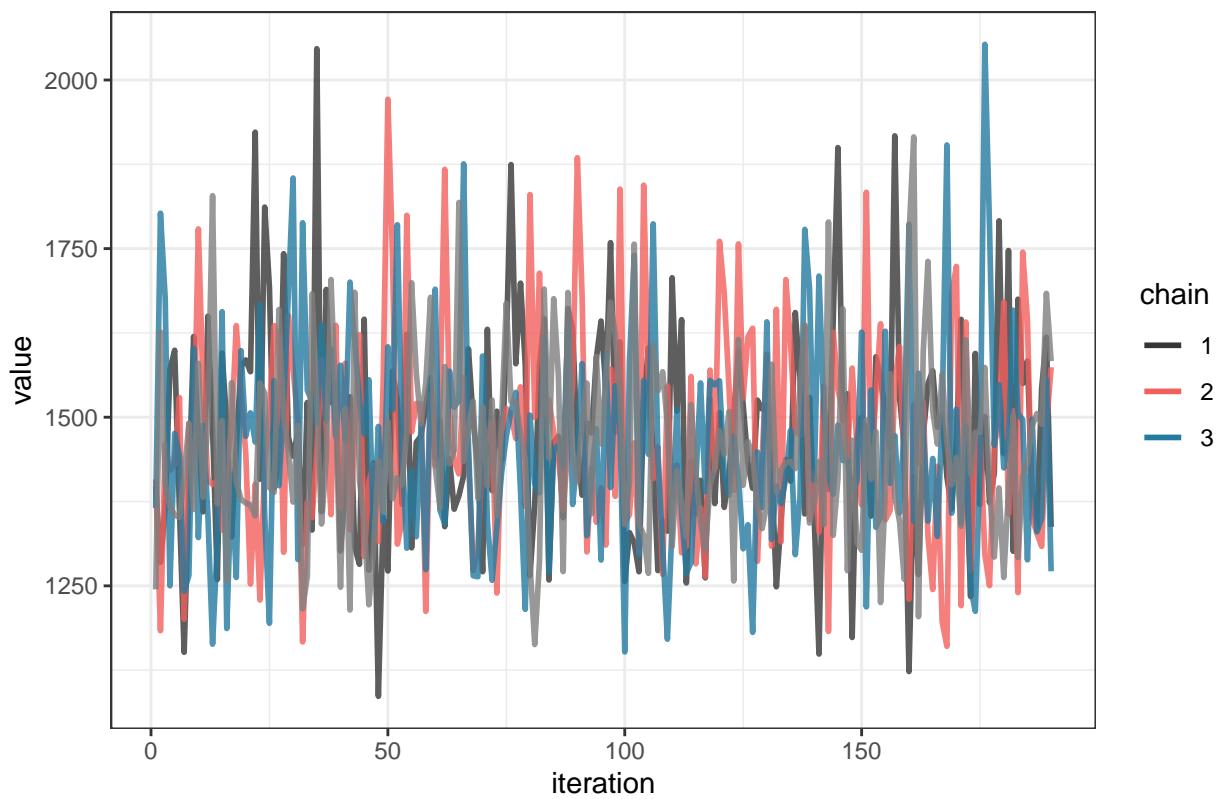
Traceplot of



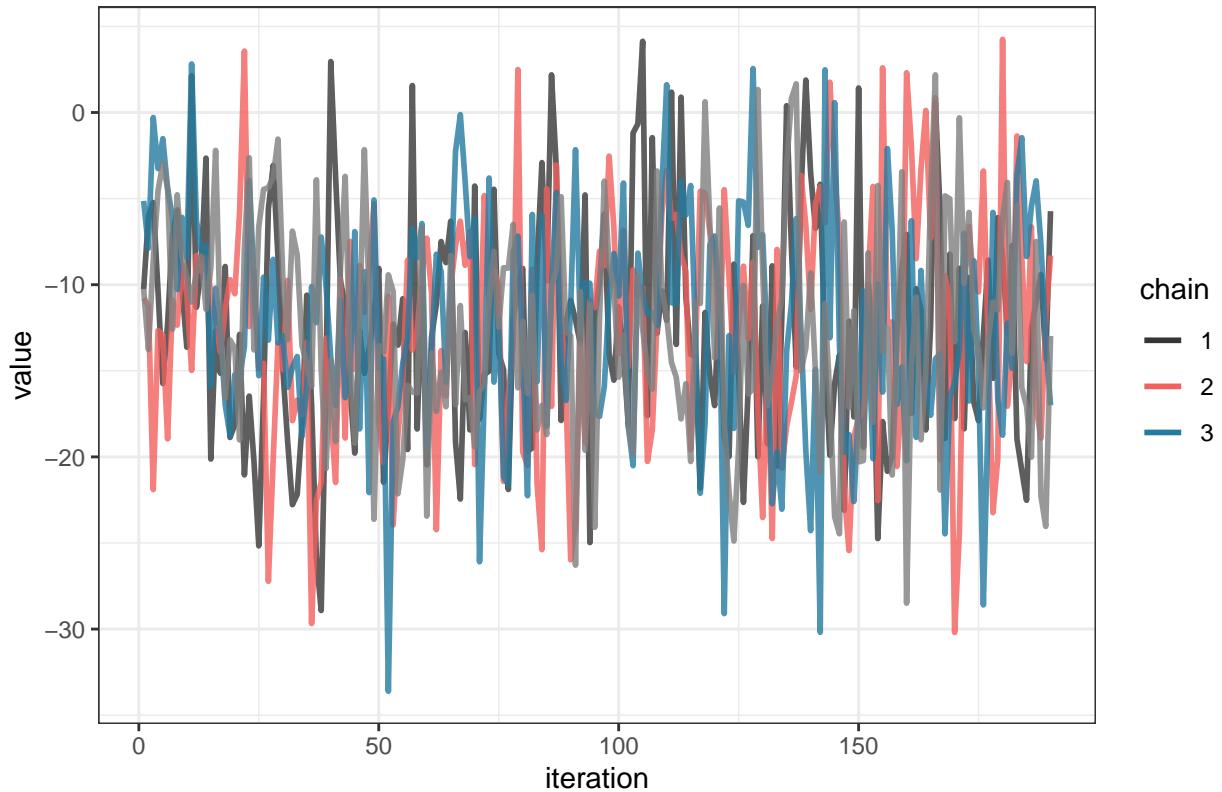
Traceplot of .1



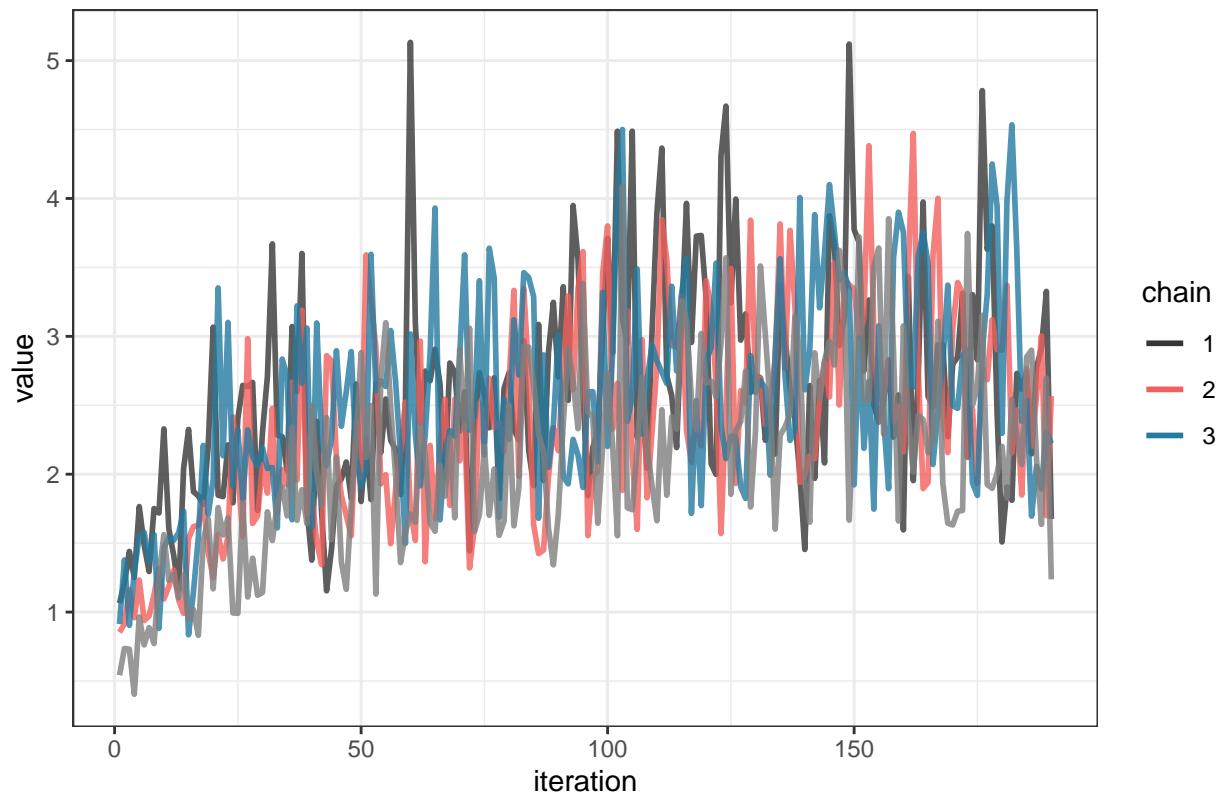
Traceplot of $D[1, 1]$



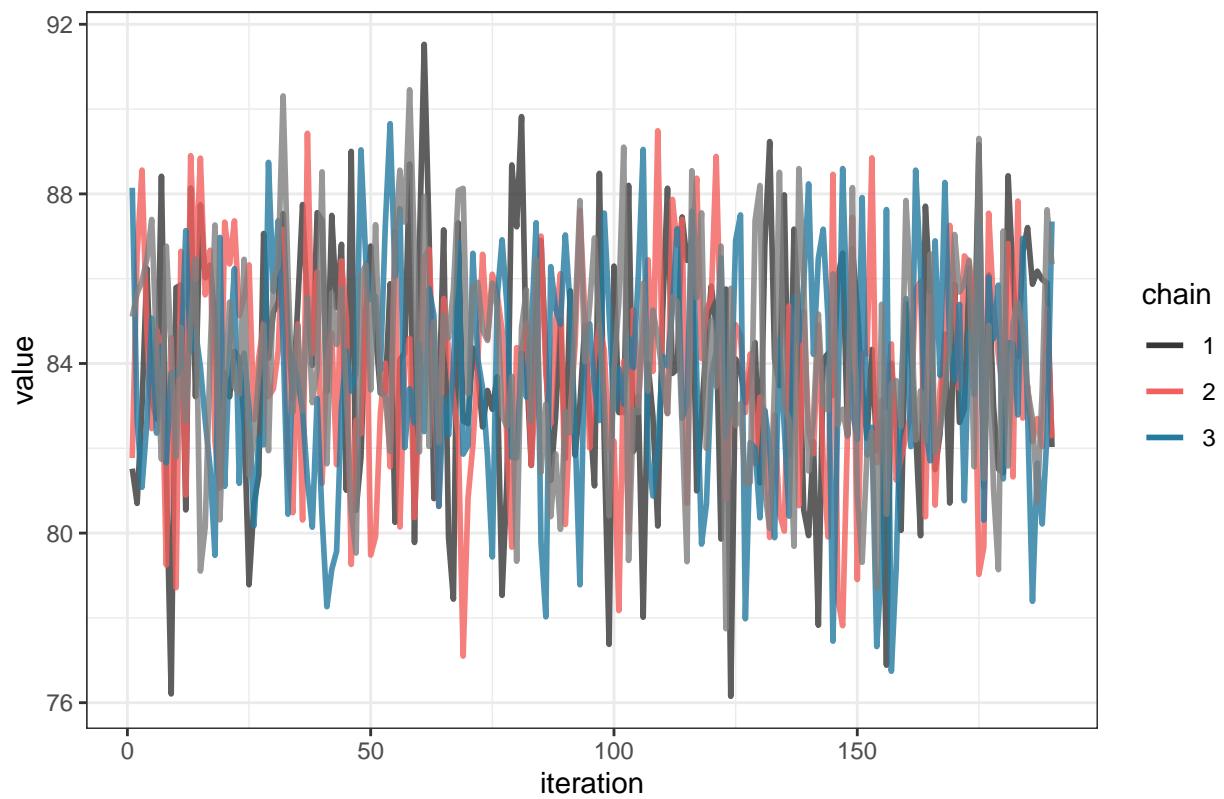
Traceplot of $D[2, 1]$



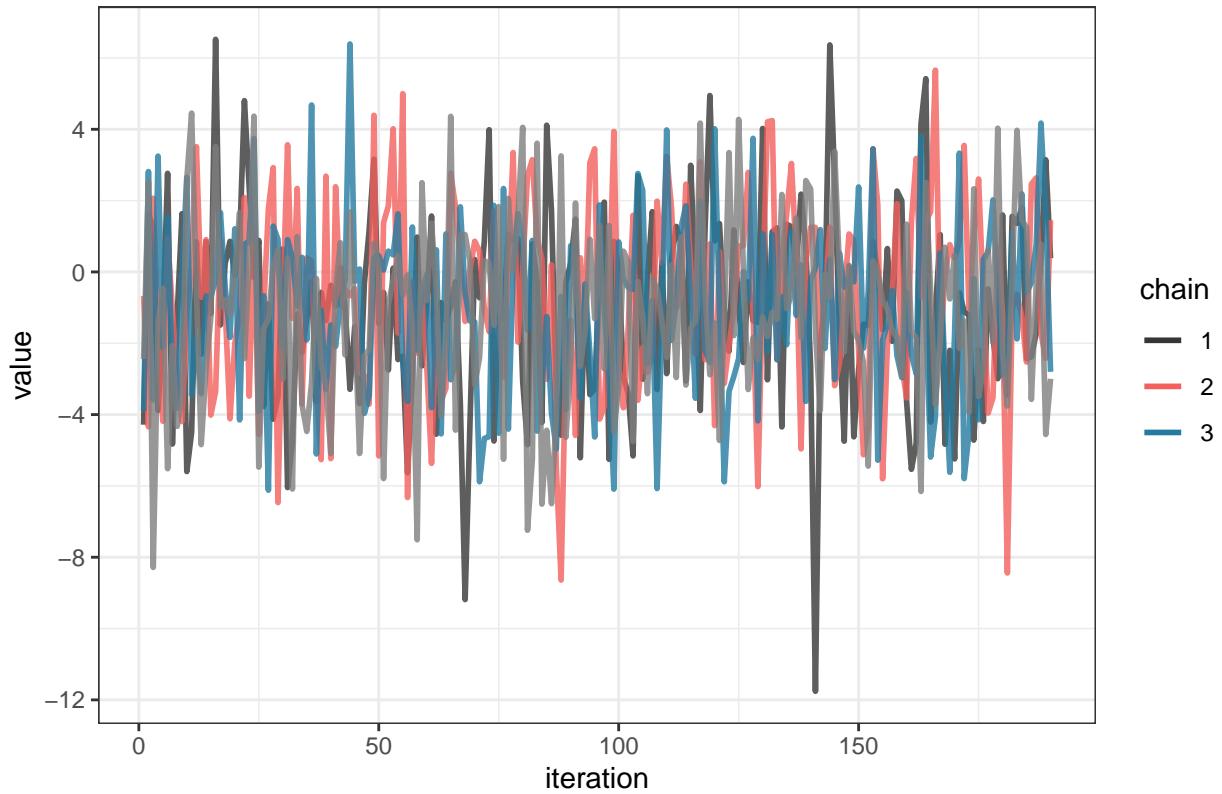
Traceplot of $D[2, 2]$



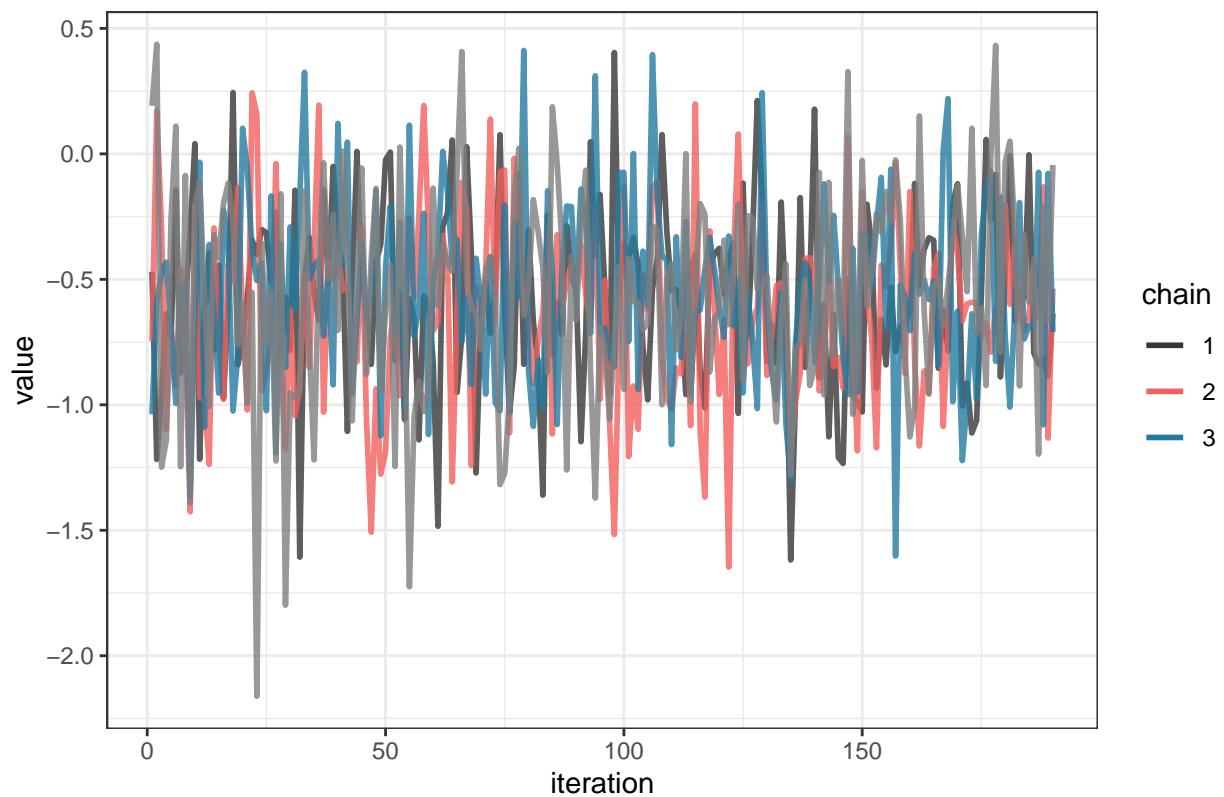
Traceplot of (Intercept)



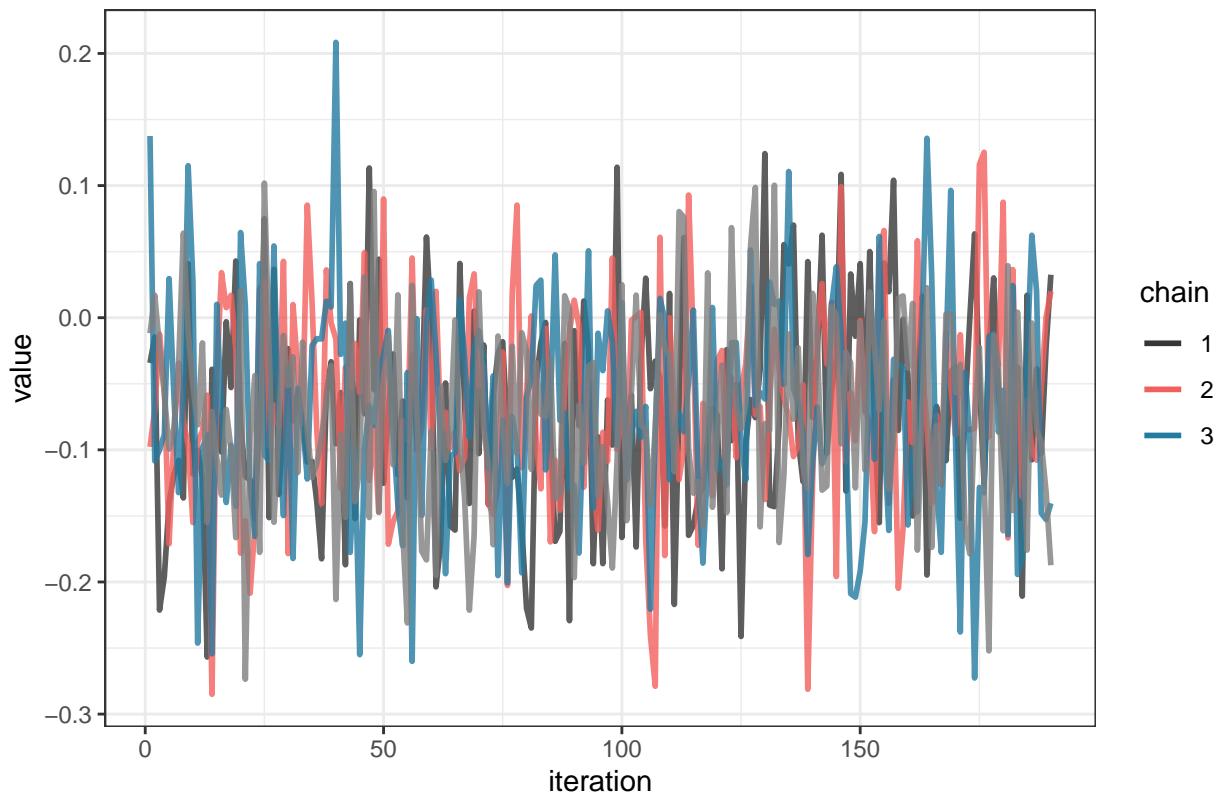
Traceplot of LOWC31.1



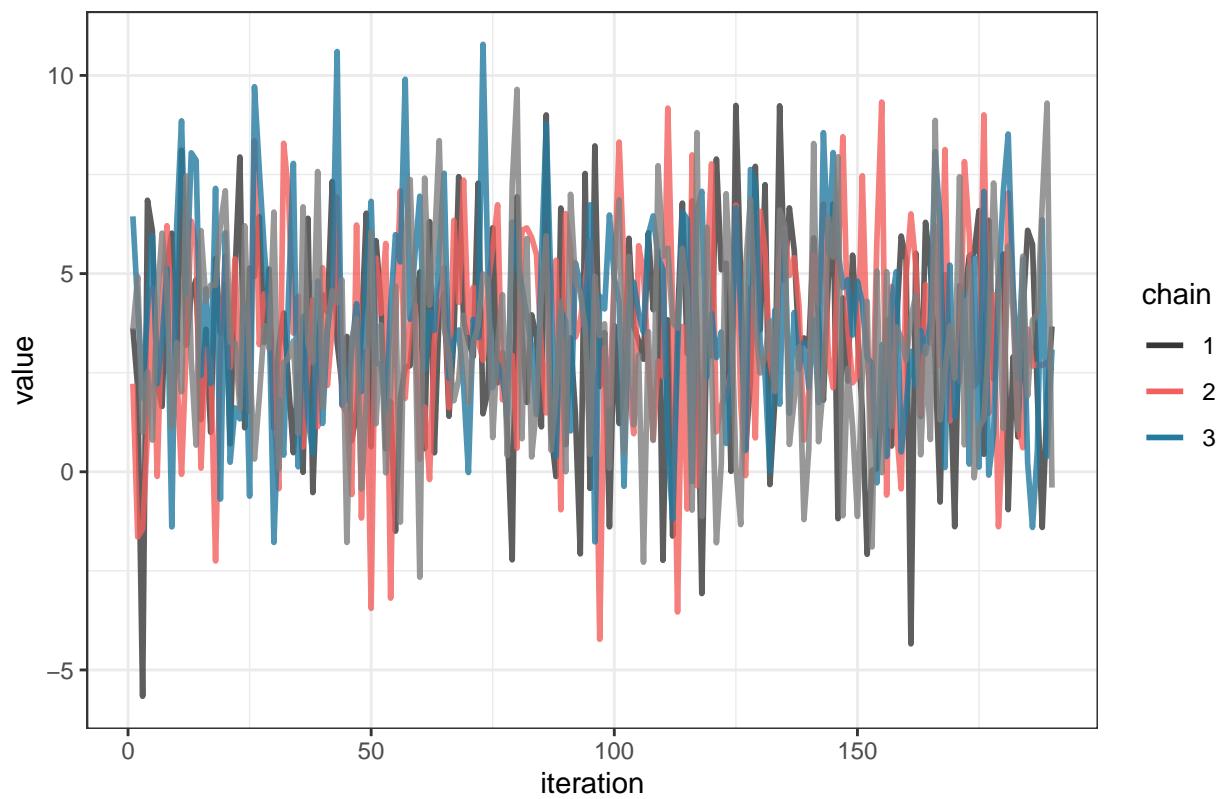
Traceplot of time



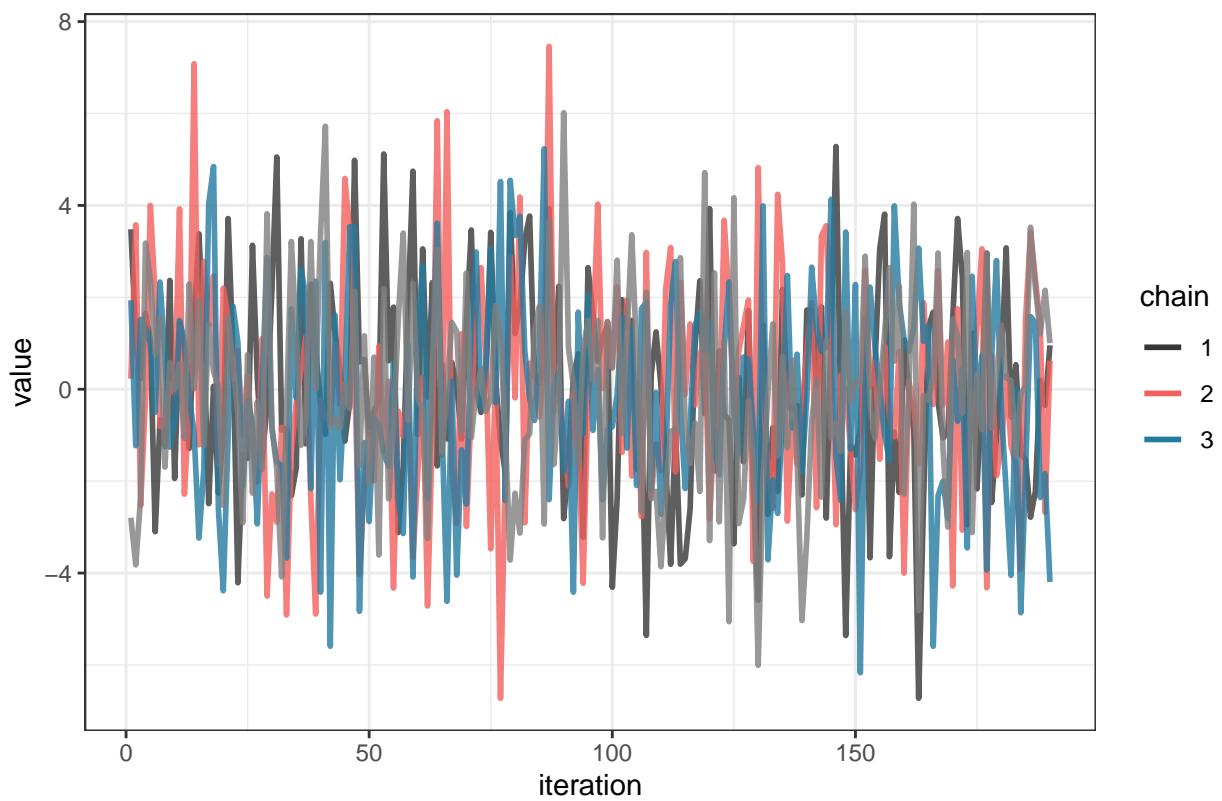
Traceplot of ageatbiopsy.1



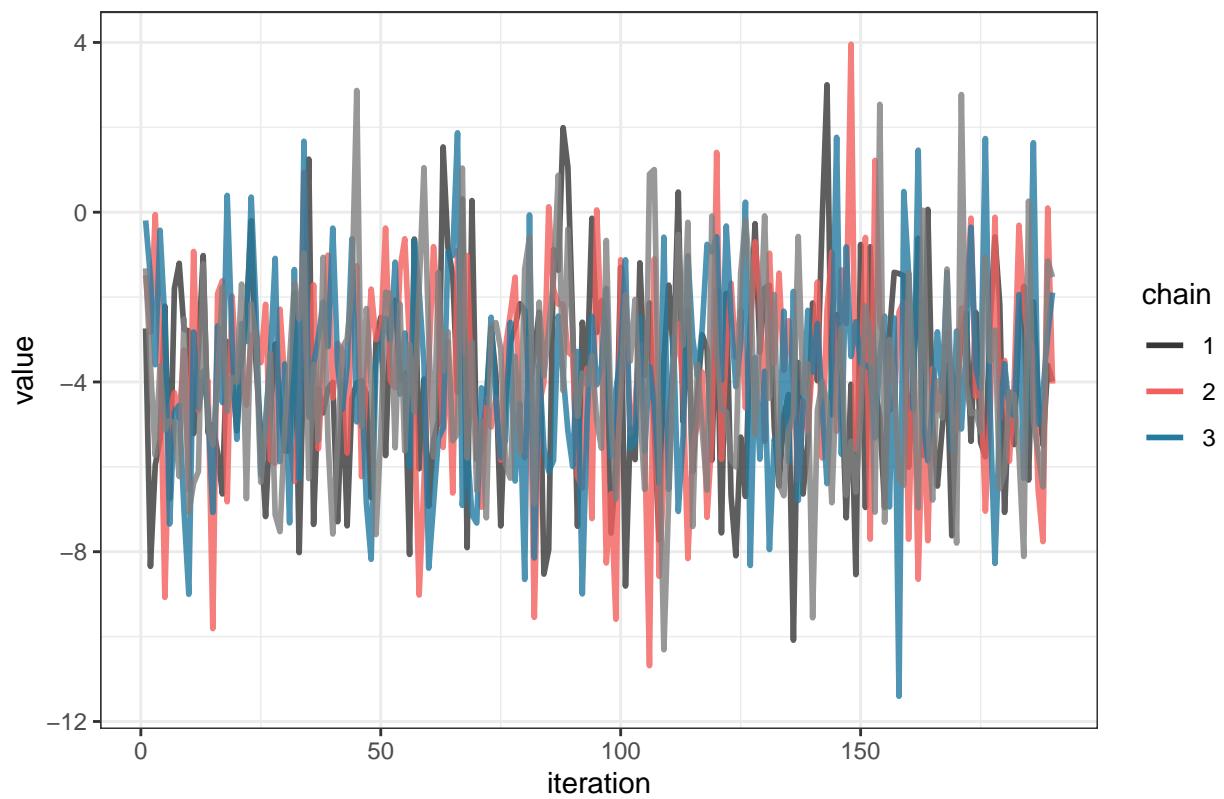
Traceplot of sex.1



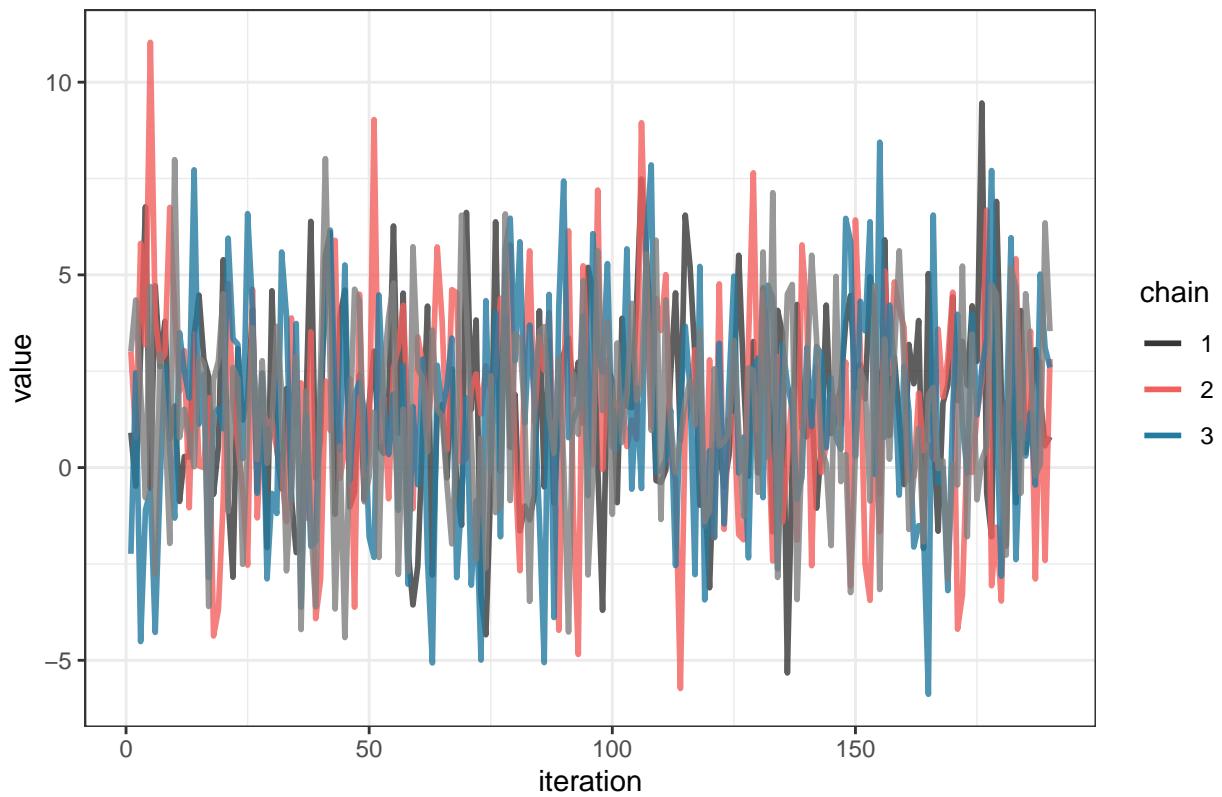
Traceplot of black.1



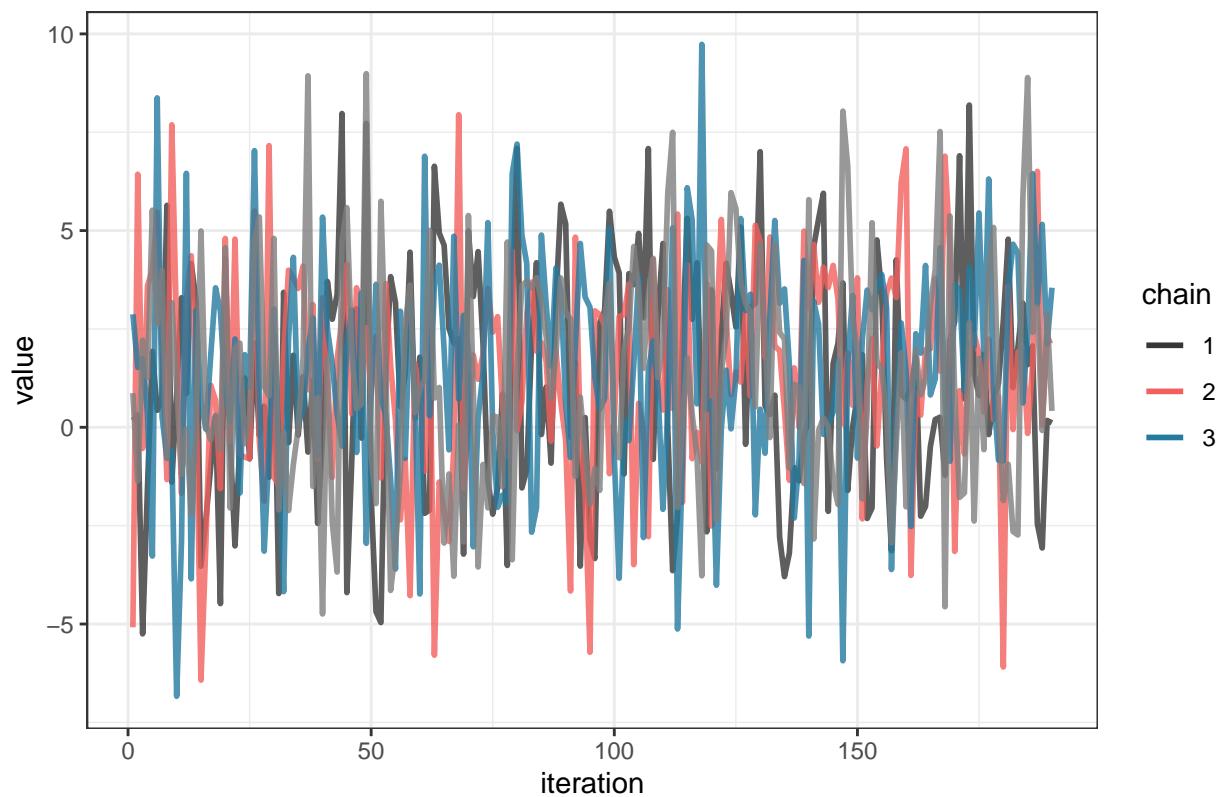
Traceplot of hypertension.1



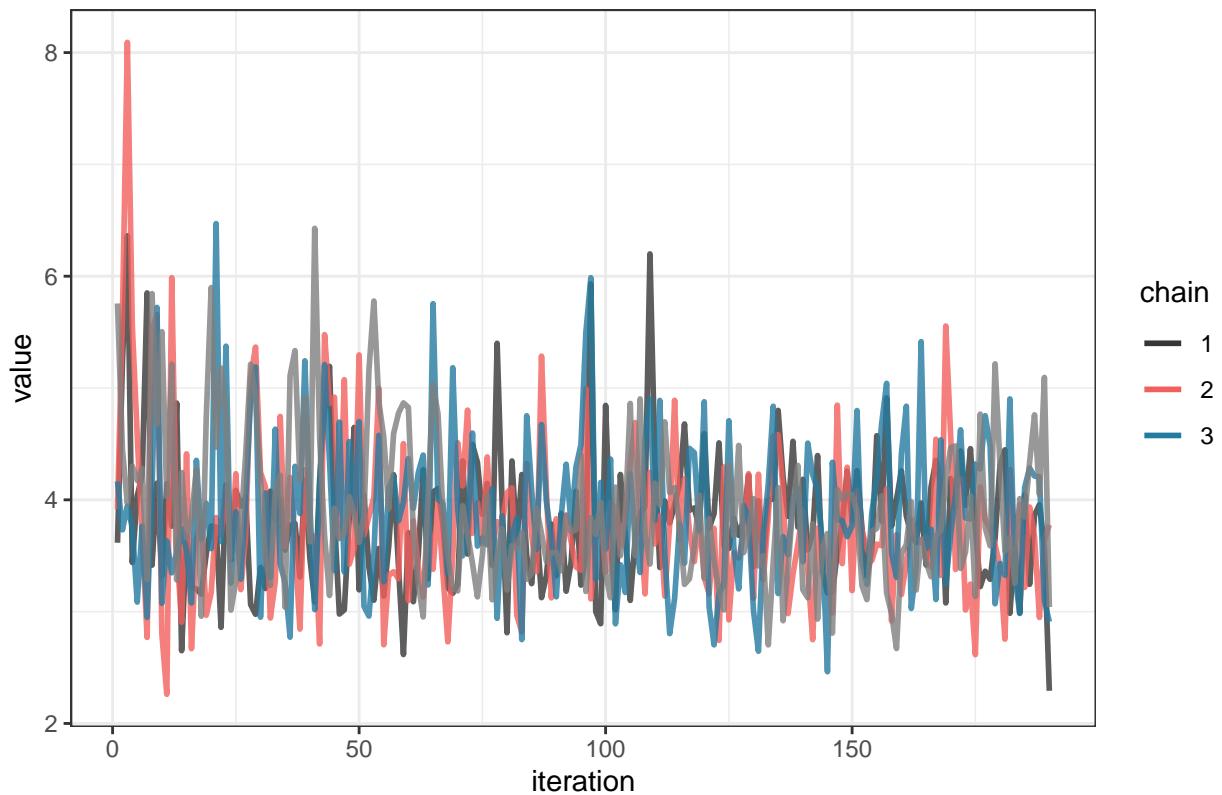
Traceplot of mmf.1



Traceplot of cyc.1

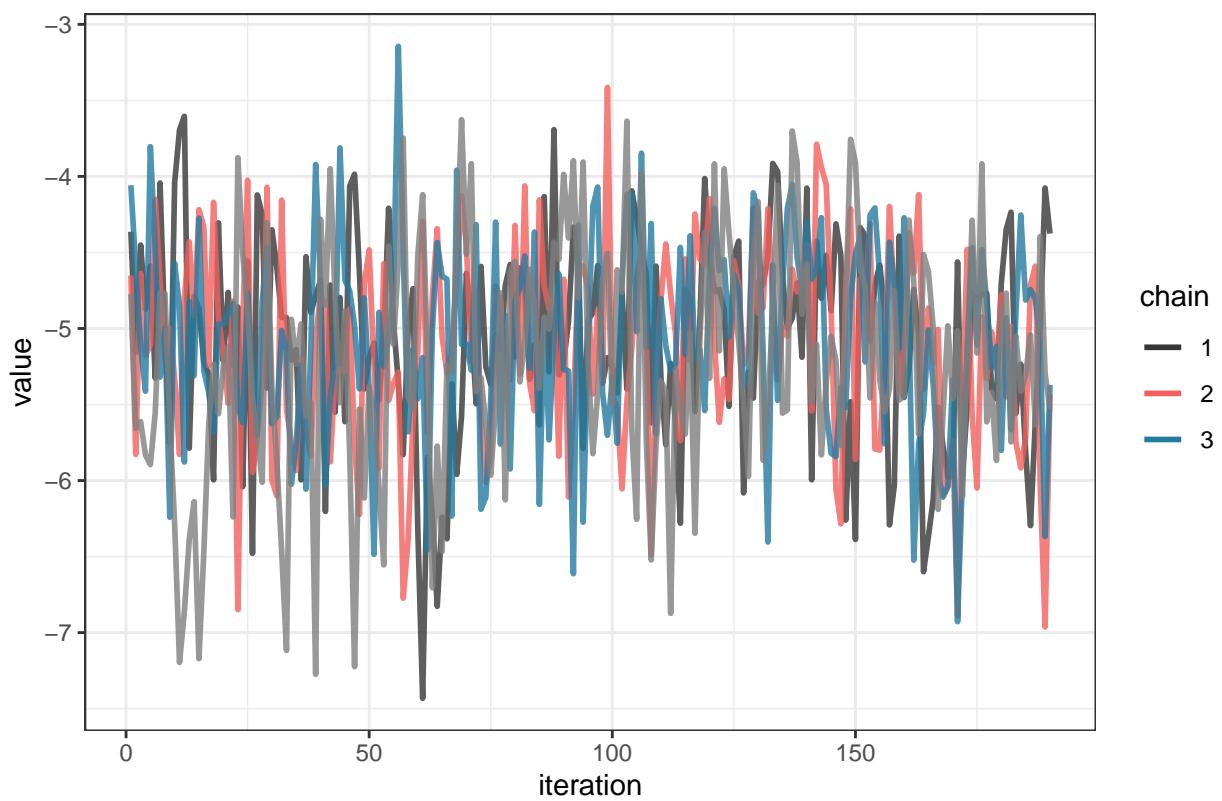


Traceplot of sigmas_1

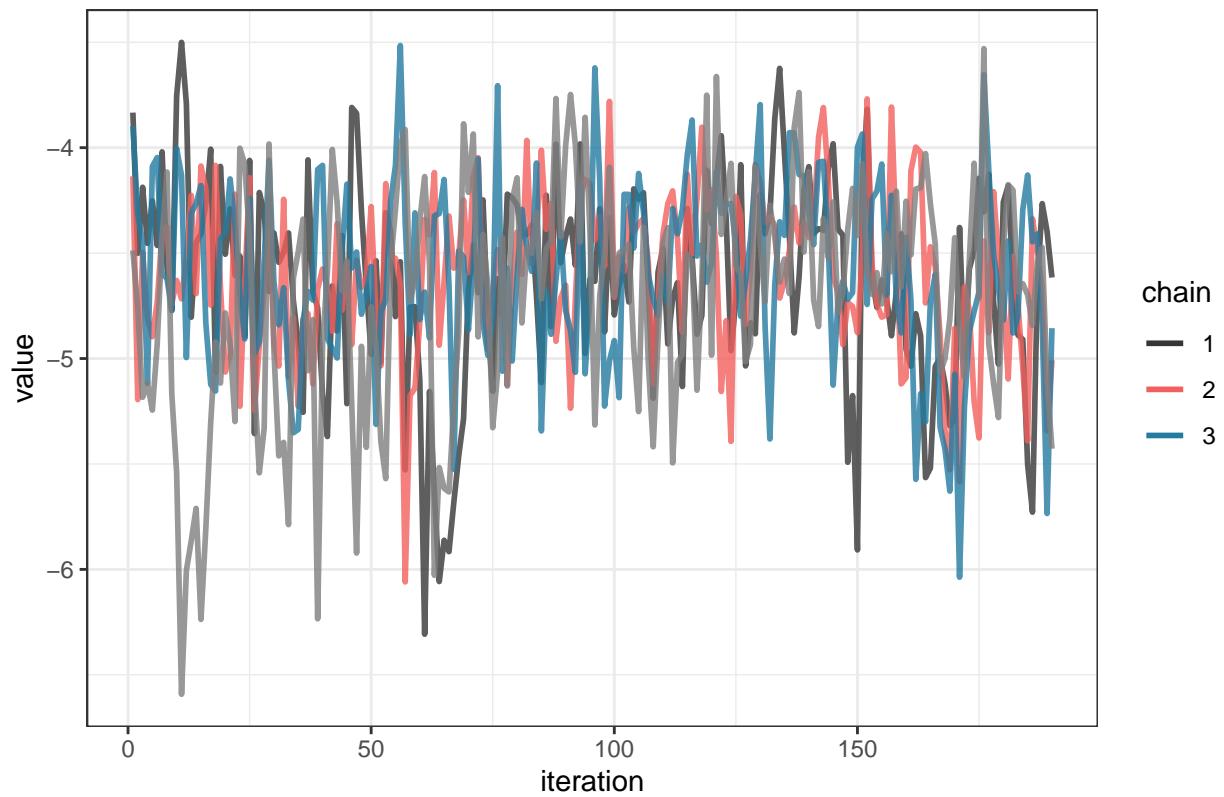


```
traceplt1 <- ggtraceplot(jointFit1)
```

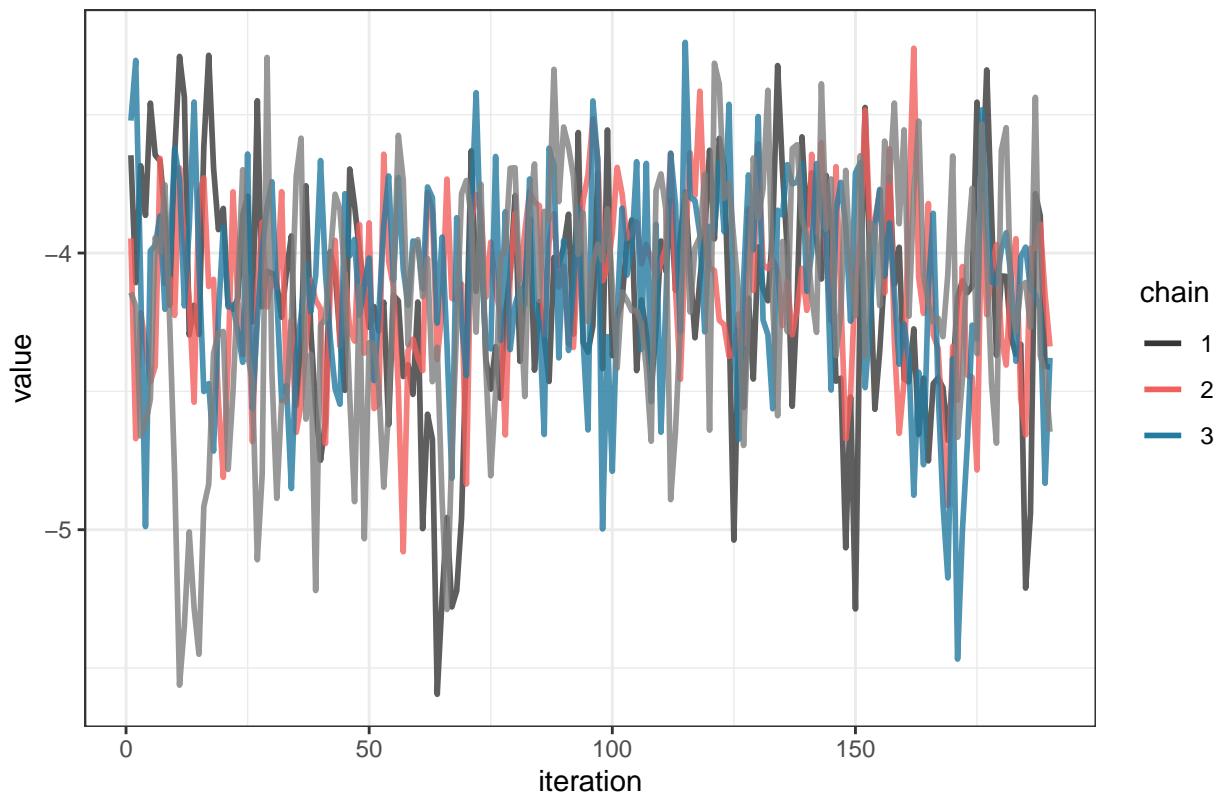
Traceplot of bs_gammas_1



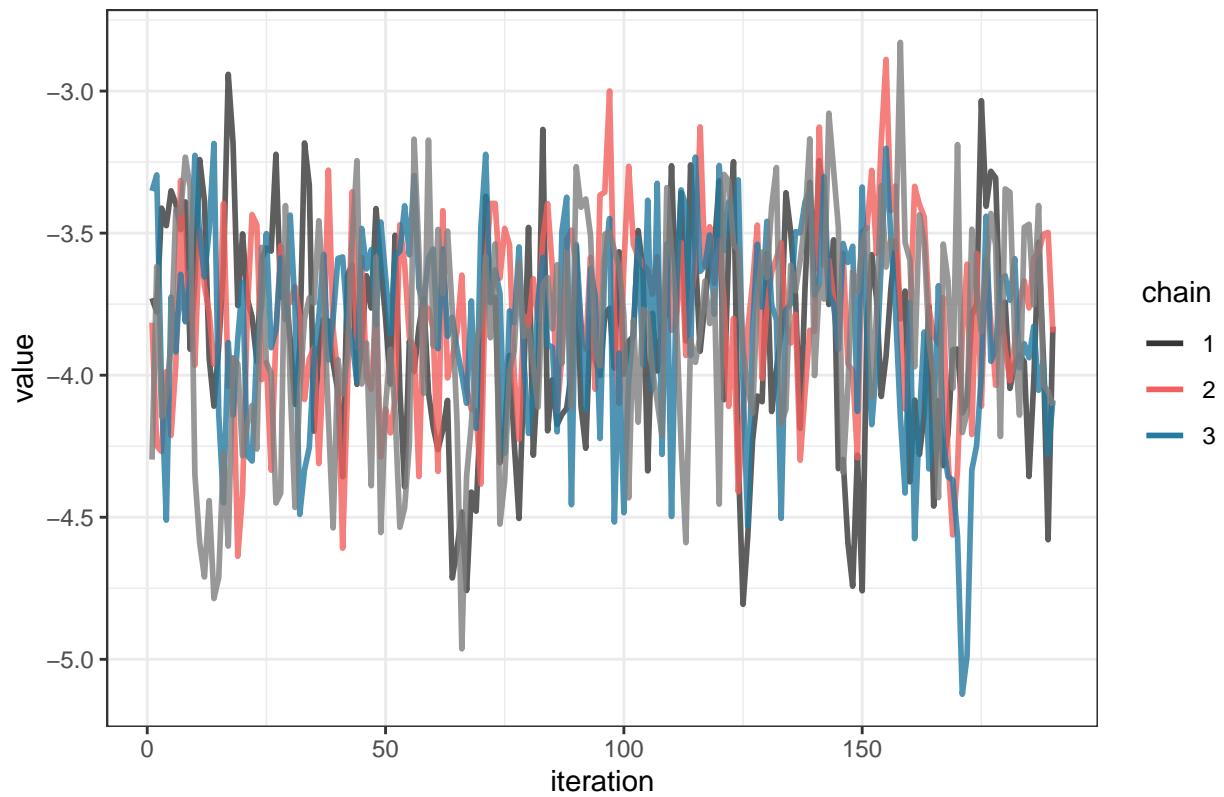
Traceplot of bs_gammas_2



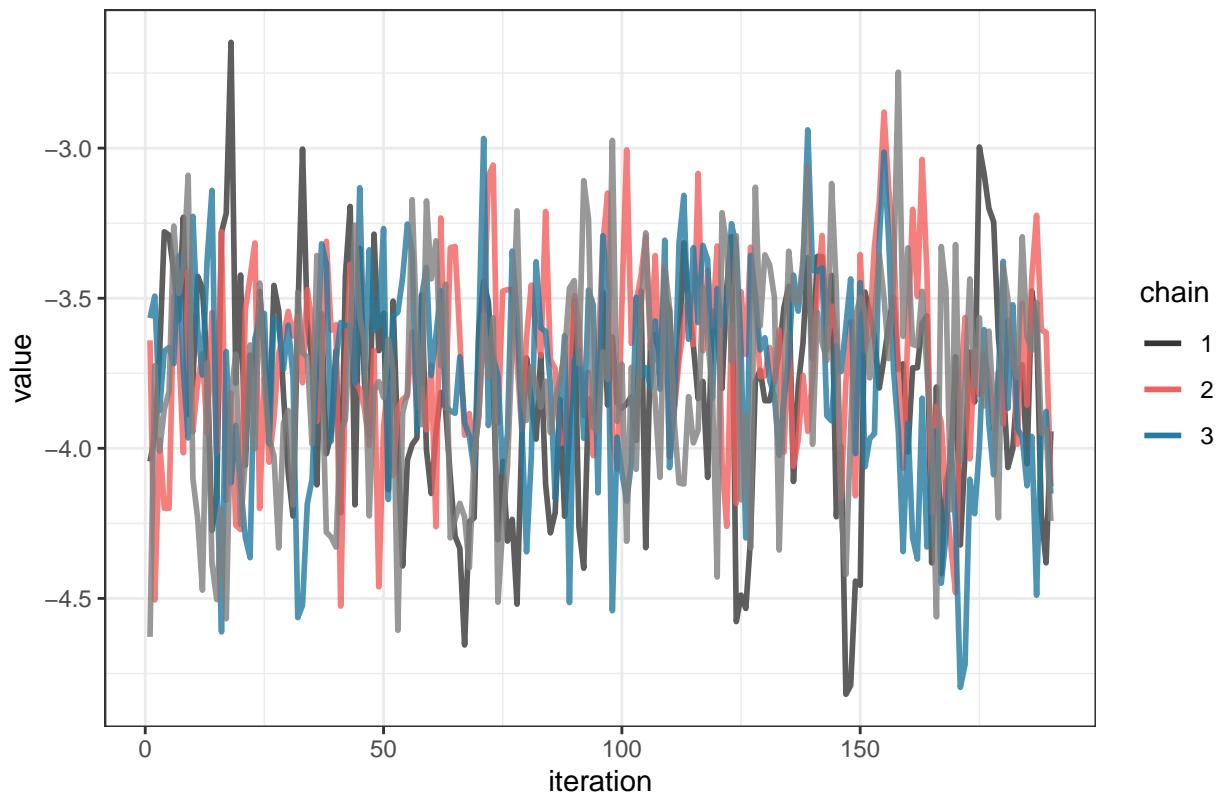
Traceplot of bs_gammas_3



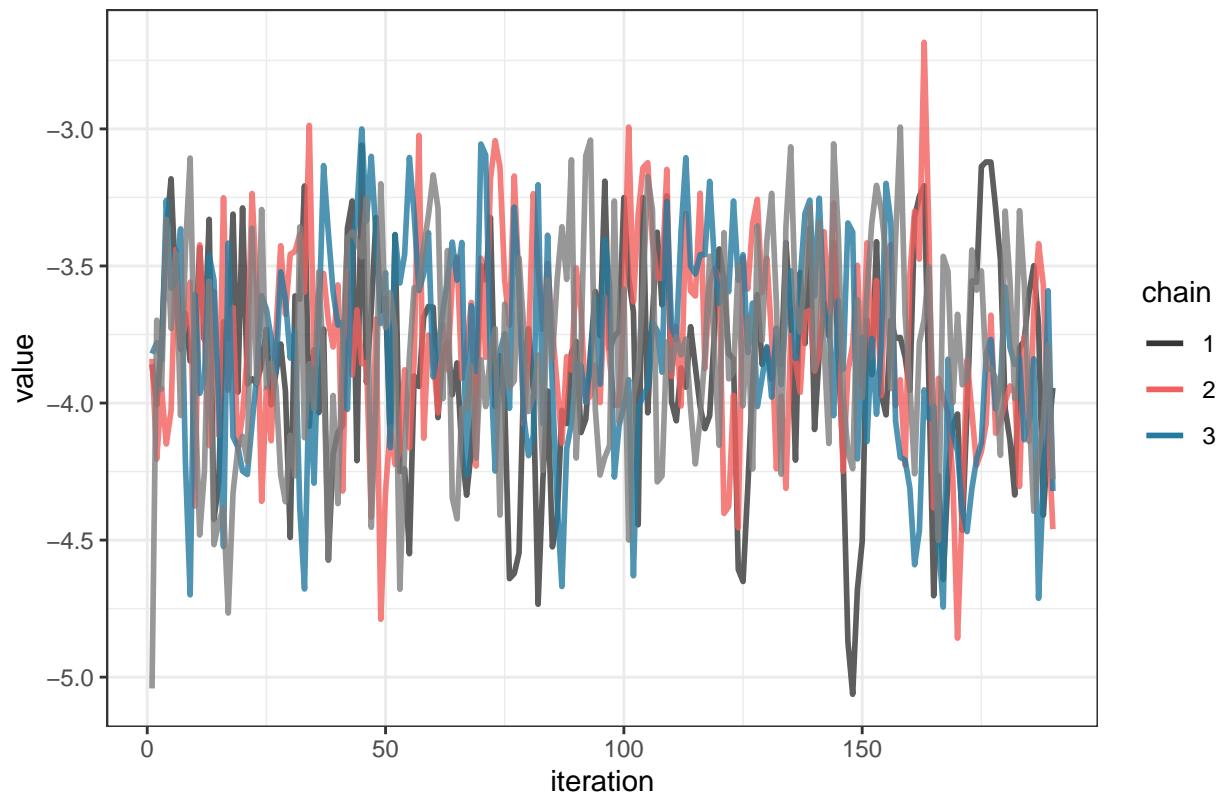
Traceplot of bs_gammas_4



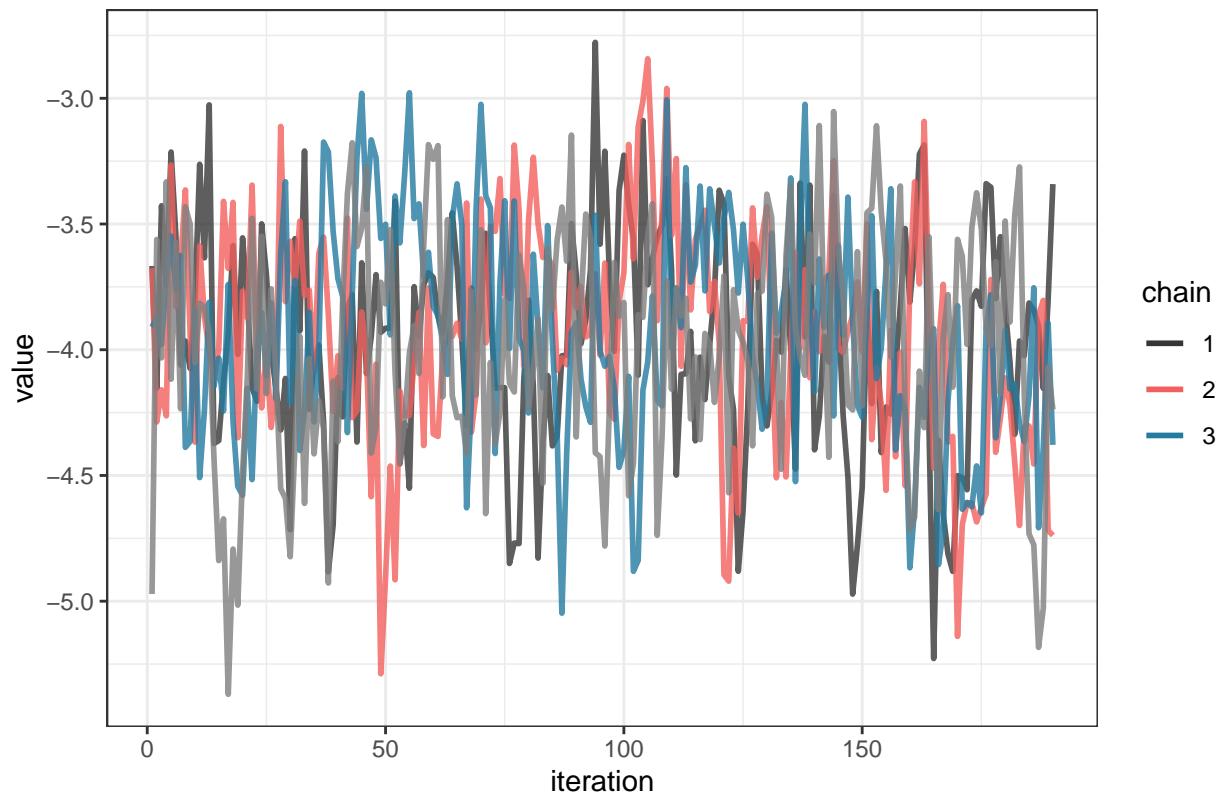
Traceplot of bs_gammas_5



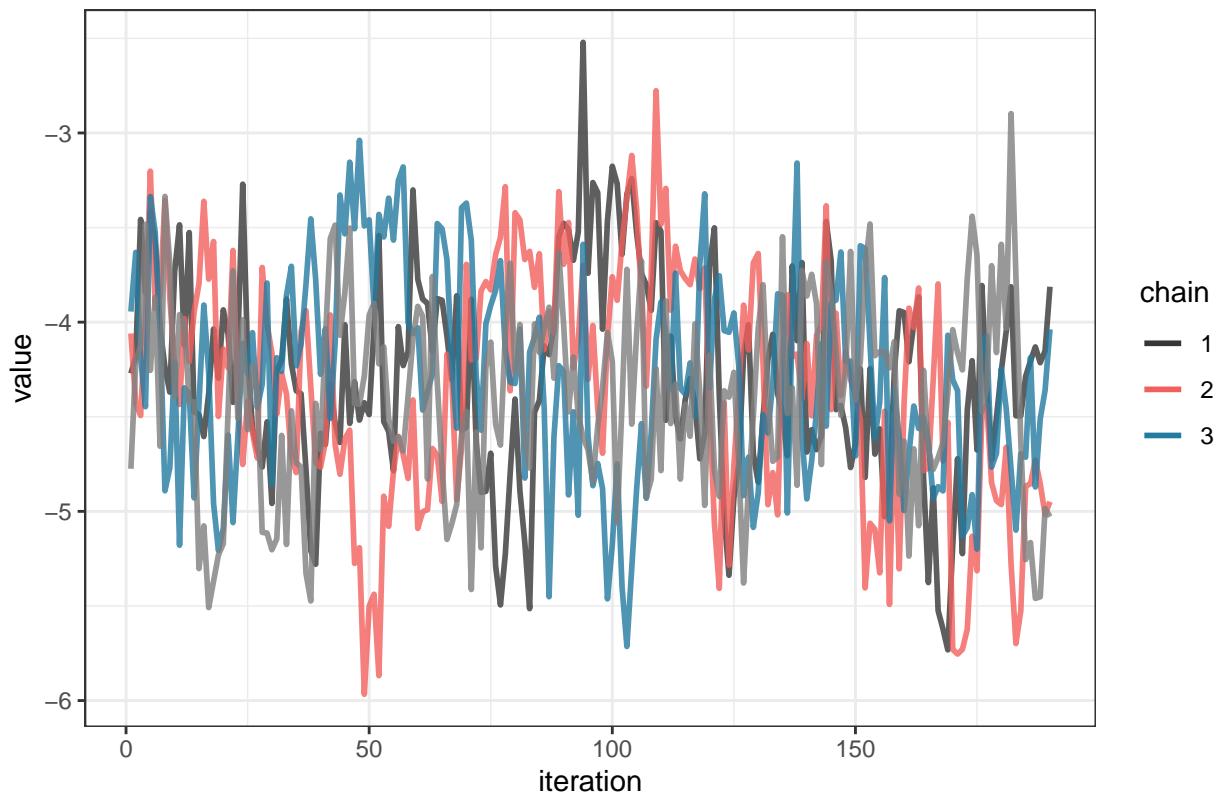
Traceplot of bs_gammas_6



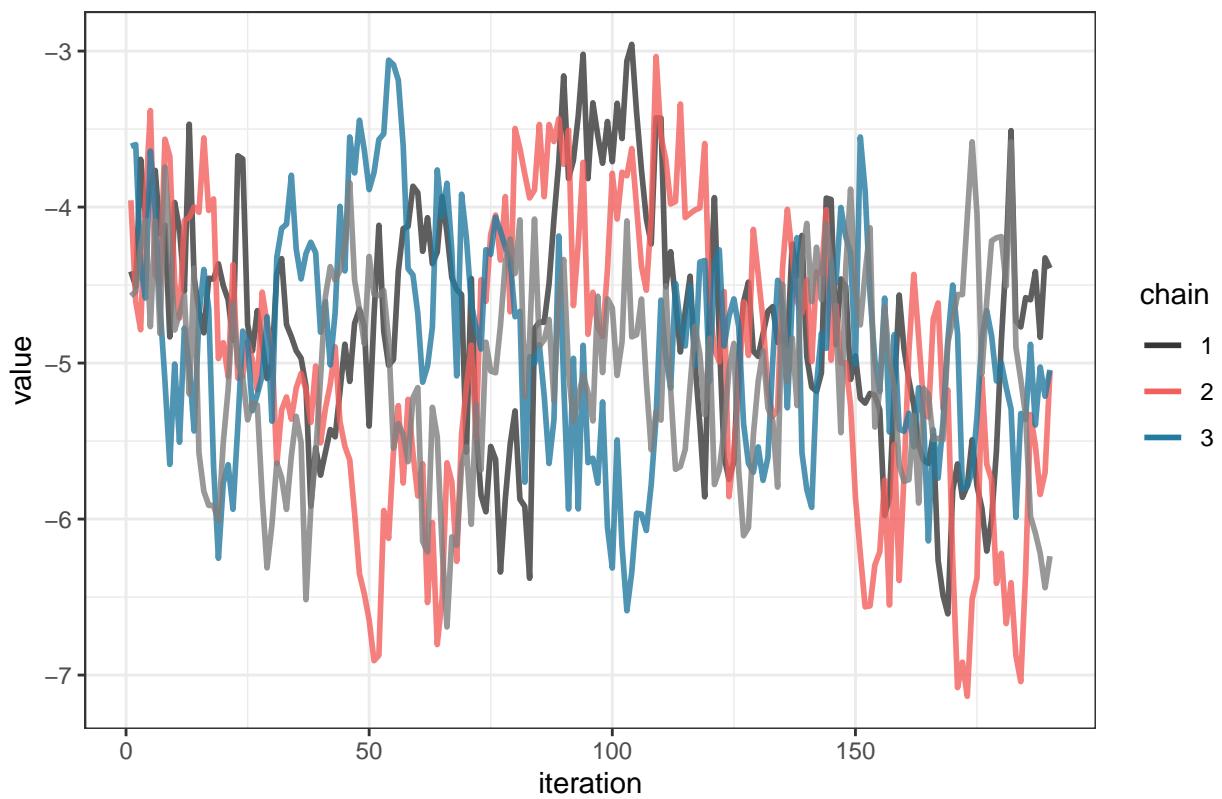
Traceplot of bs_gammas_7



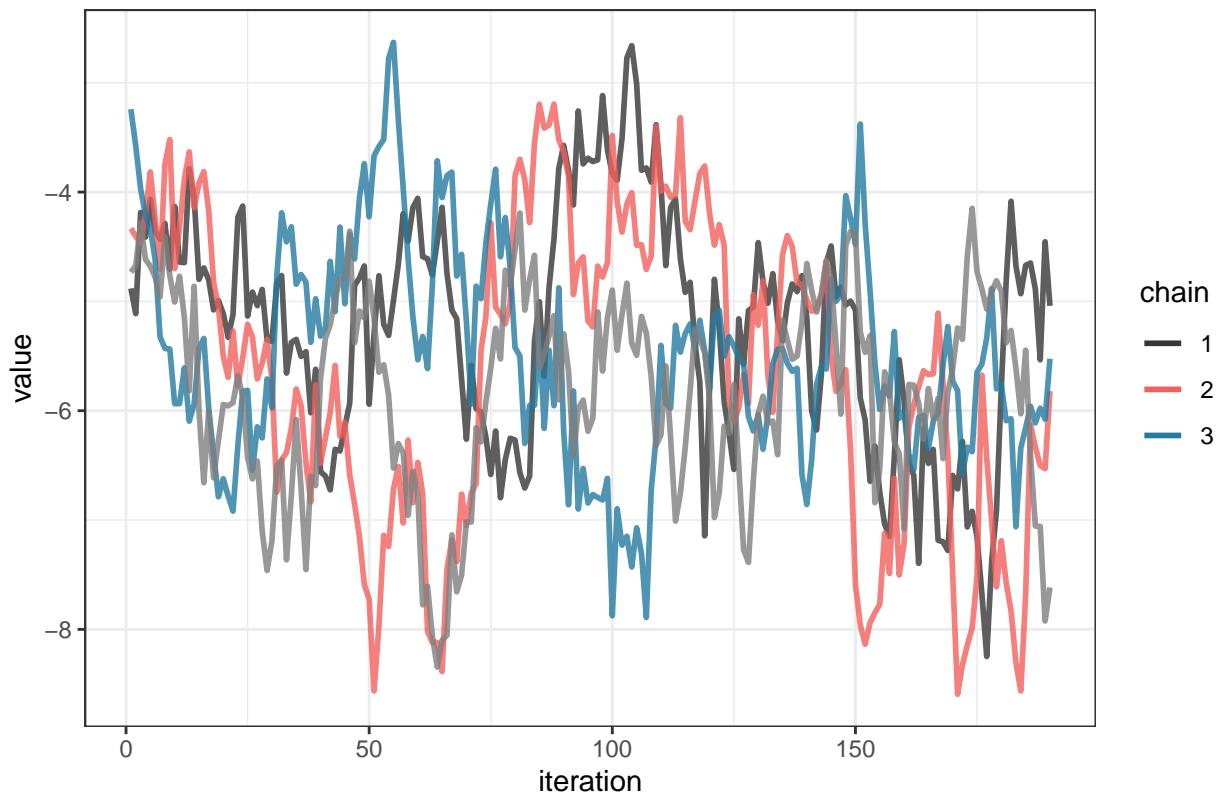
Traceplot of bs_gammas_8



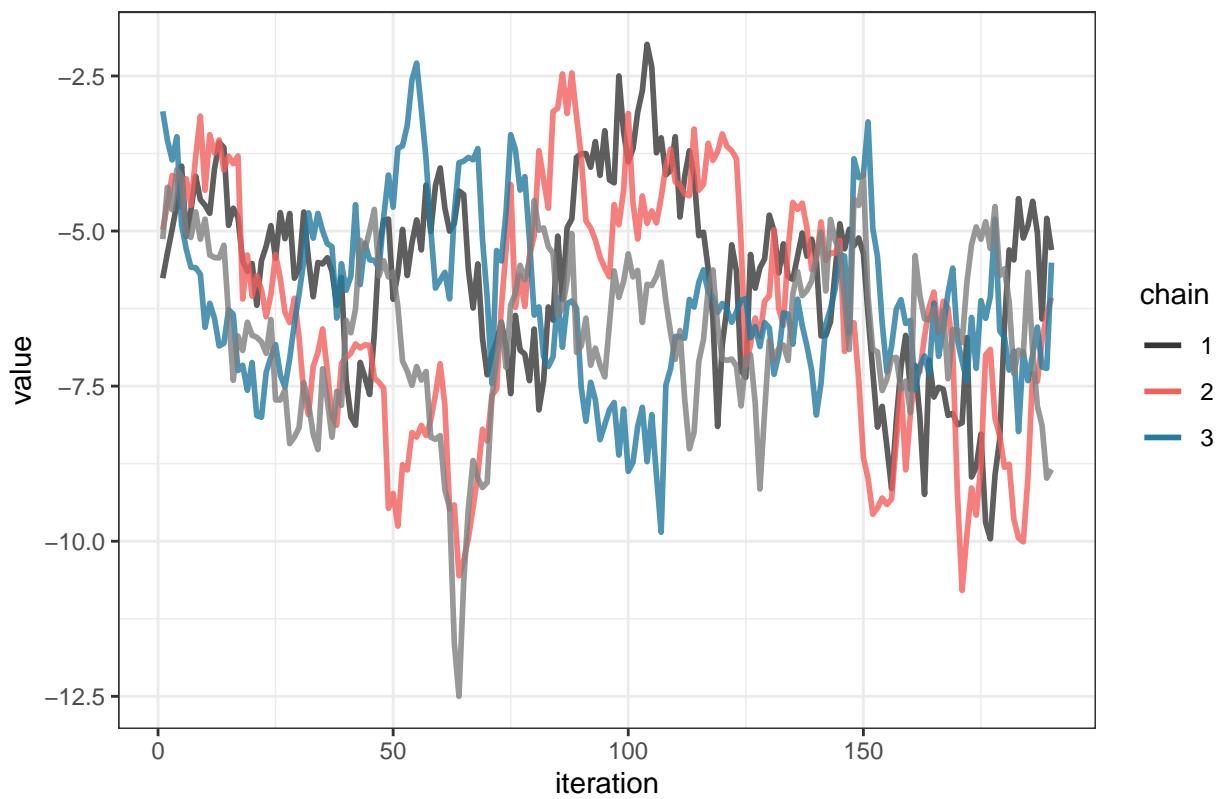
Traceplot of bs_gammas_9



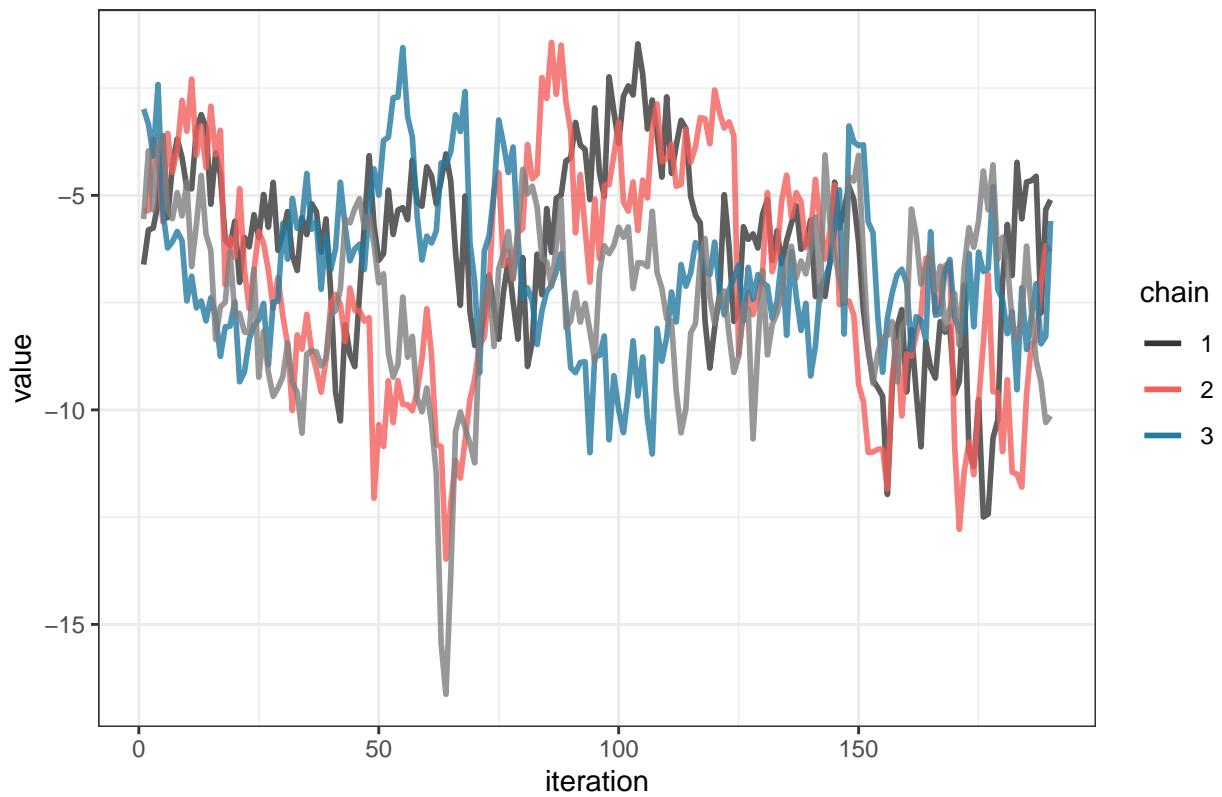
Traceplot of bs_gammas_10



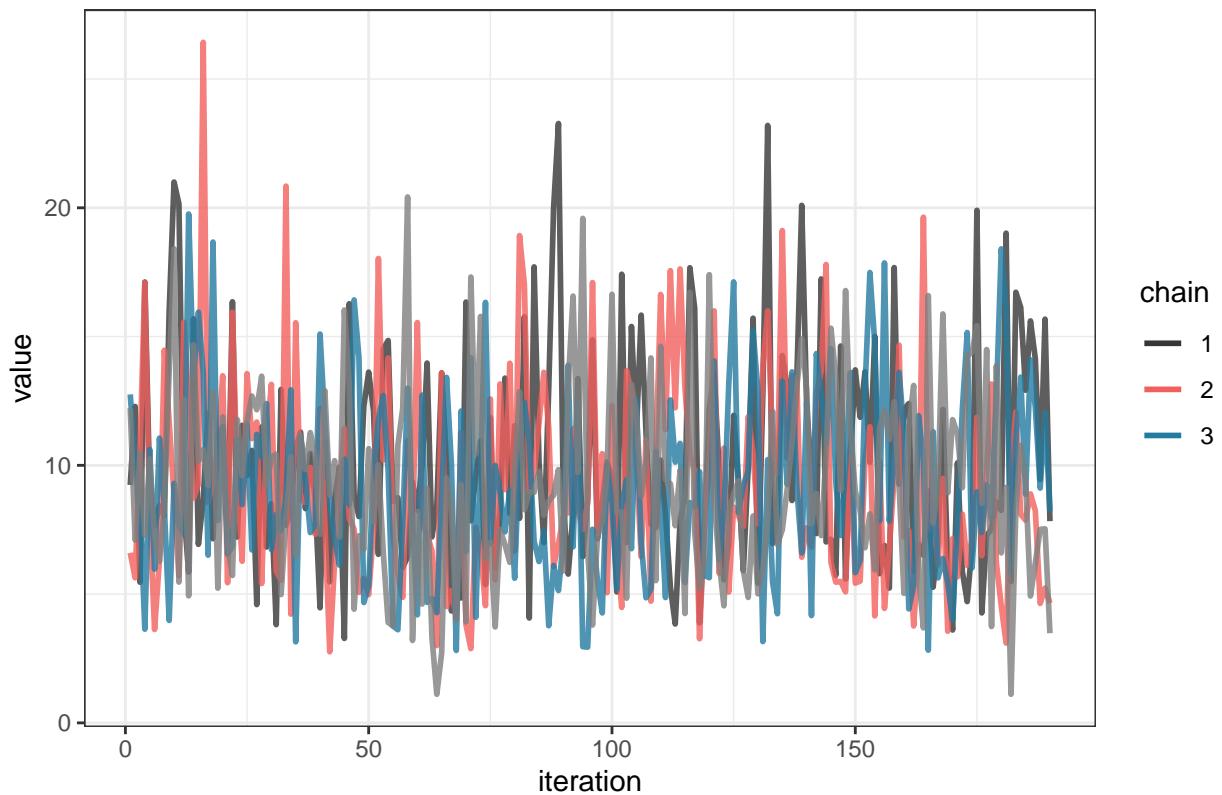
Traceplot of bs_gammas_11



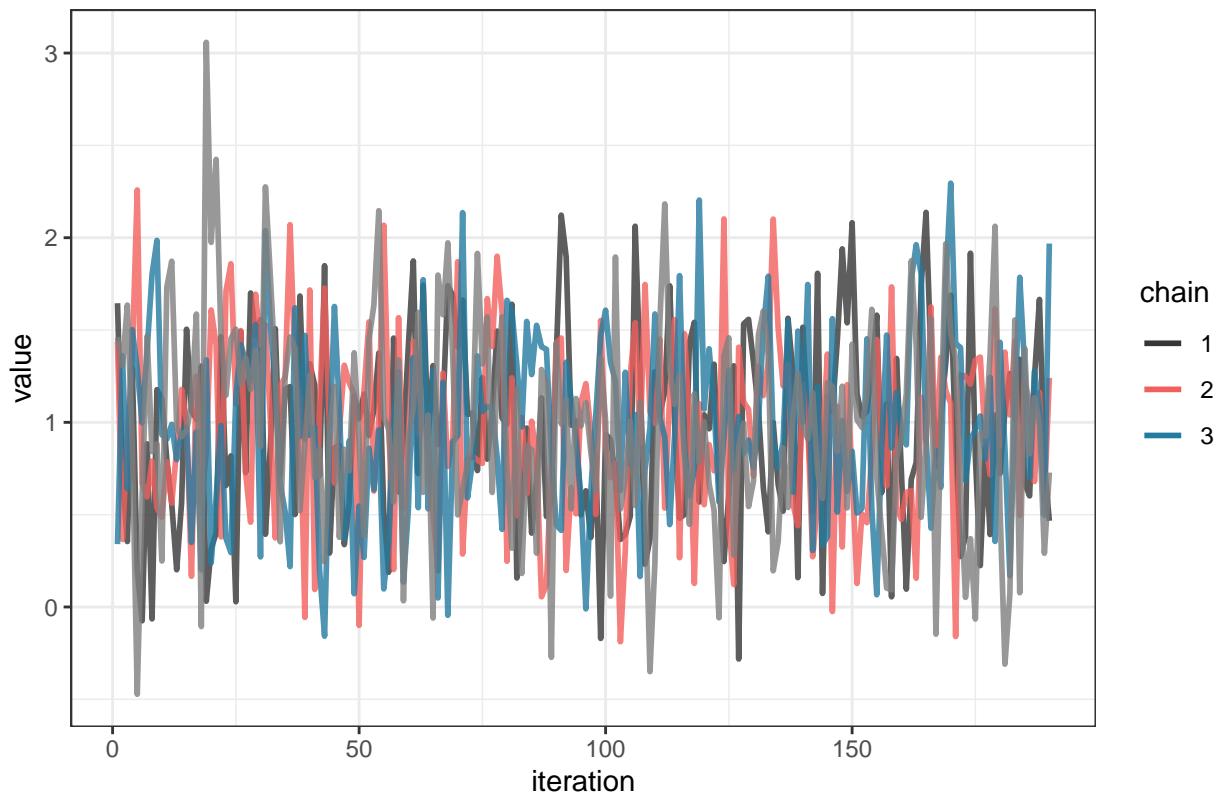
Traceplot of bs_gammas_12



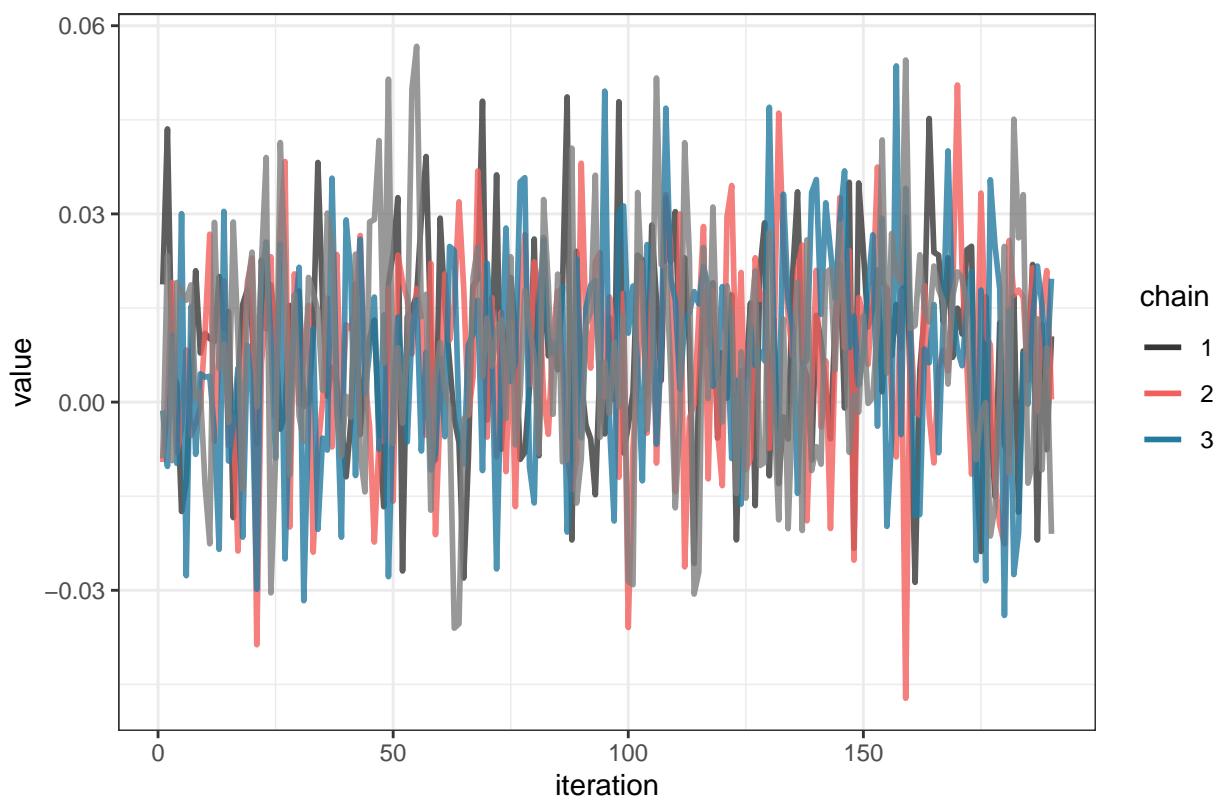
Traceplot of tau_bs_gammas



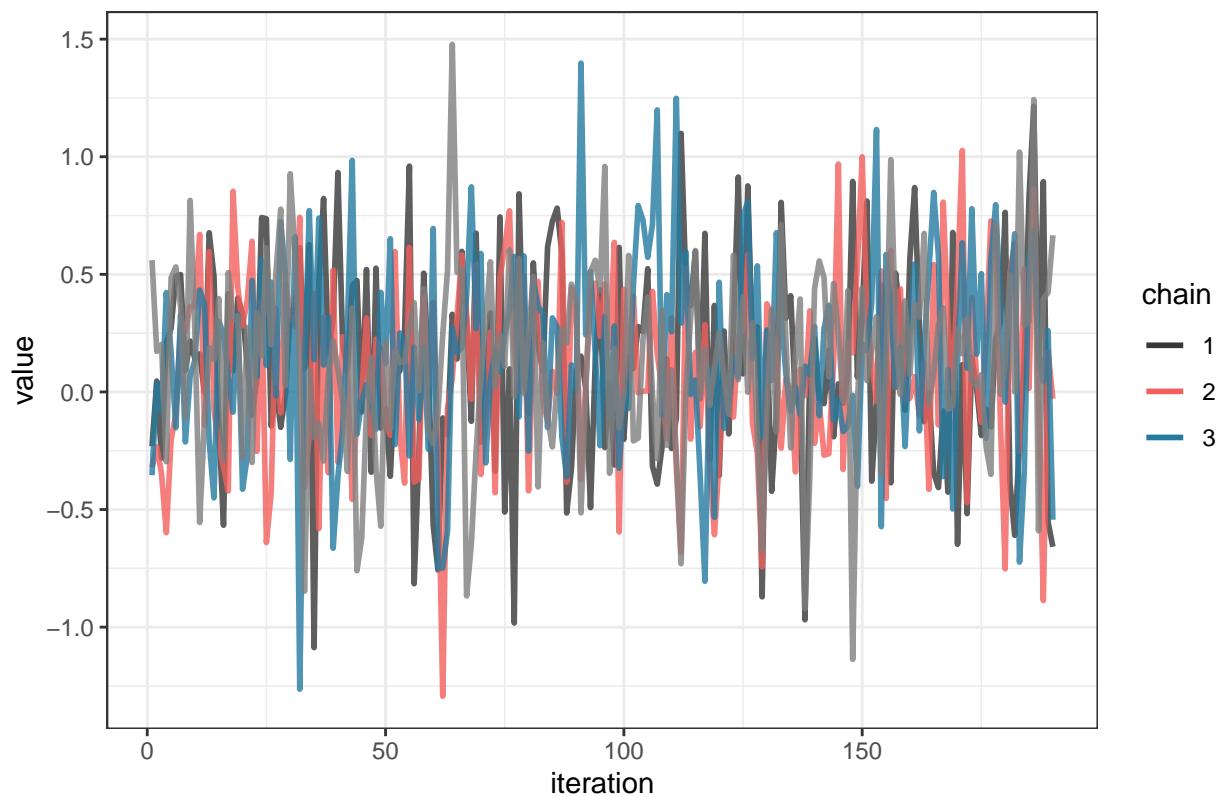
Traceplot of LOWC31



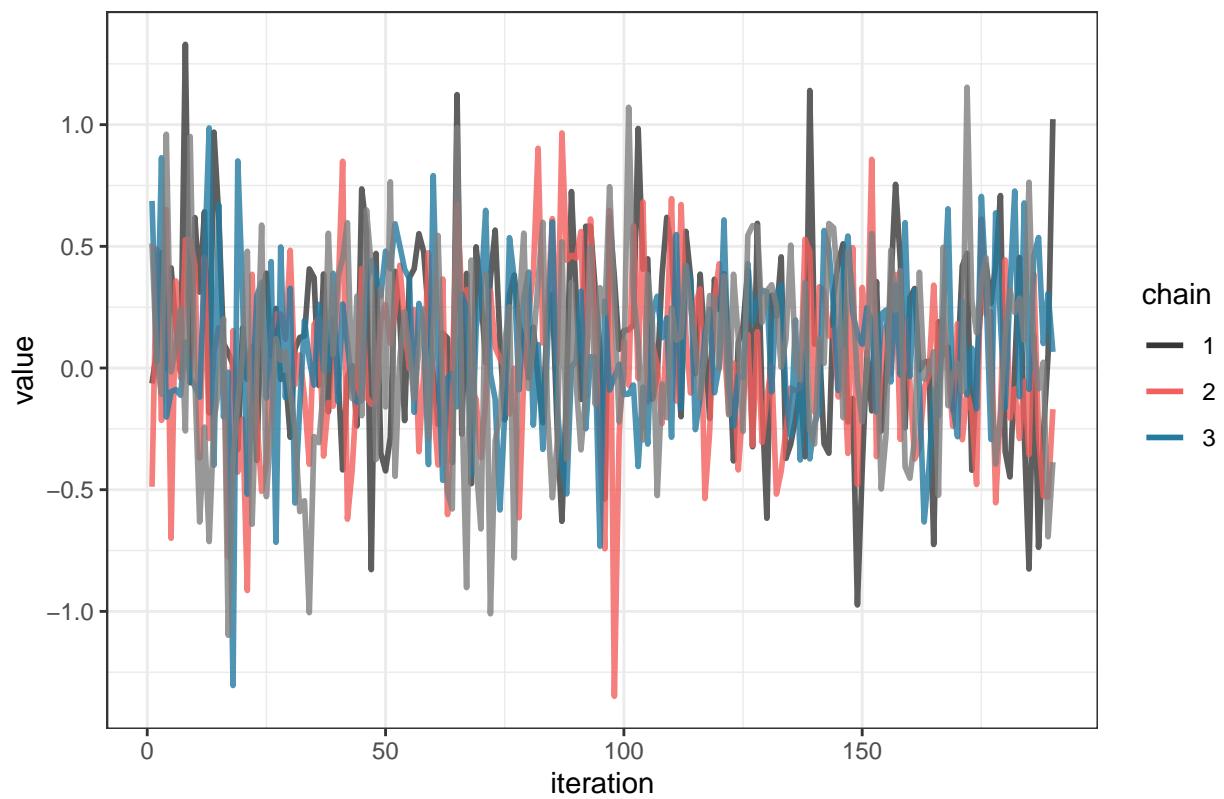
Traceplot of ageatbiopsy



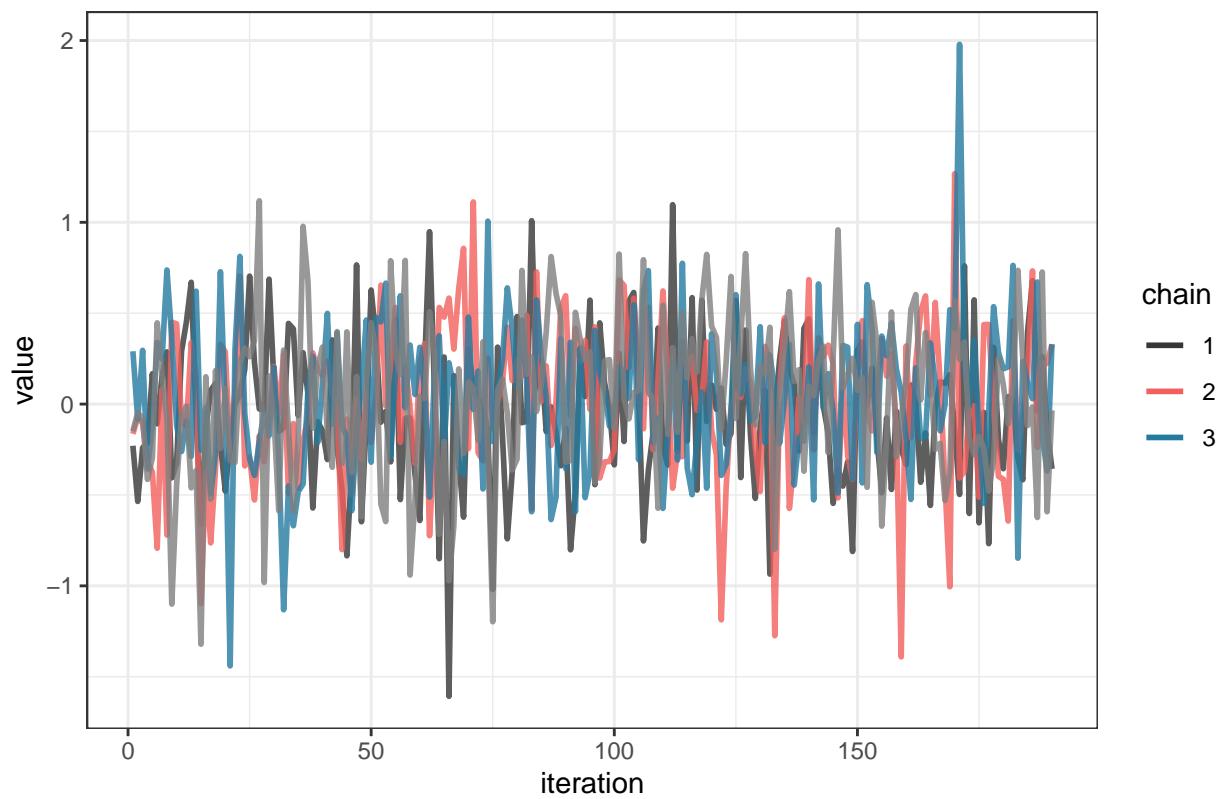
Traceplot of sex



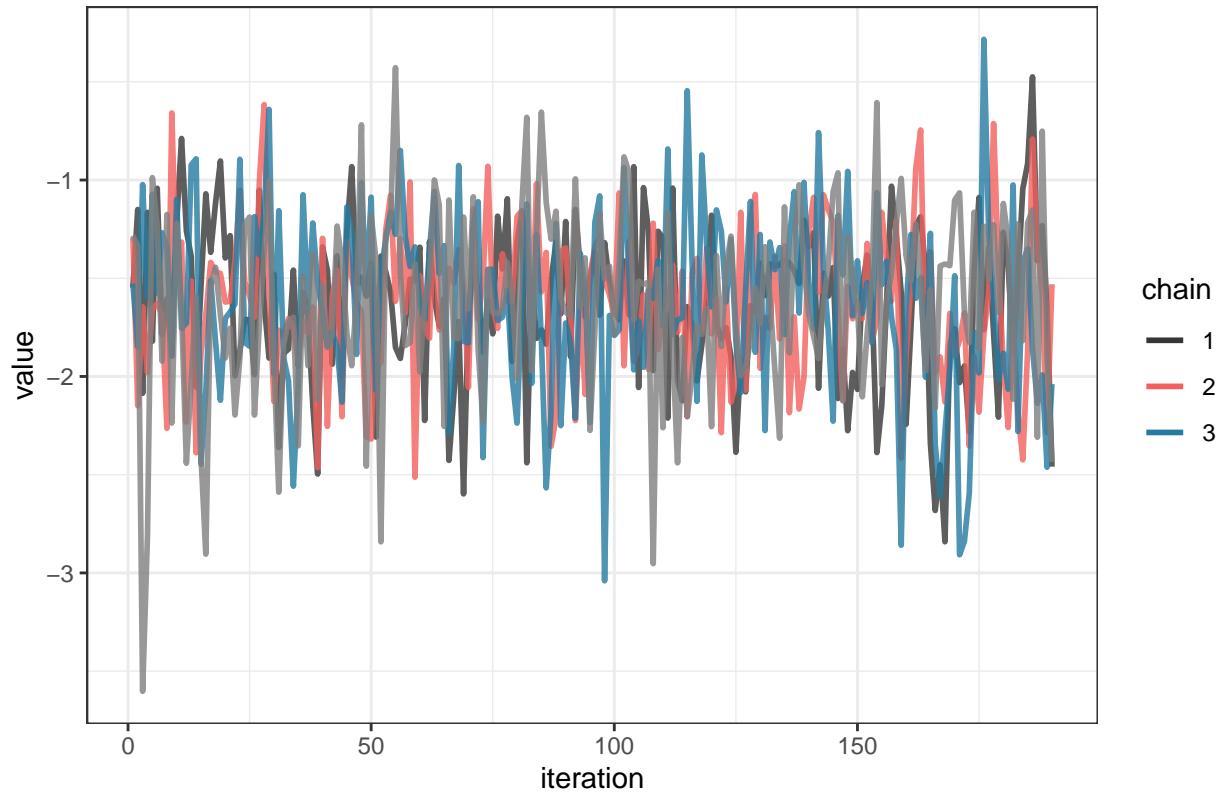
Traceplot of black



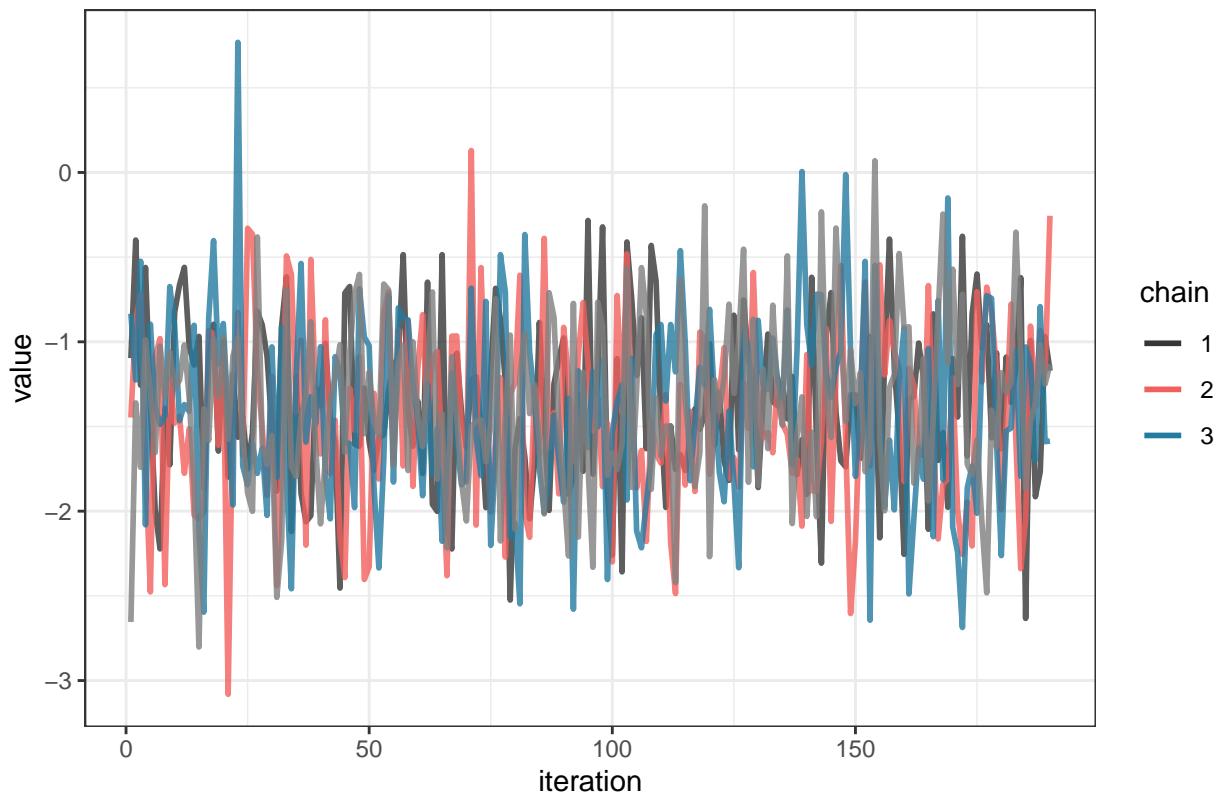
Traceplot of hypertension



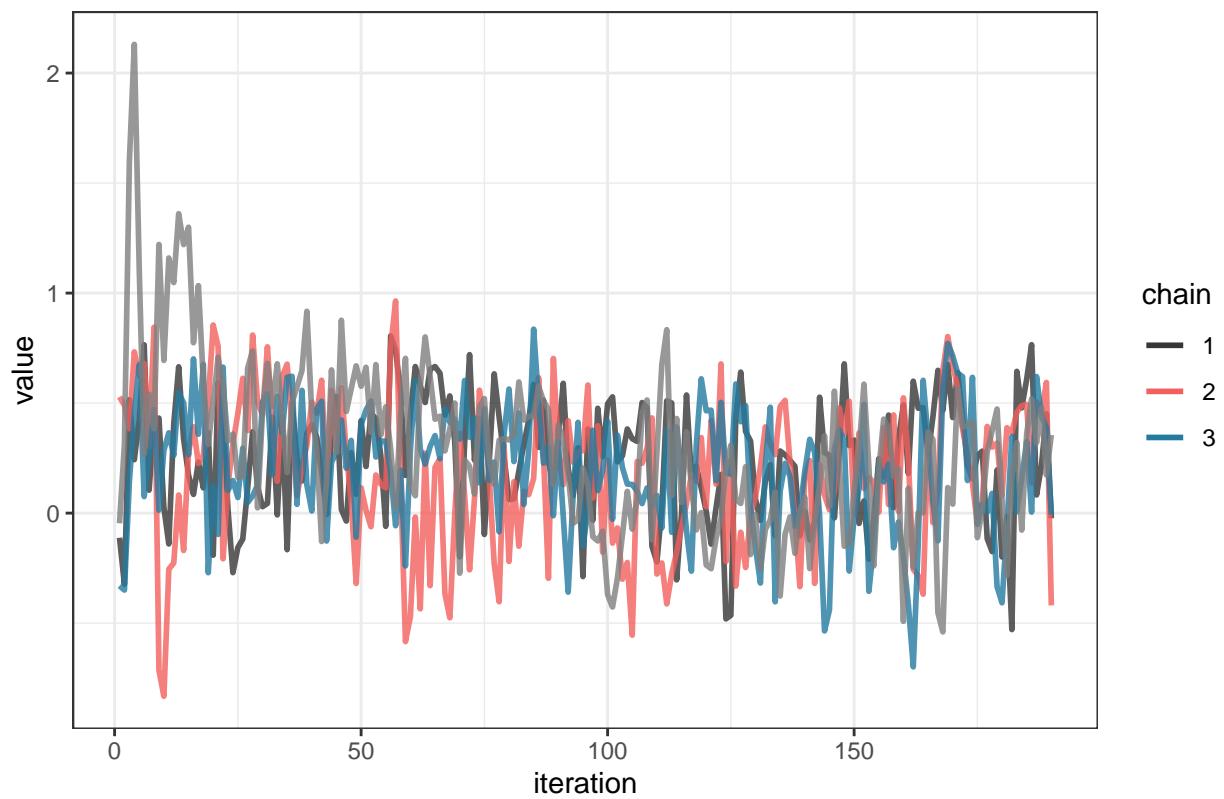
Traceplot of mmf



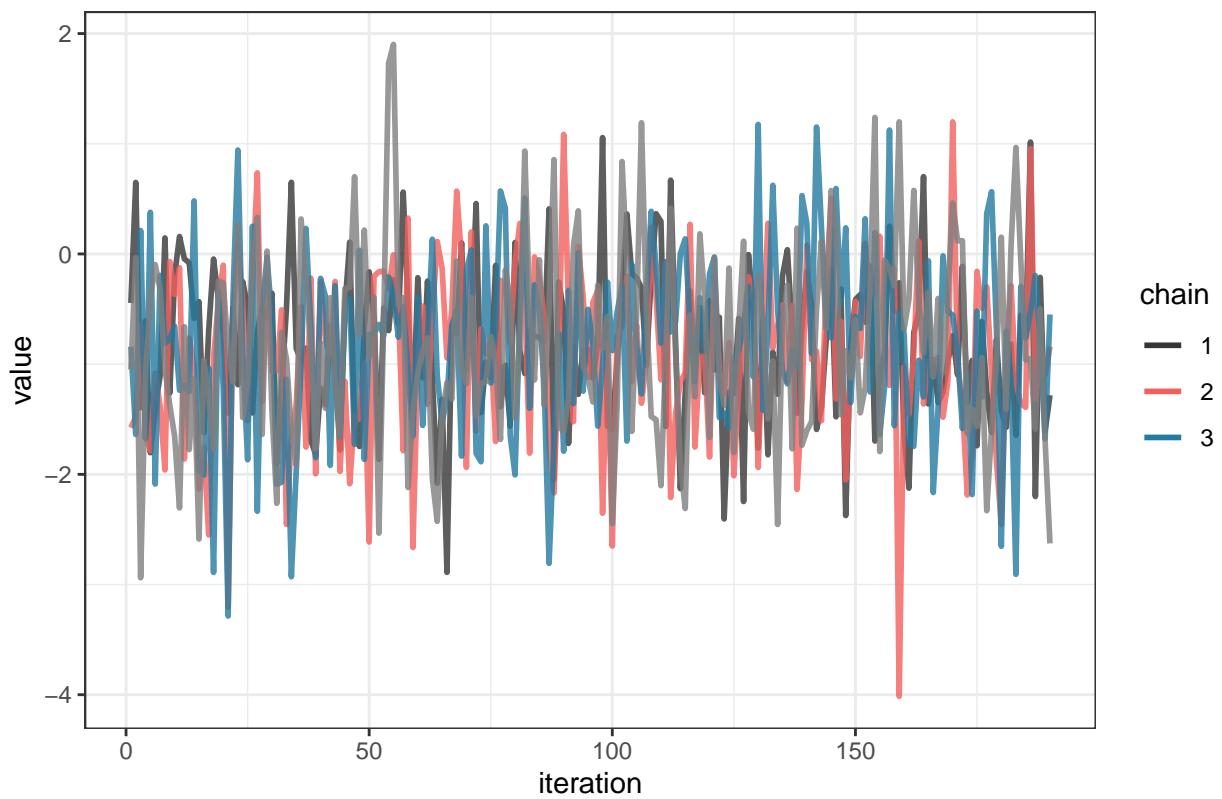
Traceplot of cyc



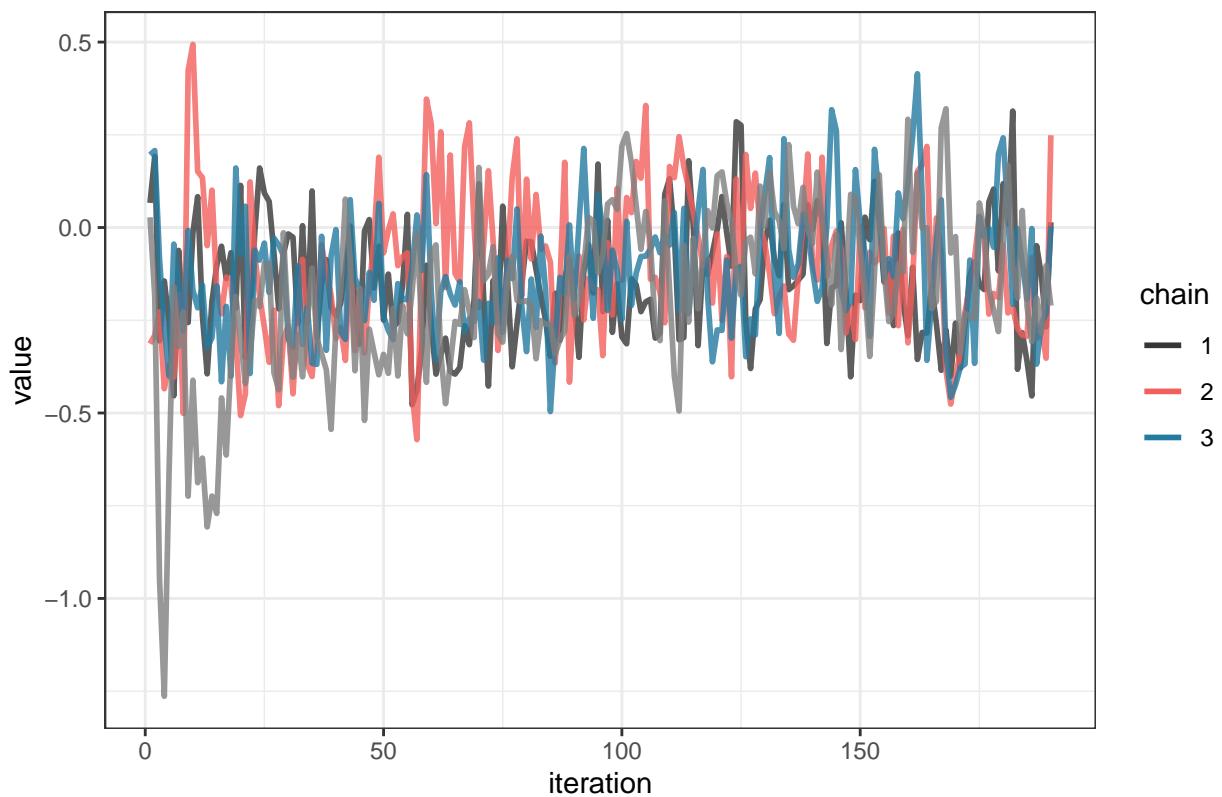
Traceplot of slope(eGFR)



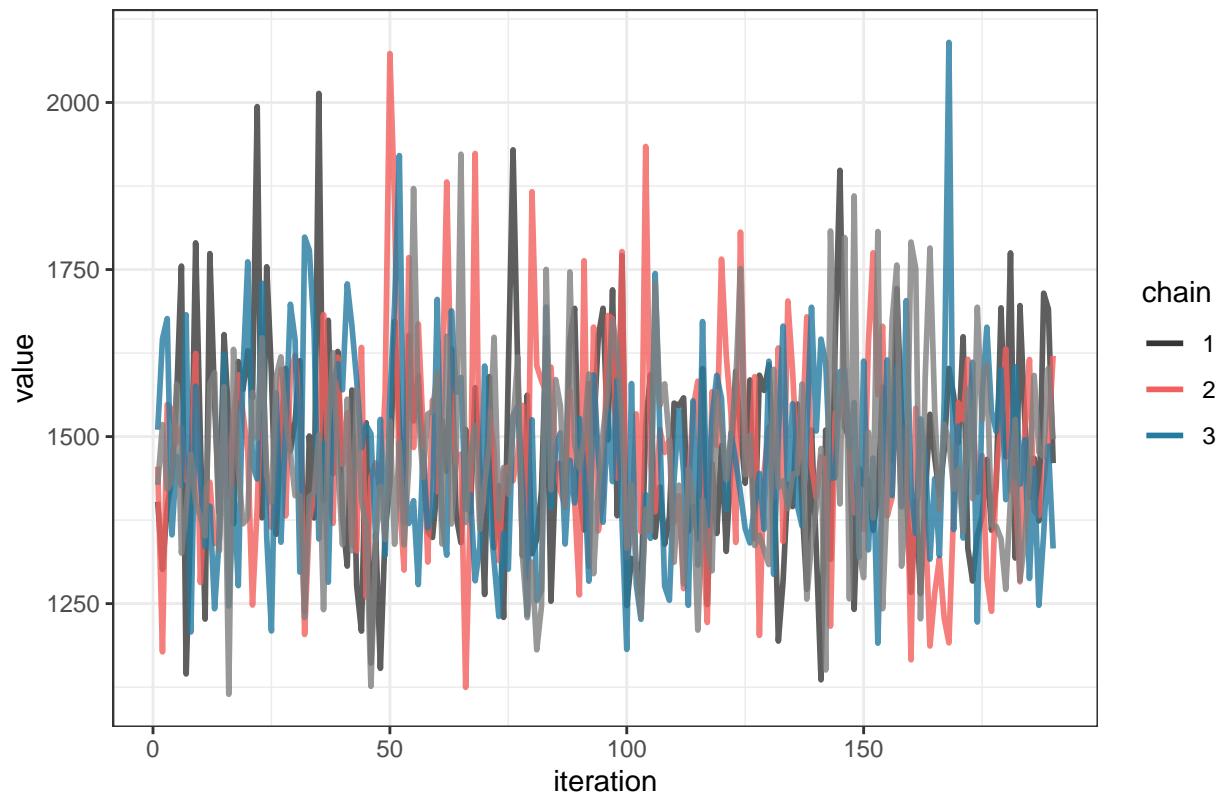
Traceplot of



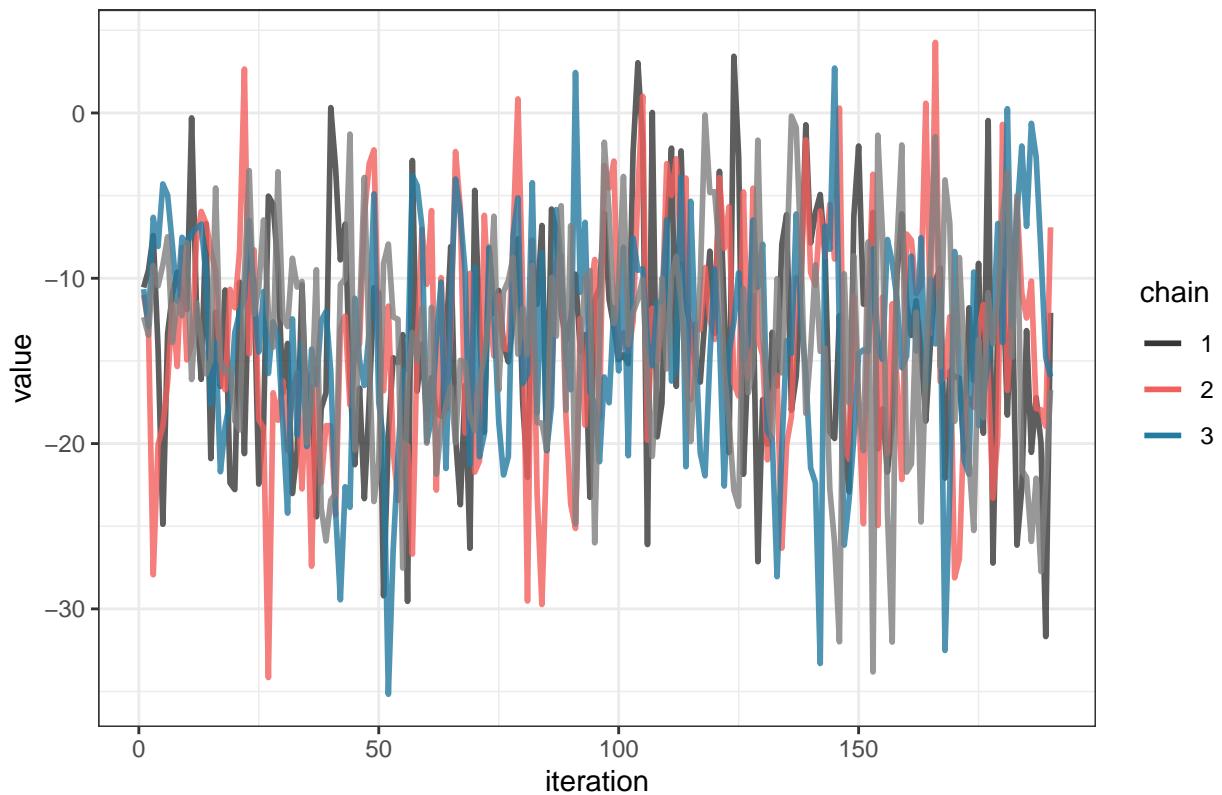
Traceplot of .1



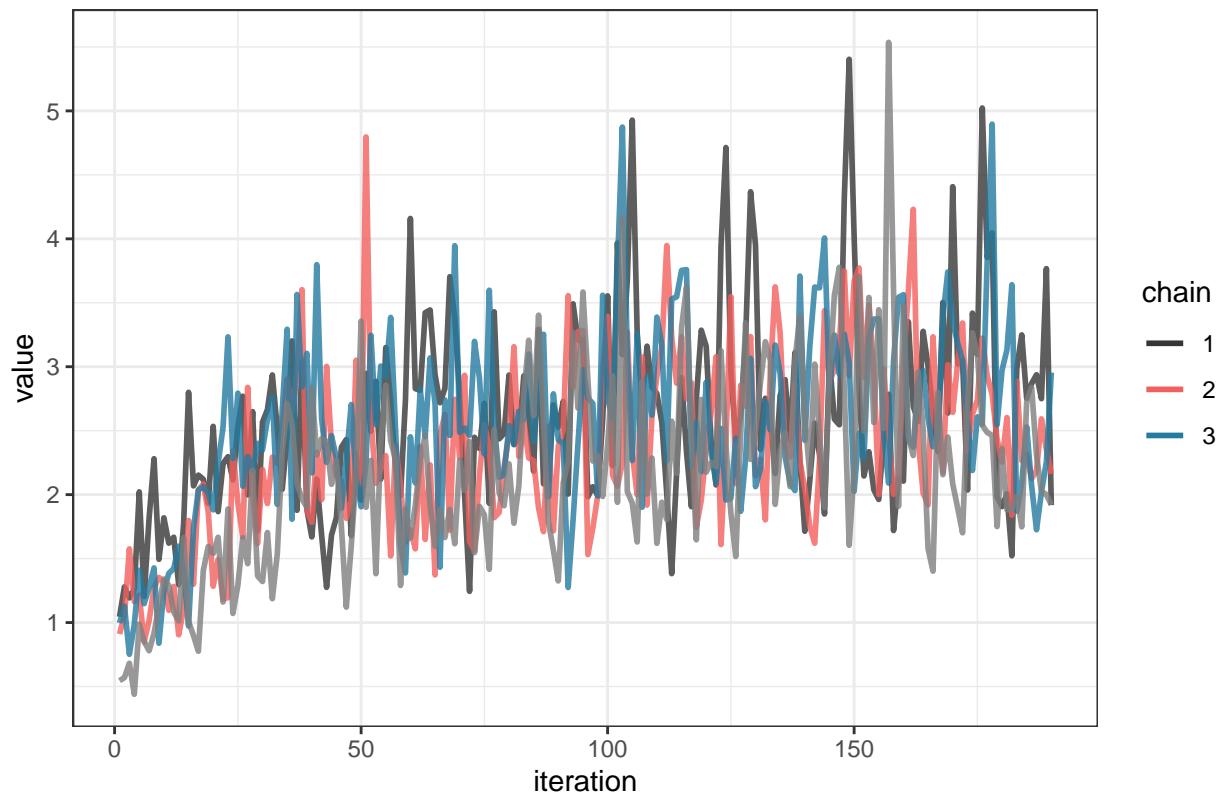
Traceplot of $D[1, 1]$



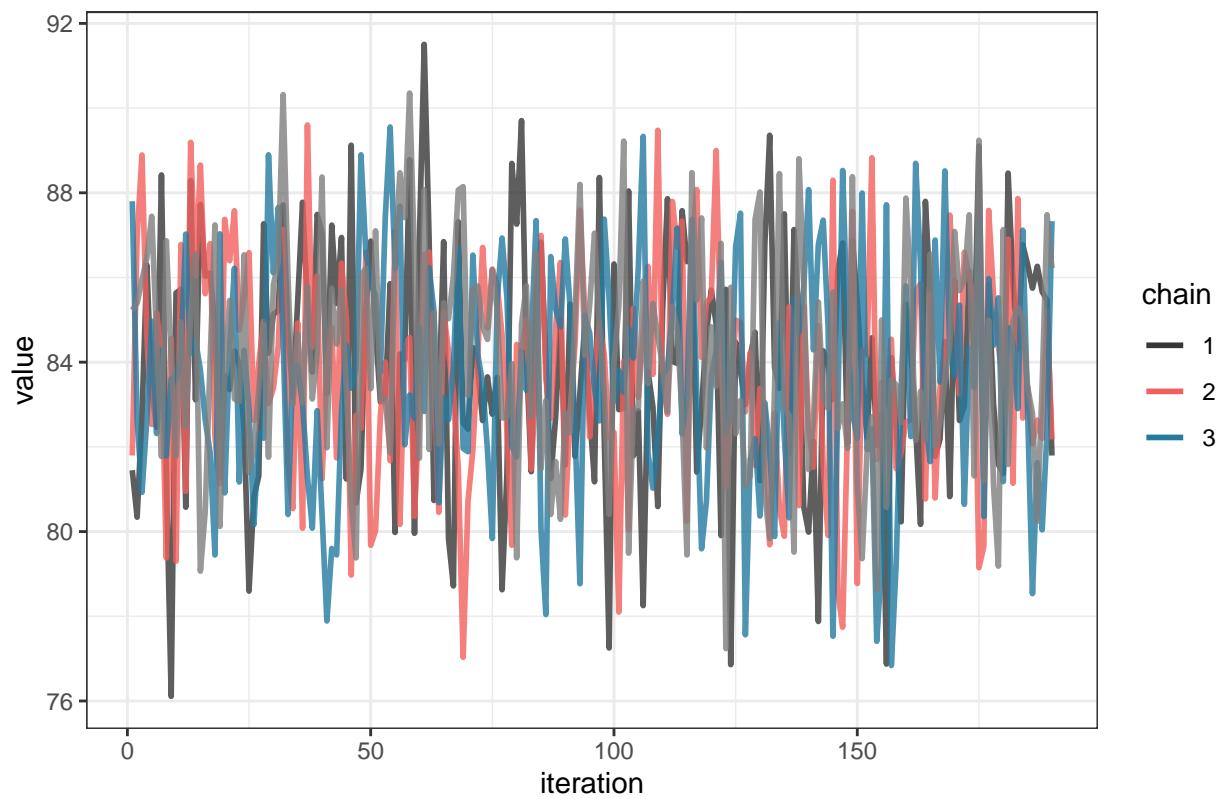
Traceplot of $D[2, 1]$



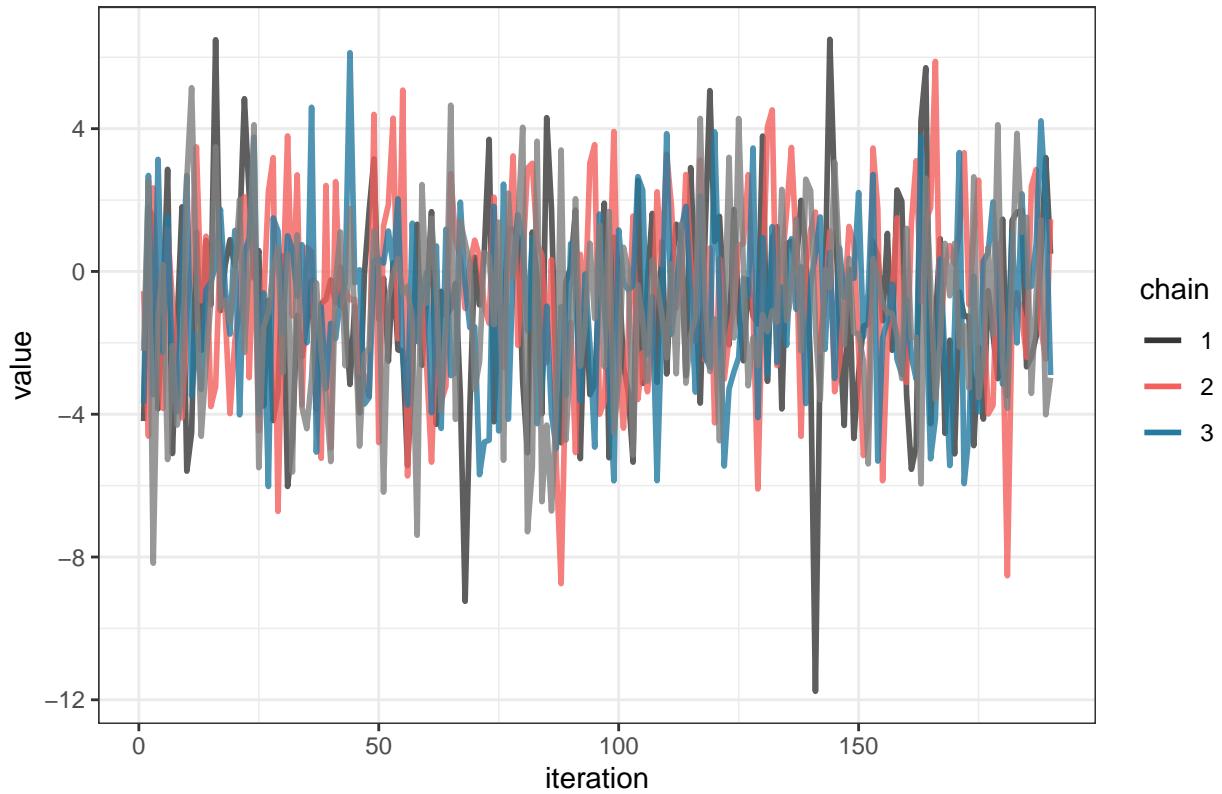
Traceplot of $D[2, 2]$



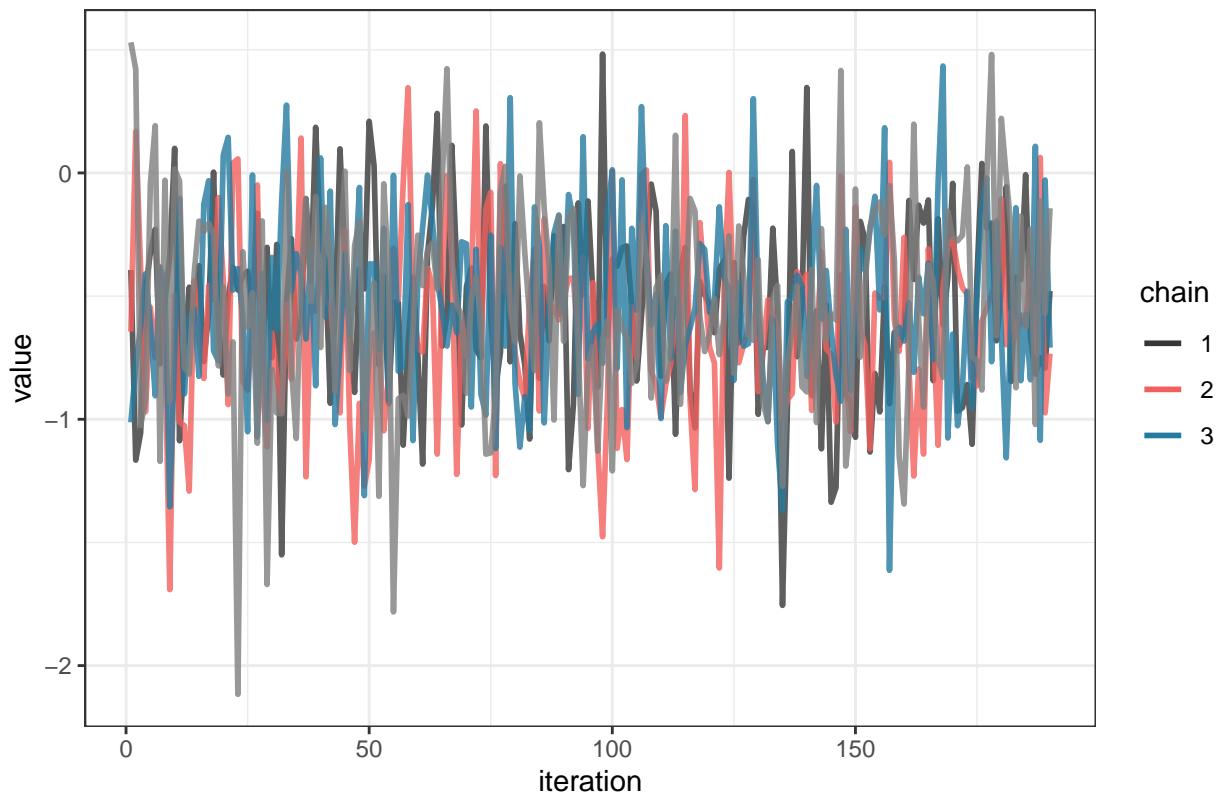
Traceplot of (Intercept)



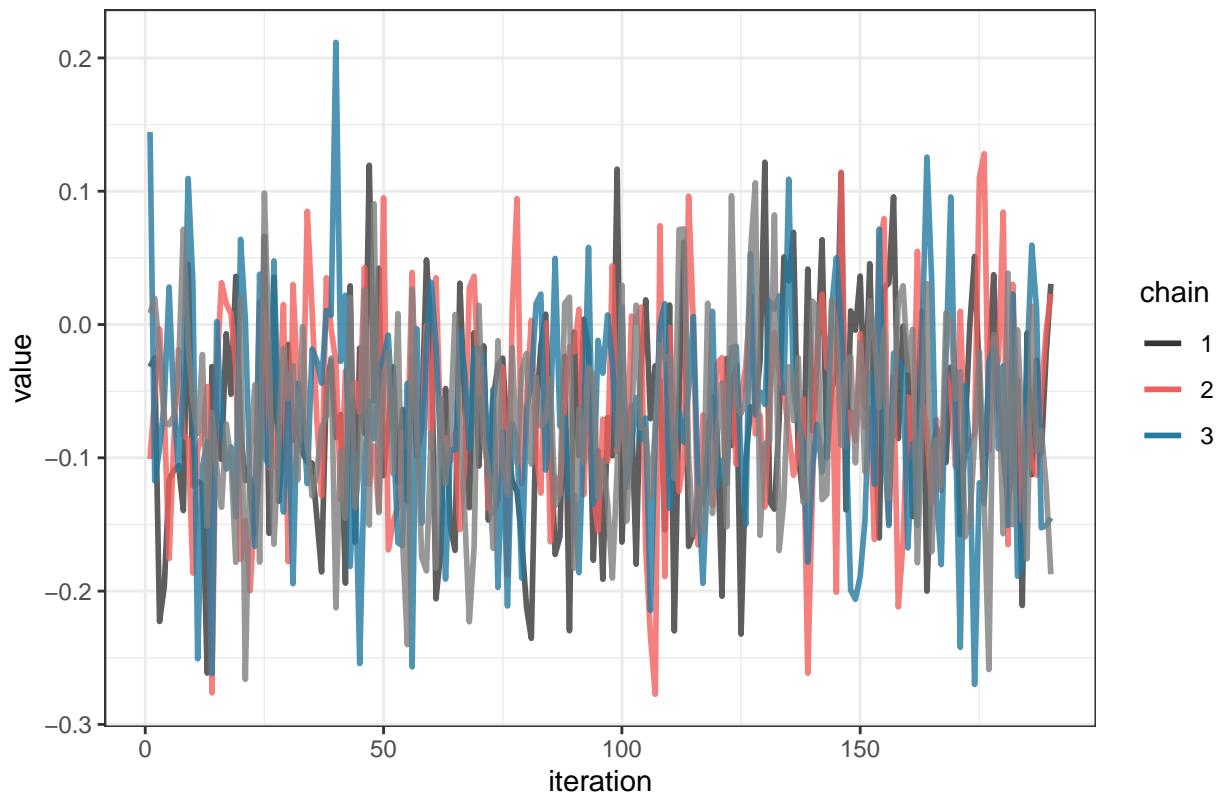
Traceplot of LOWC31.1



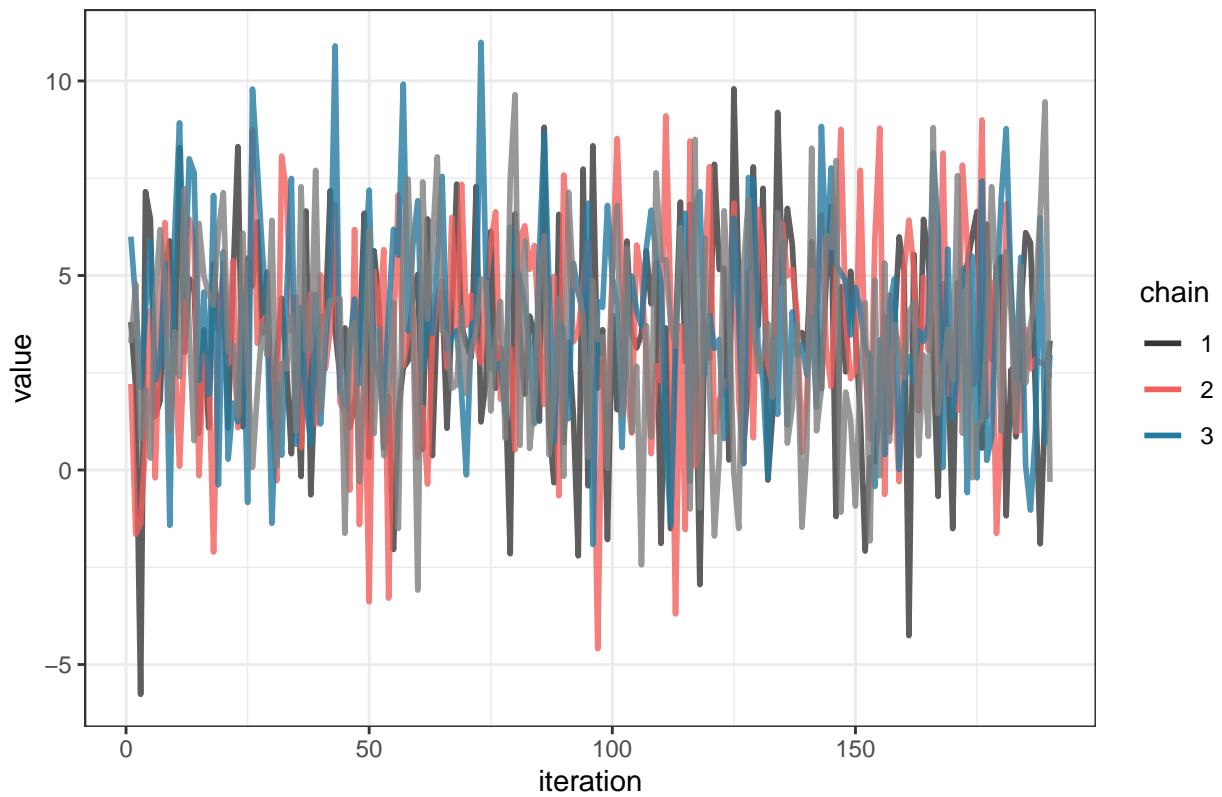
Traceplot of time



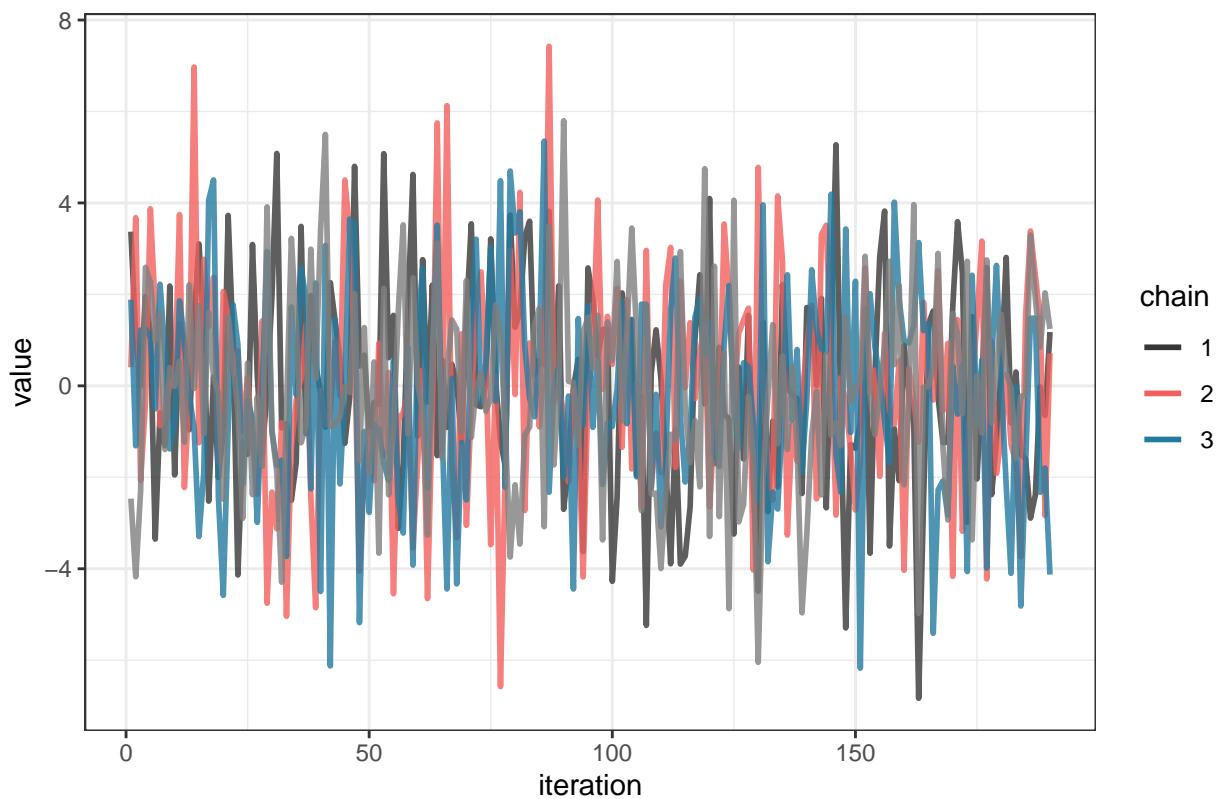
Traceplot of ageatbiopsy.1



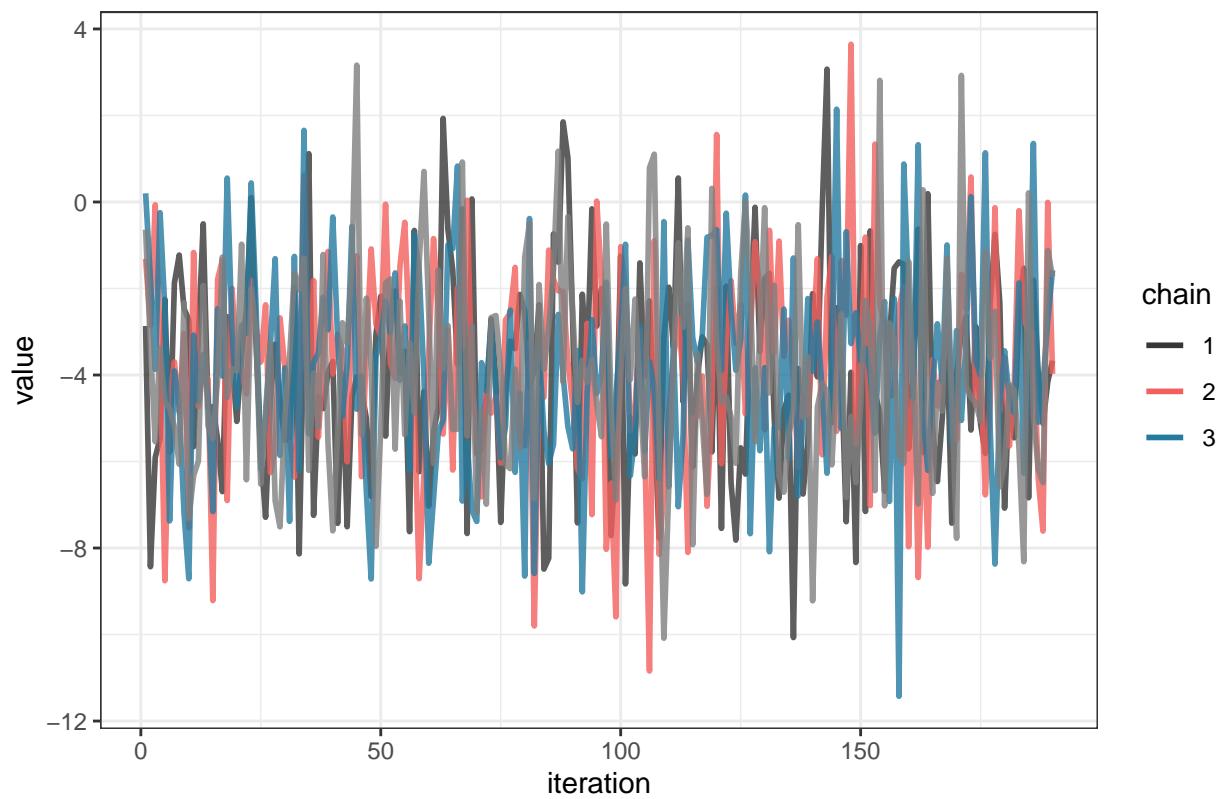
Traceplot of sex.1



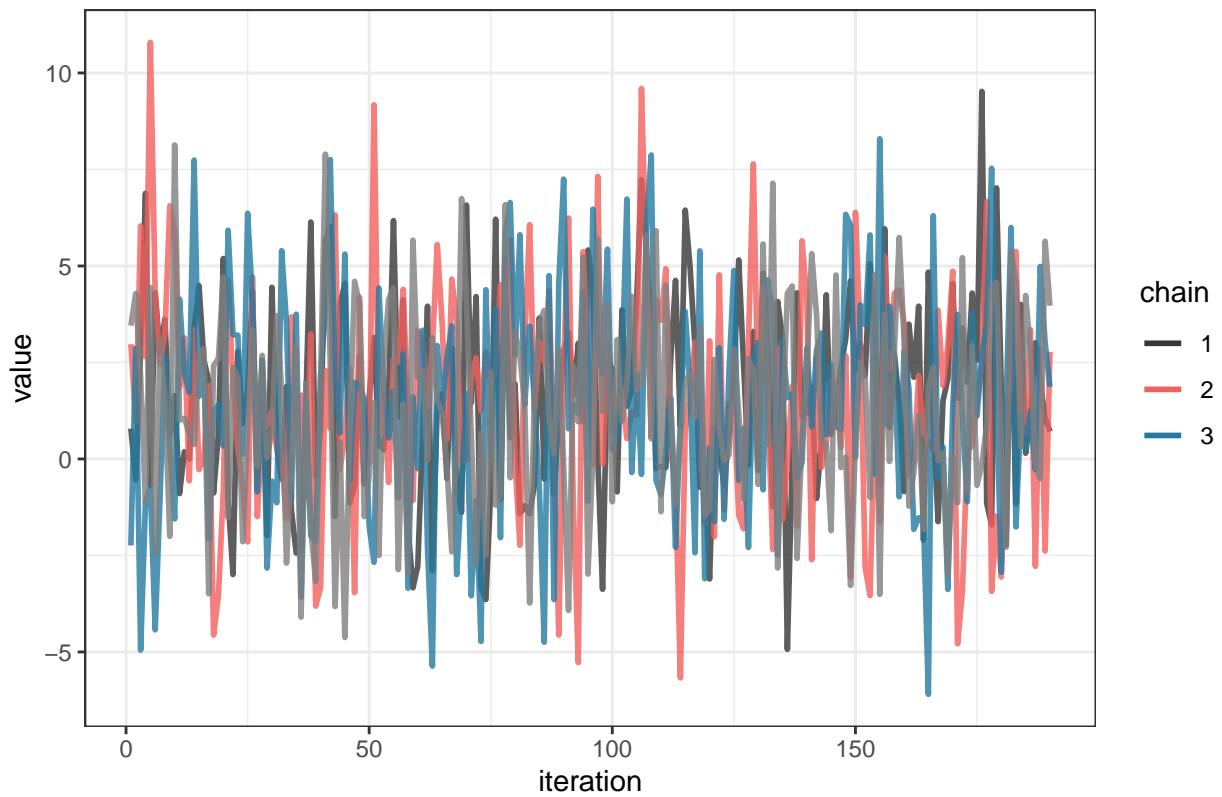
Traceplot of black.1



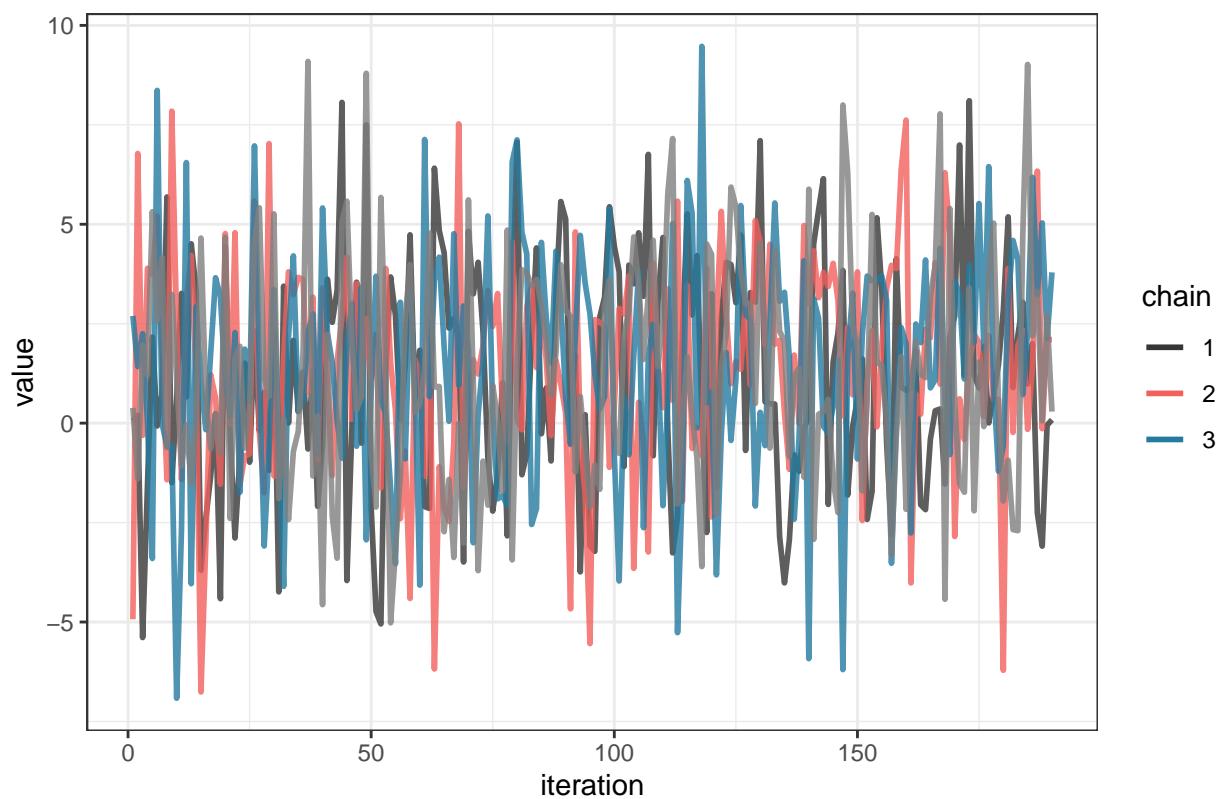
Traceplot of hypertension.1



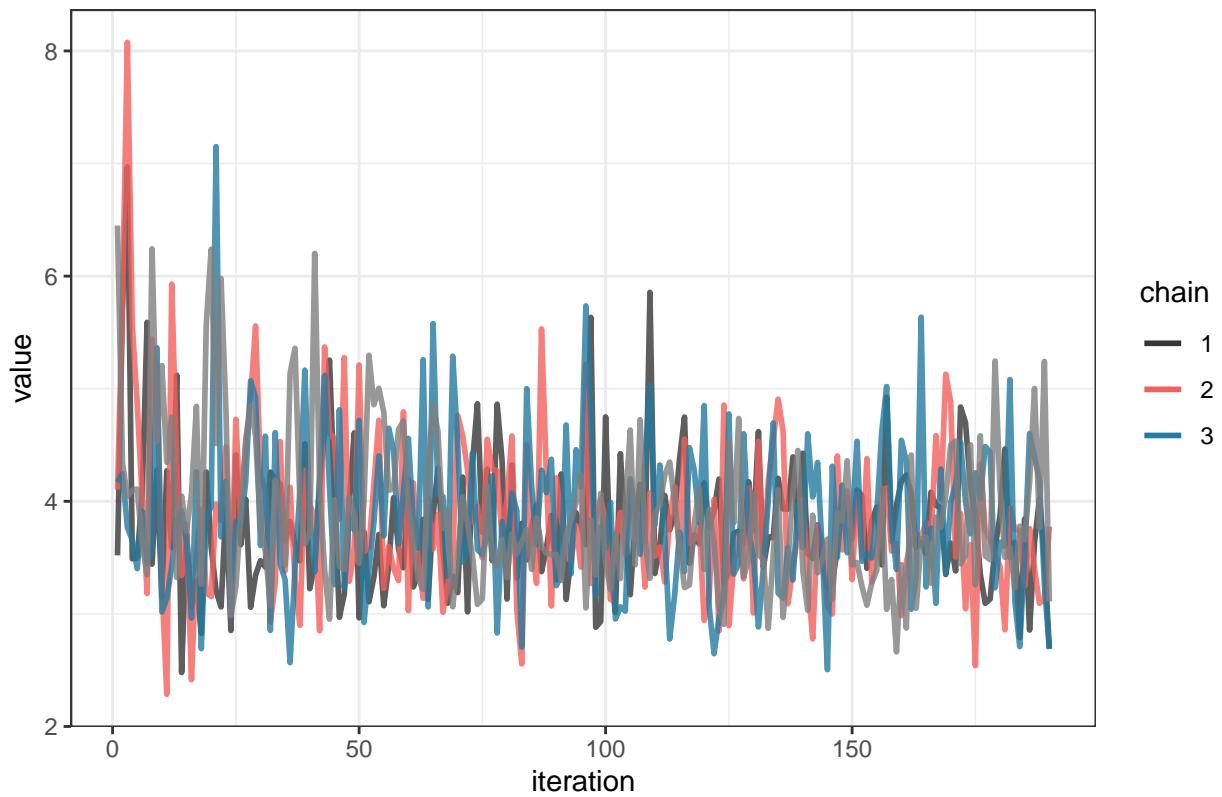
Traceplot of mmf.1



Traceplot of cyc.1

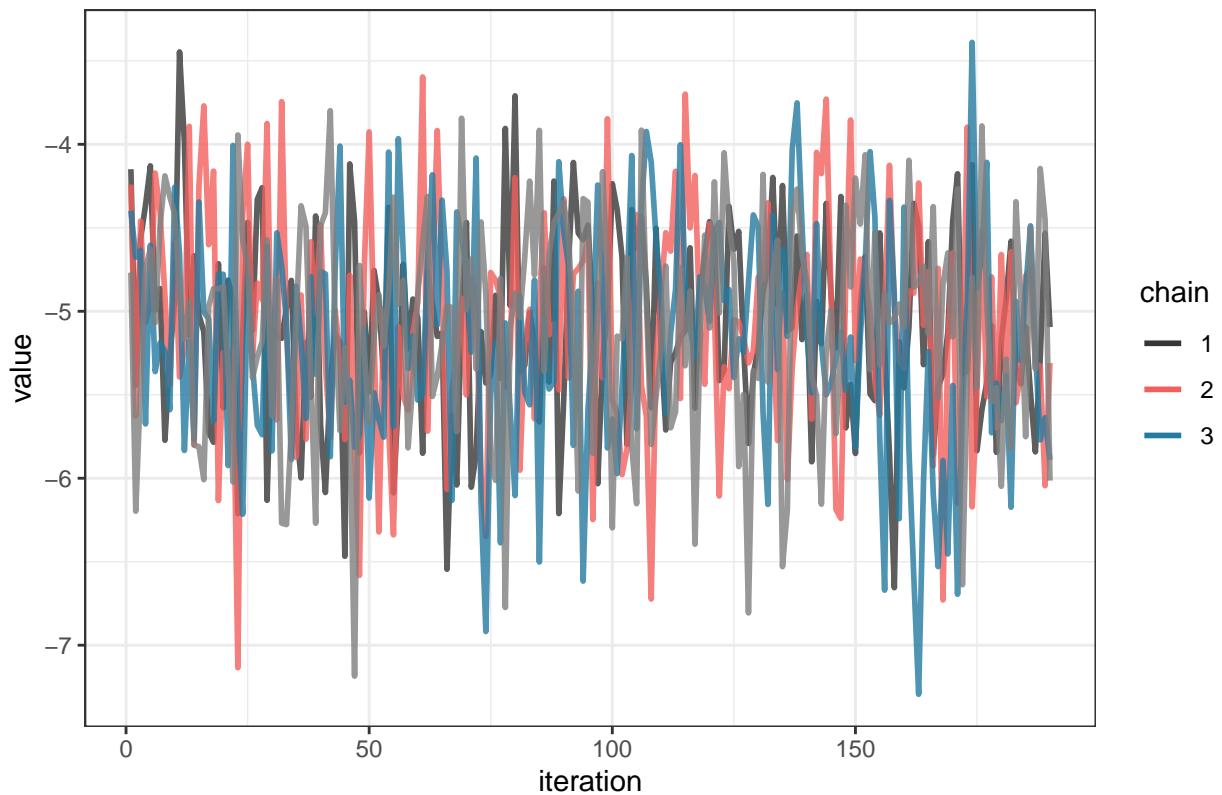


Traceplot of sigmas_1

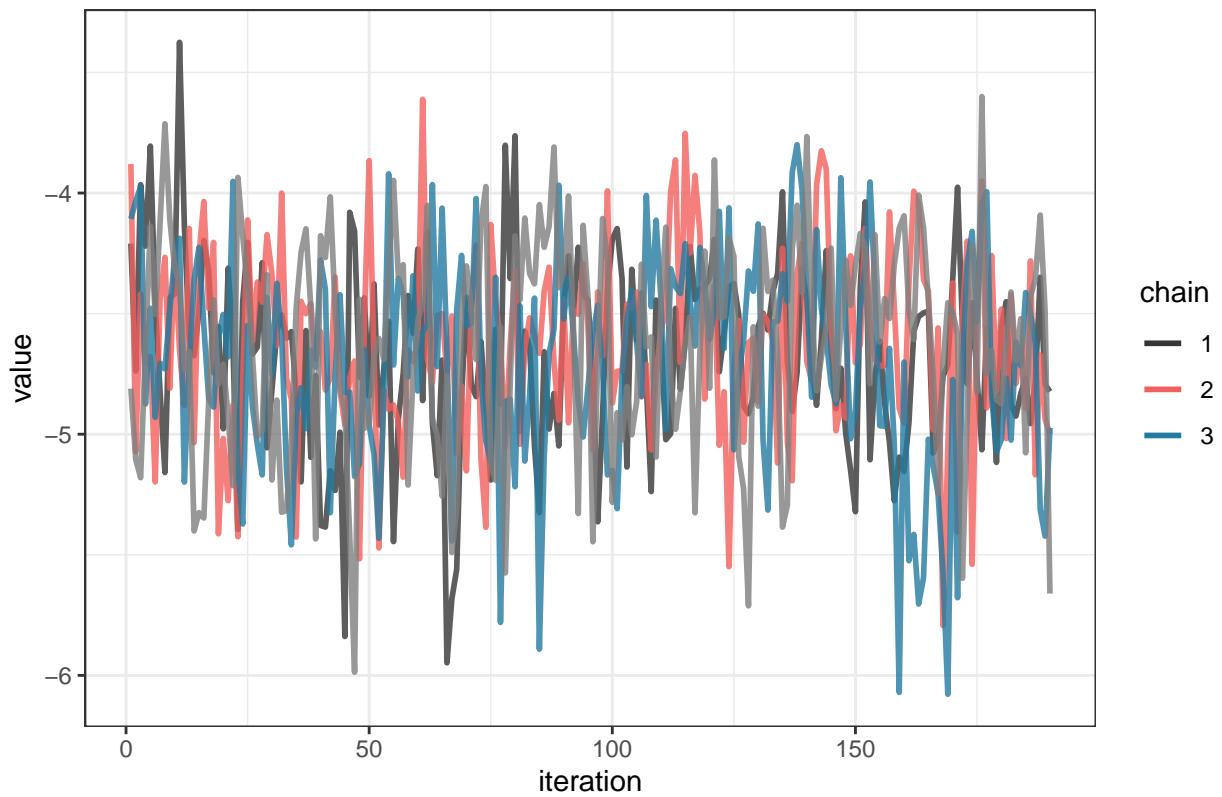


```
traceplt2 <- ggtraceplot(jointFit2)
```

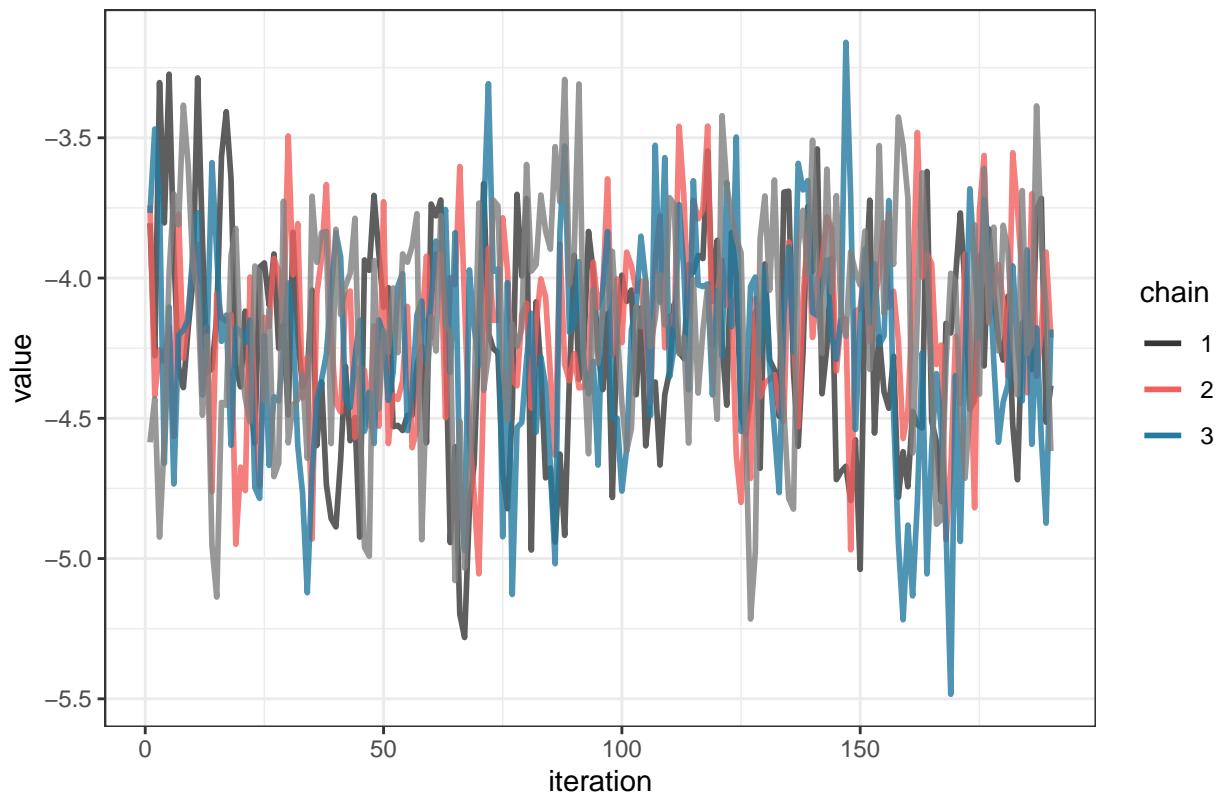
Traceplot of bs_gammas_1



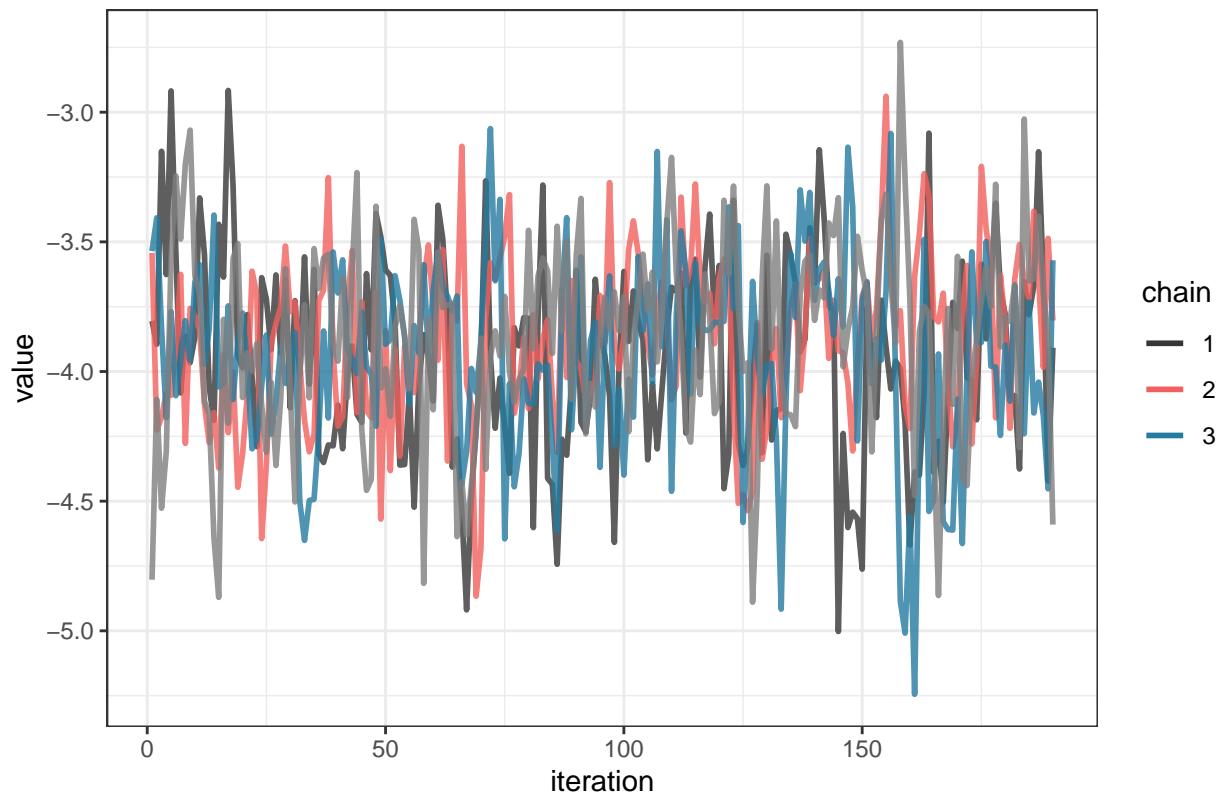
Traceplot of bs_gammas_2



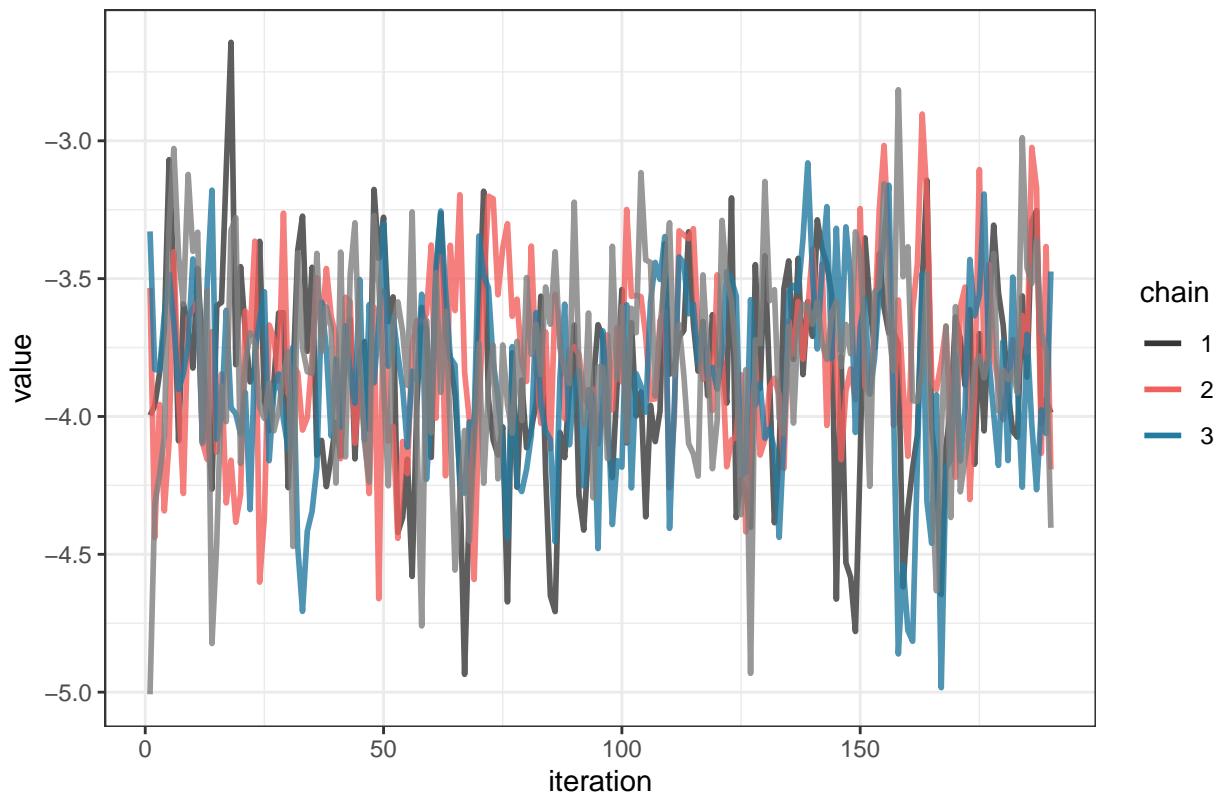
Traceplot of bs_gammas_3



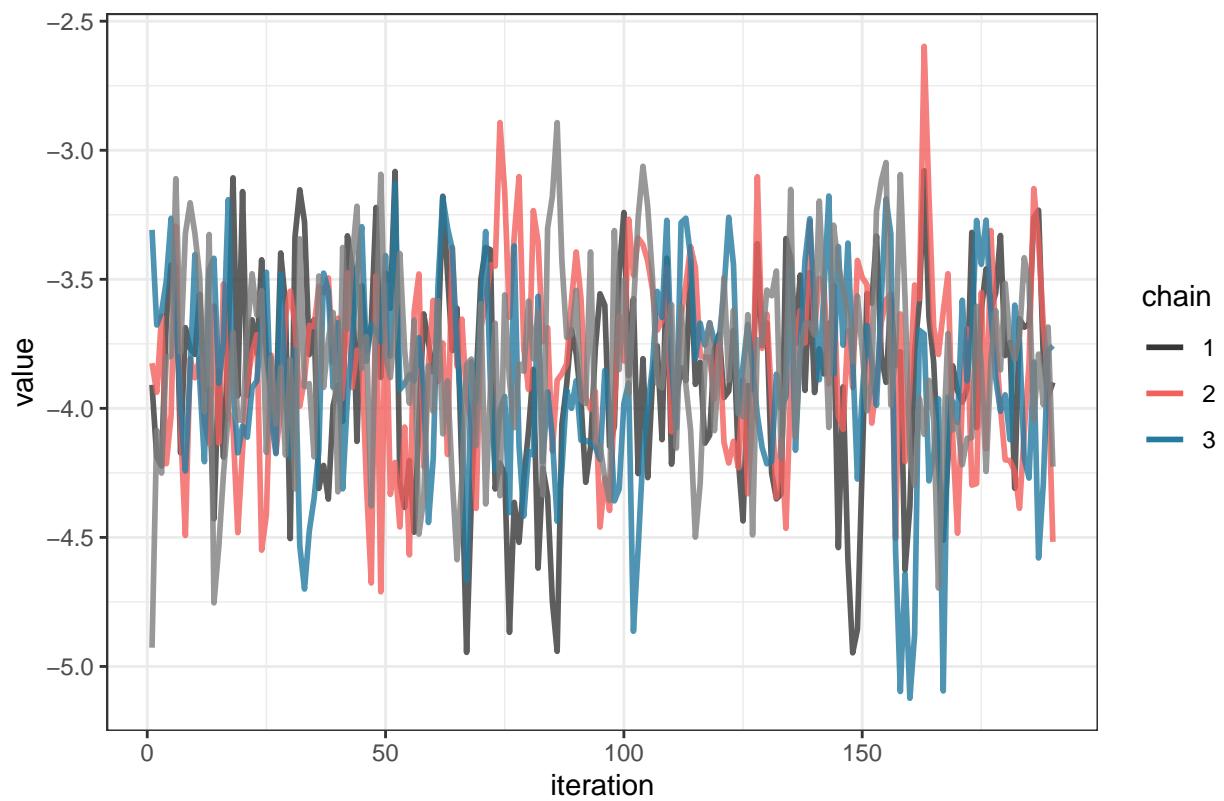
Traceplot of bs_gammas_4



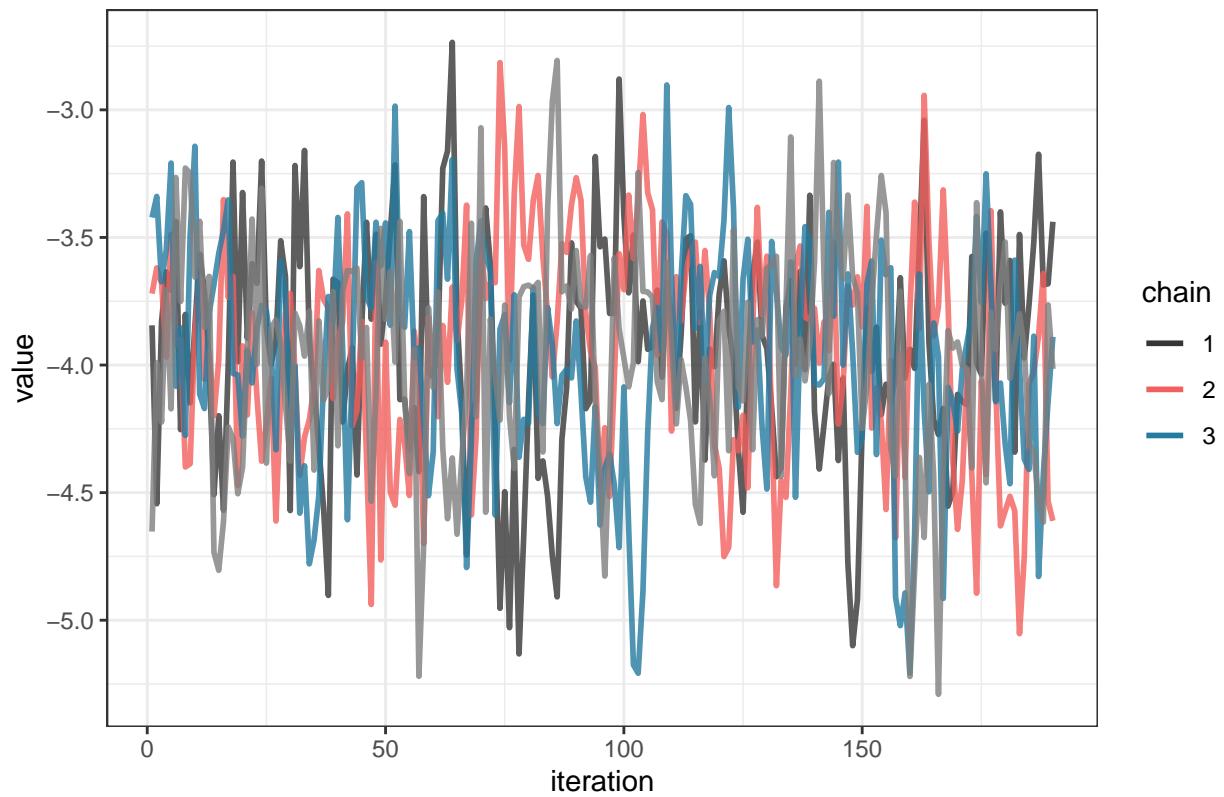
Traceplot of bs_gammas_5



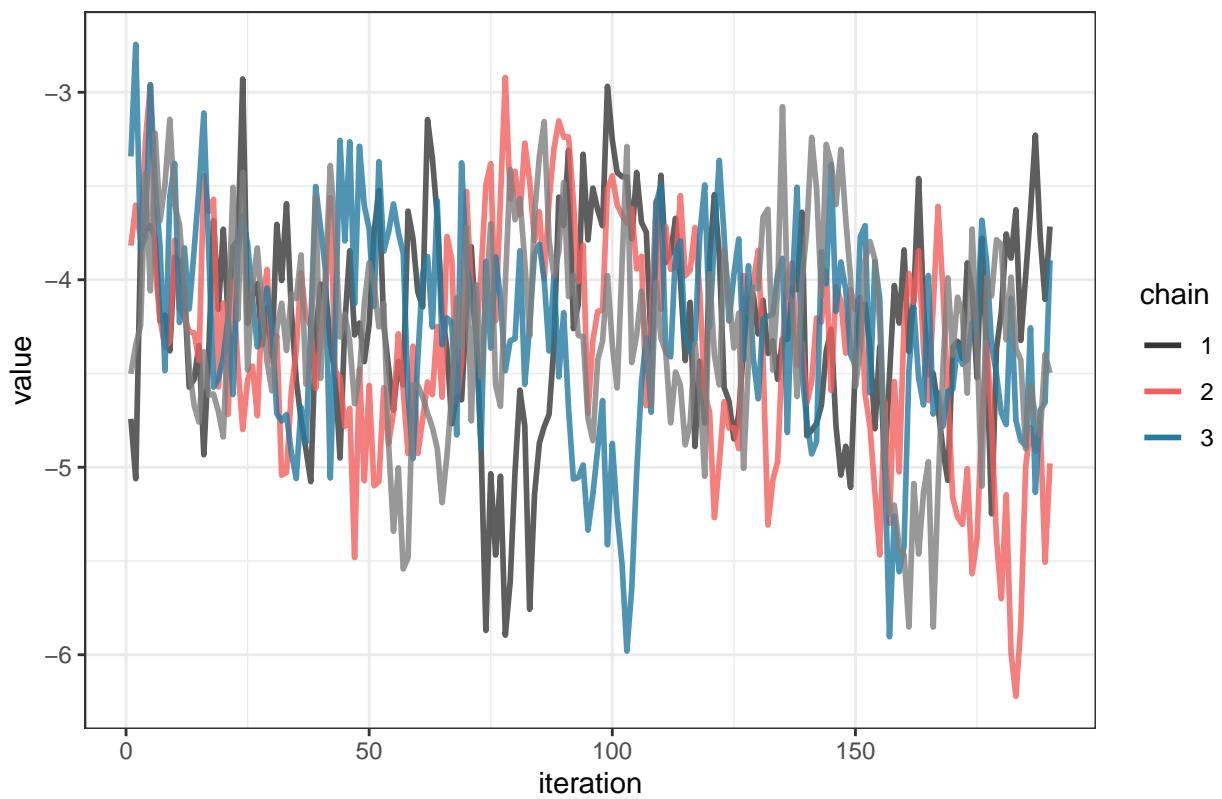
Traceplot of bs_gammas_6



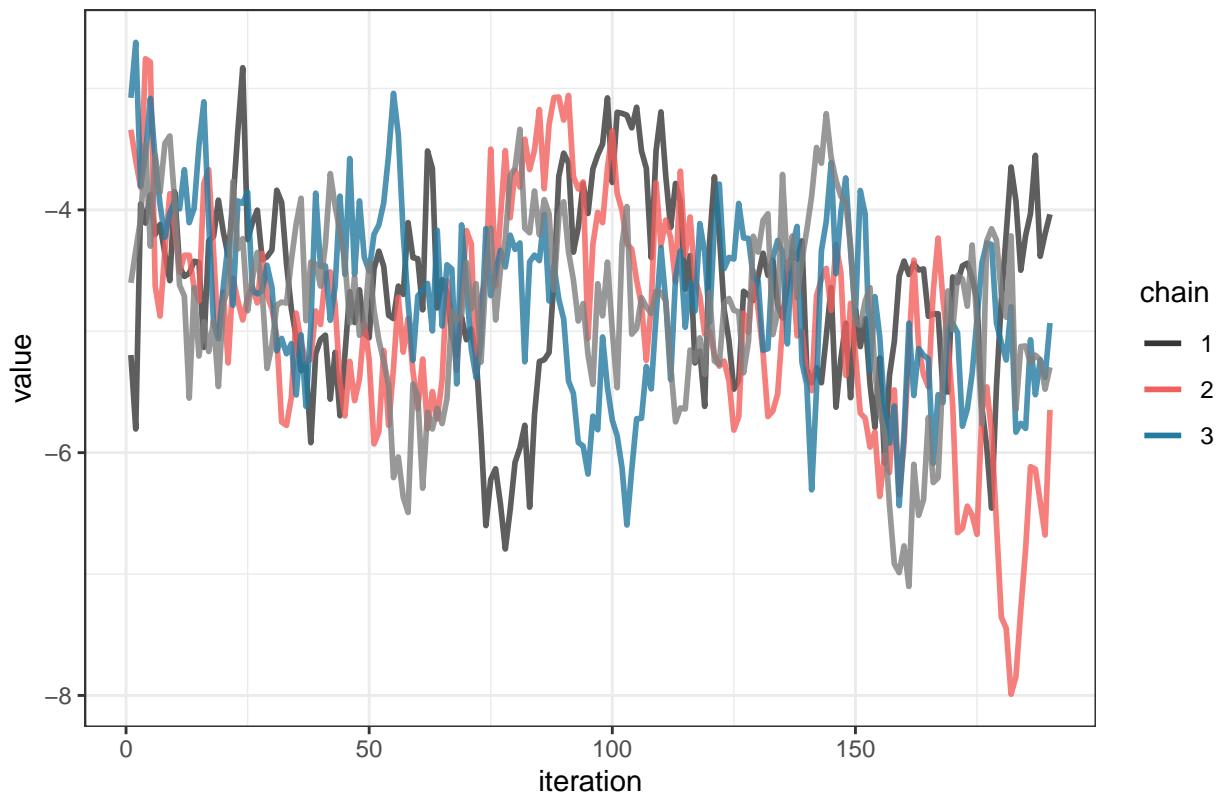
Traceplot of bs_gammas_7



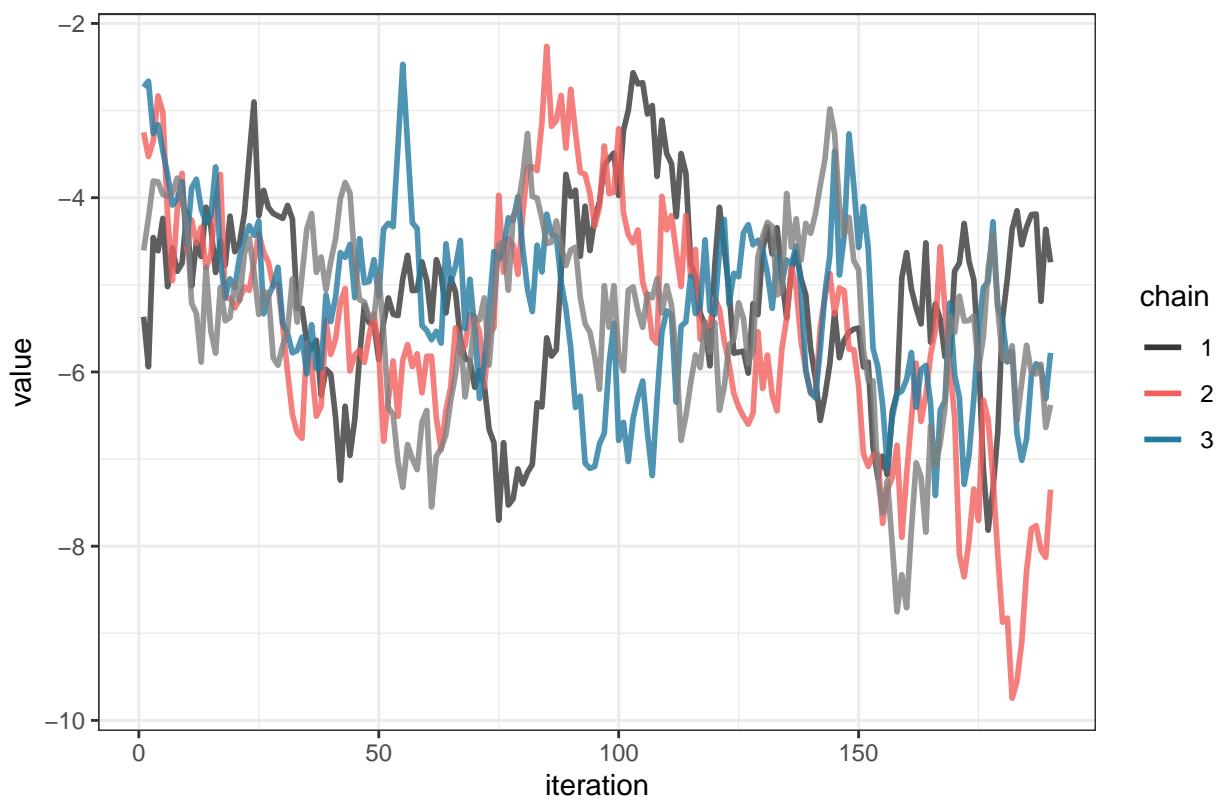
Traceplot of bs_gammas_8



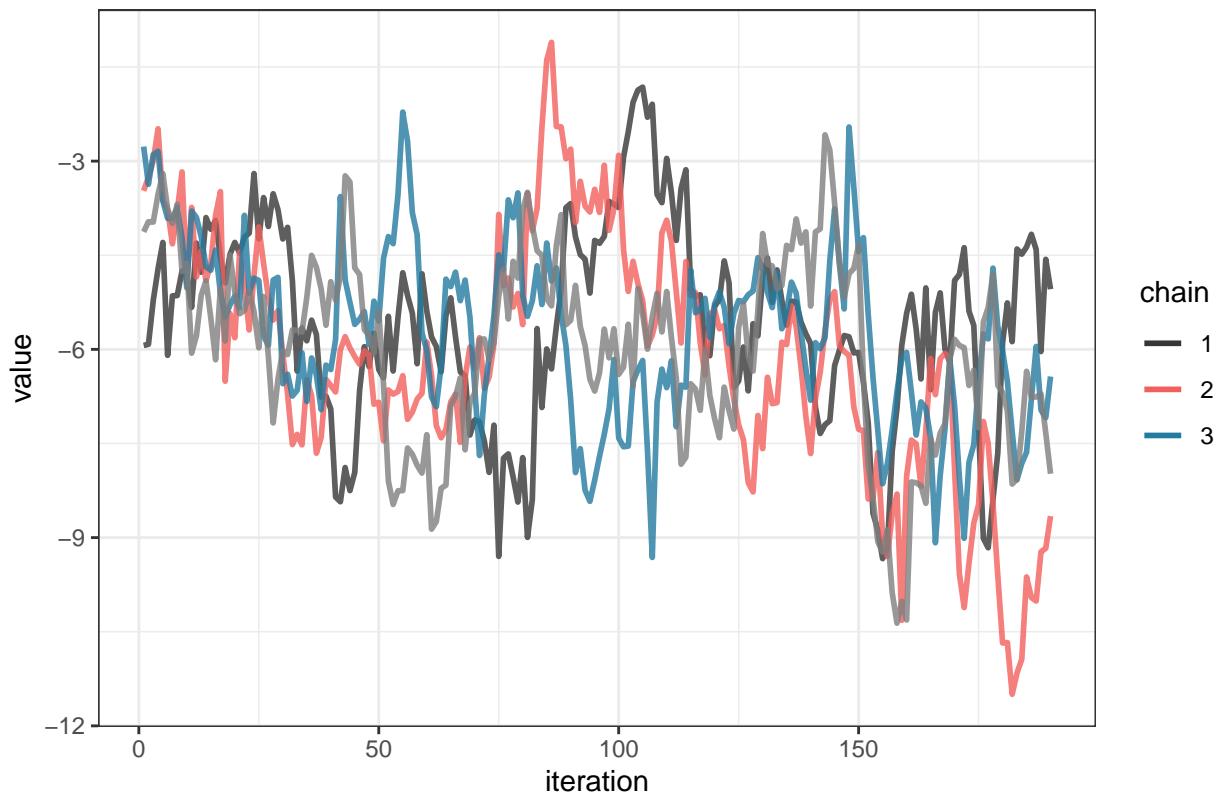
Traceplot of bs_gammas_9



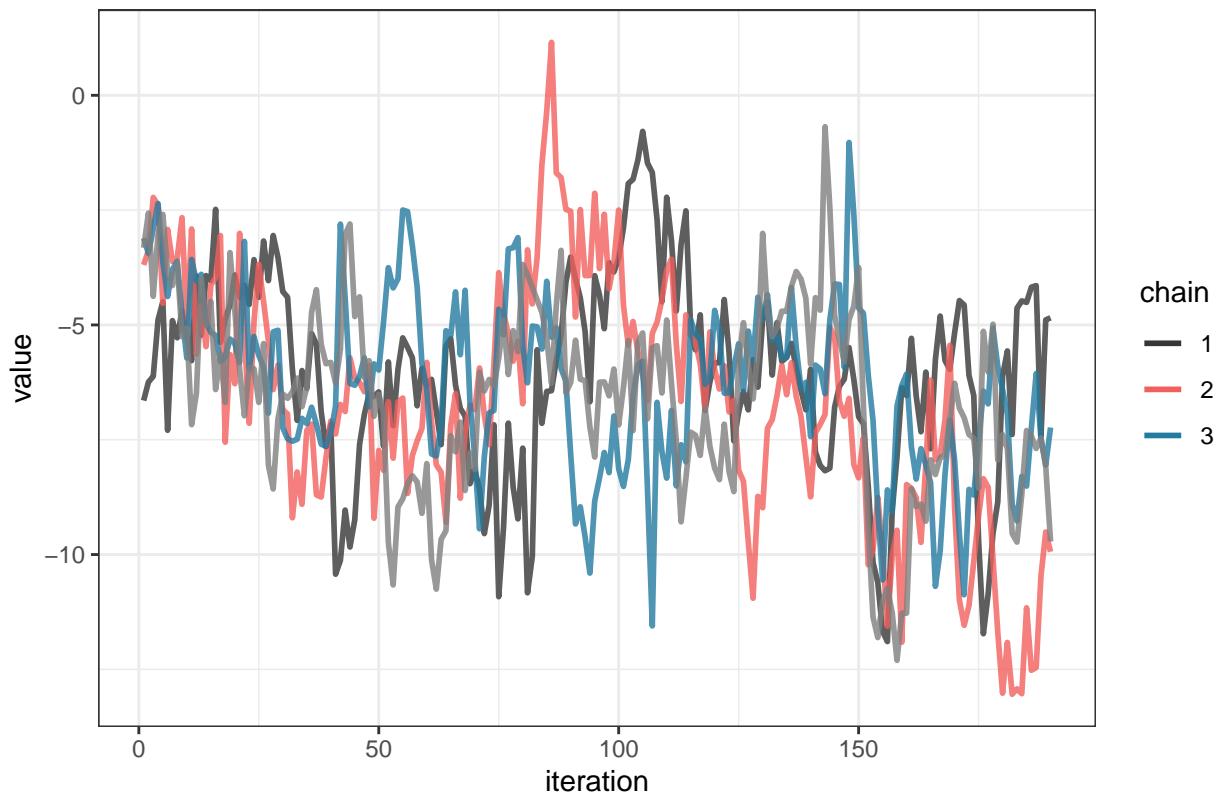
Traceplot of bs_gammas_10



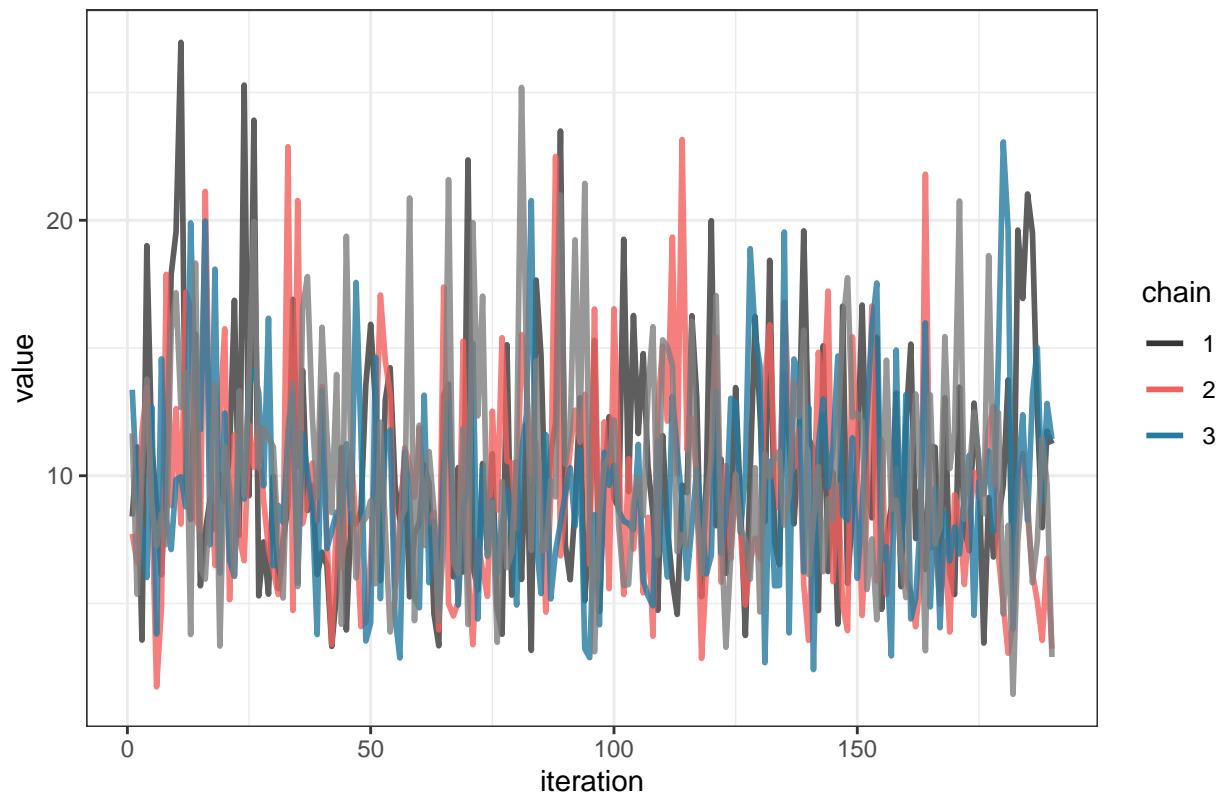
Traceplot of bs_gammas_11



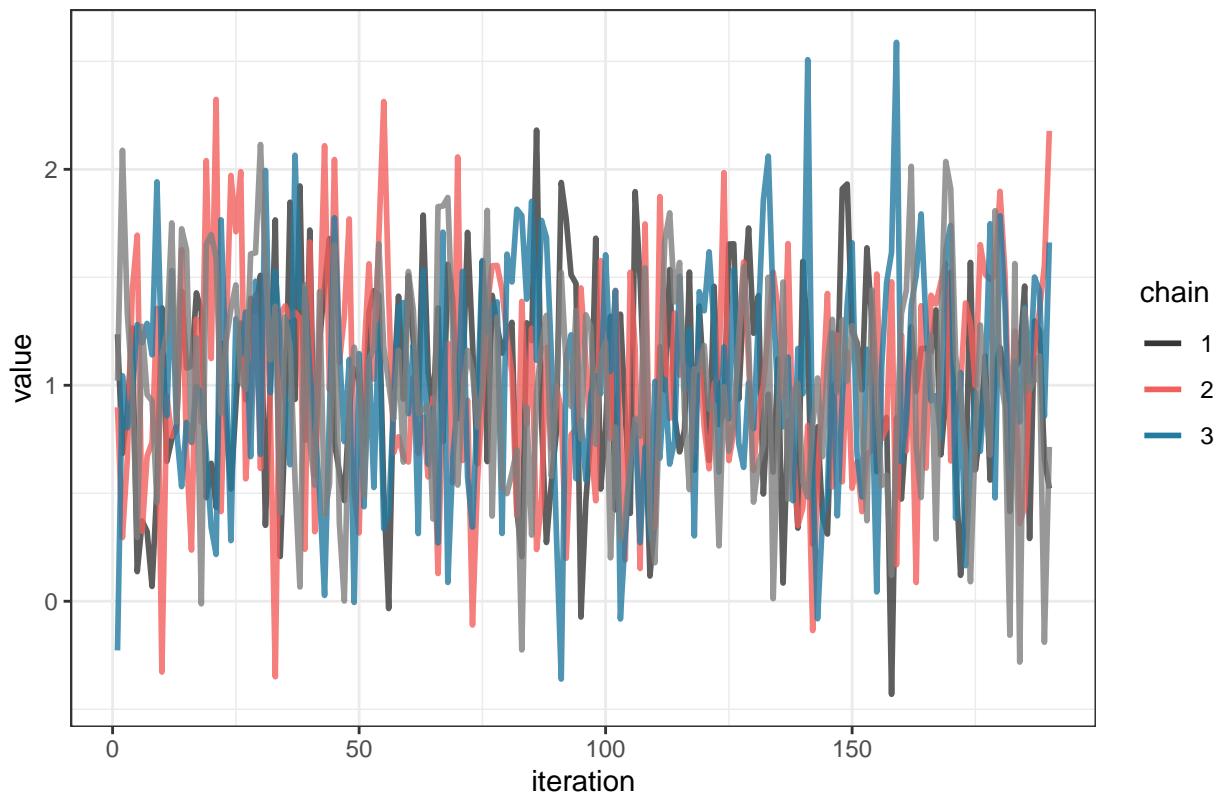
Traceplot of bs_gammas_12



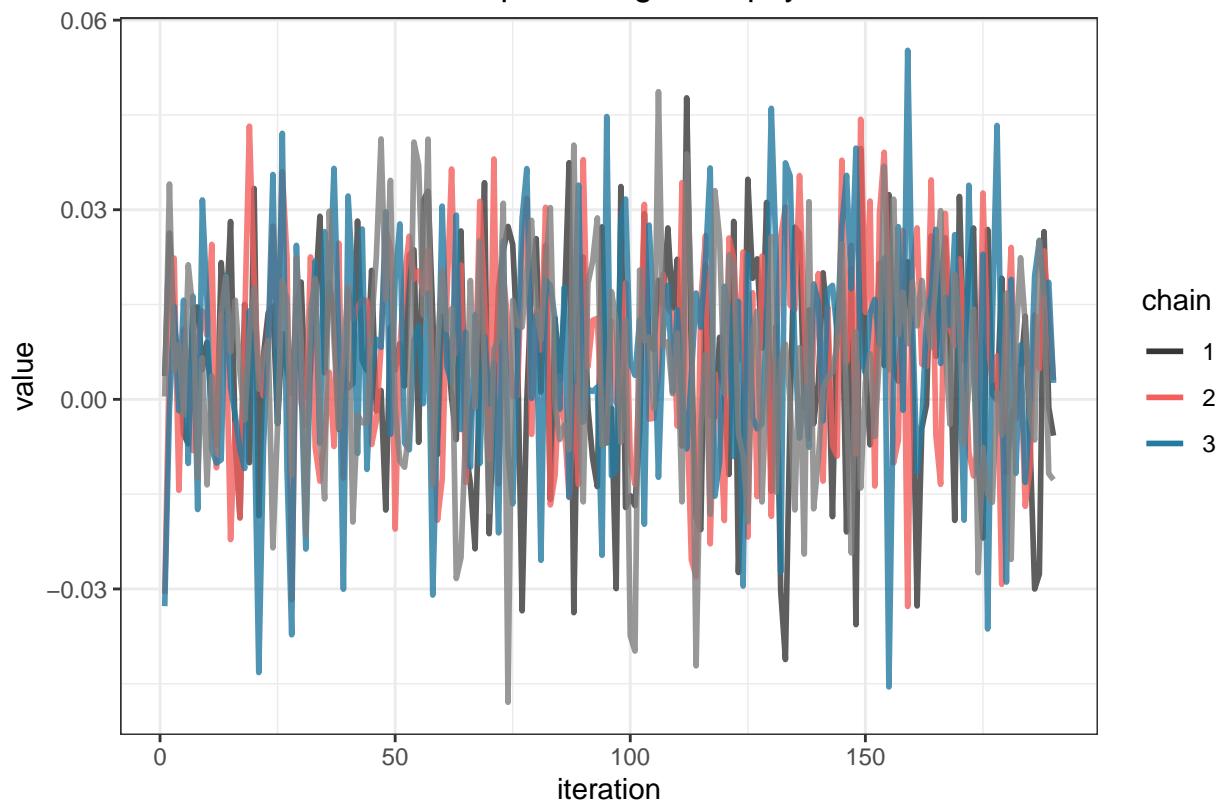
Traceplot of tau_bs_gammas



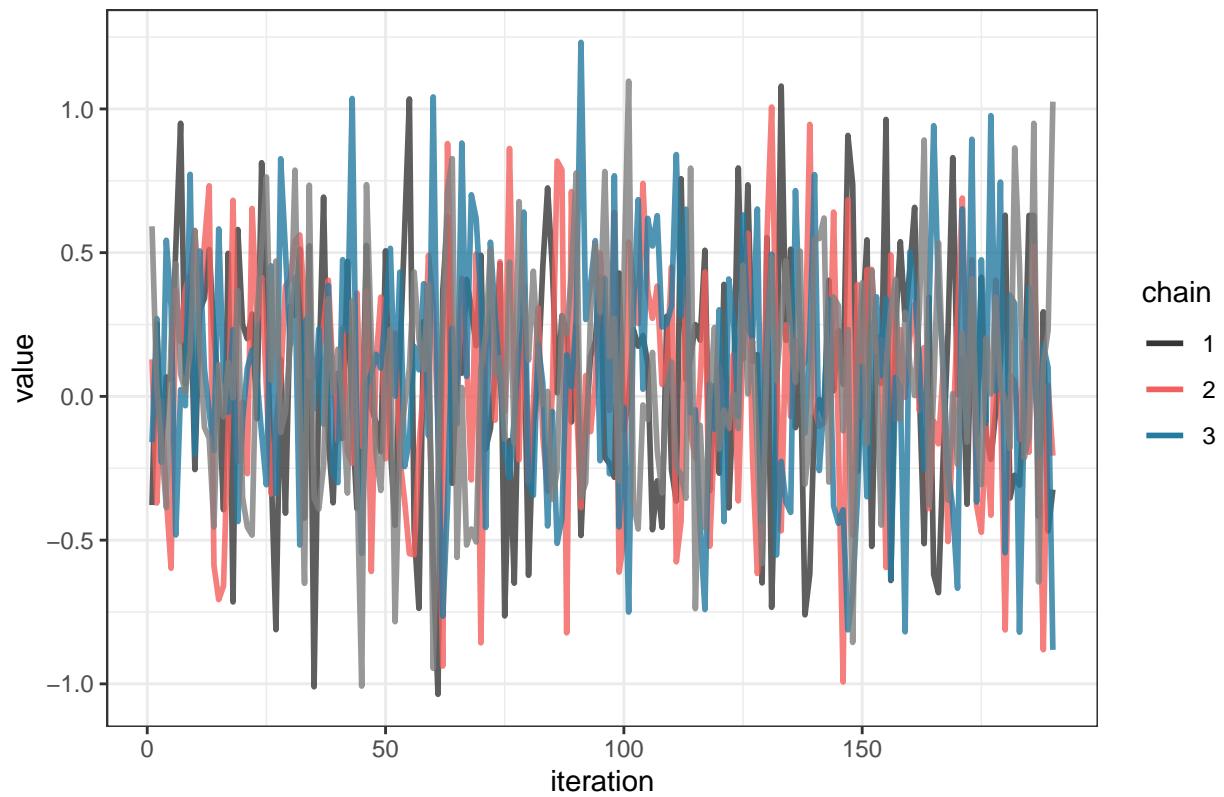
Traceplot of LOWC31



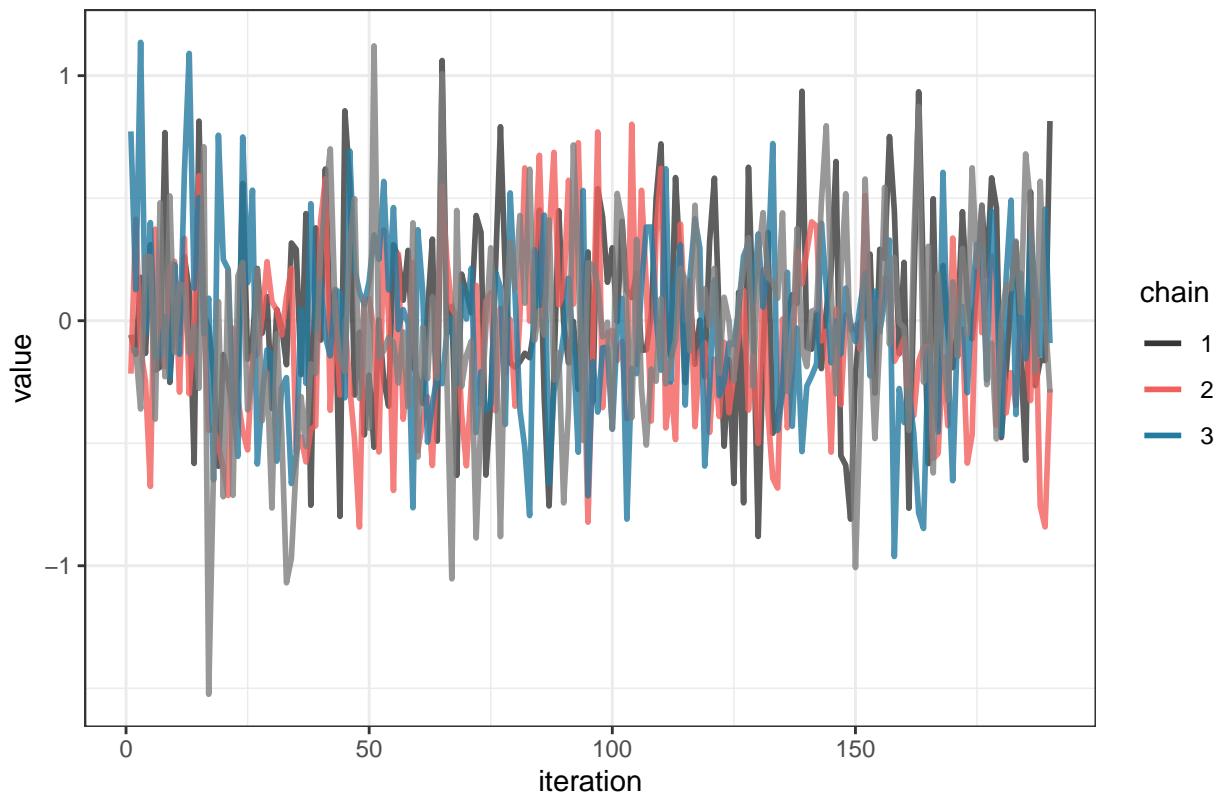
Traceplot of ageatbiopsy



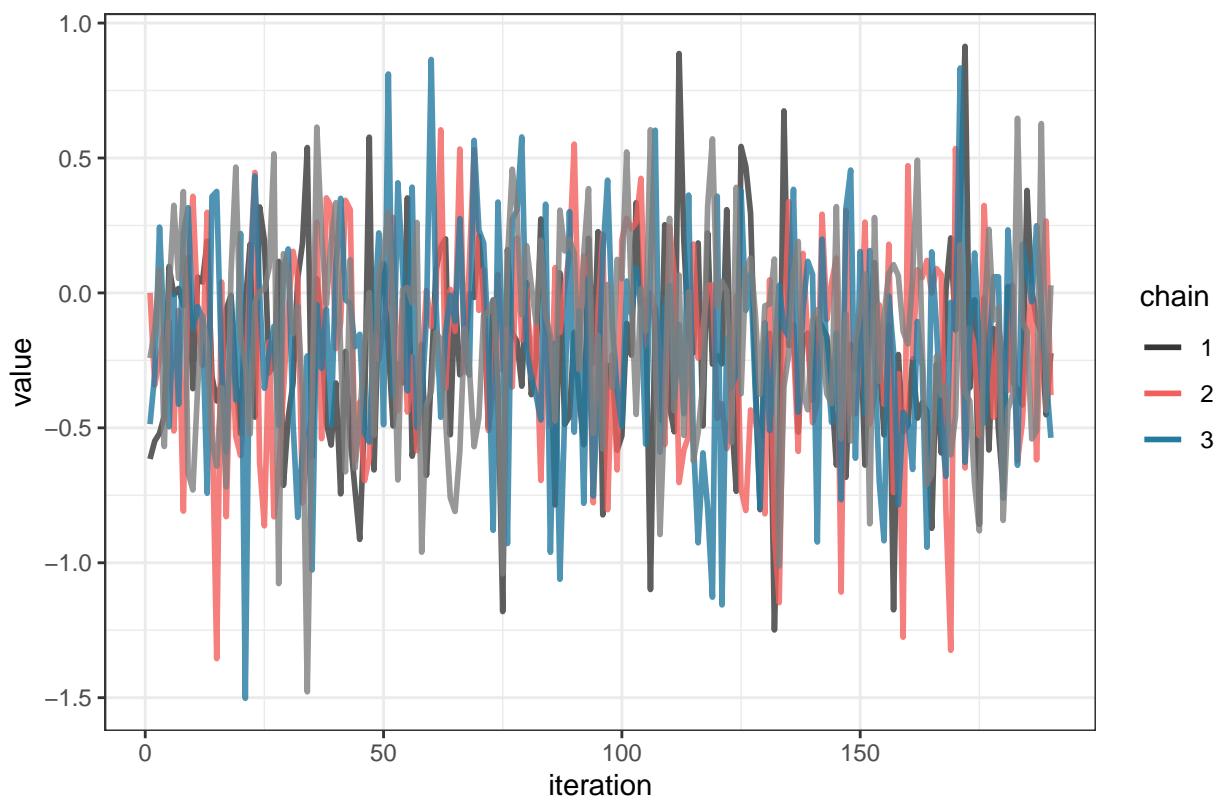
Traceplot of sex



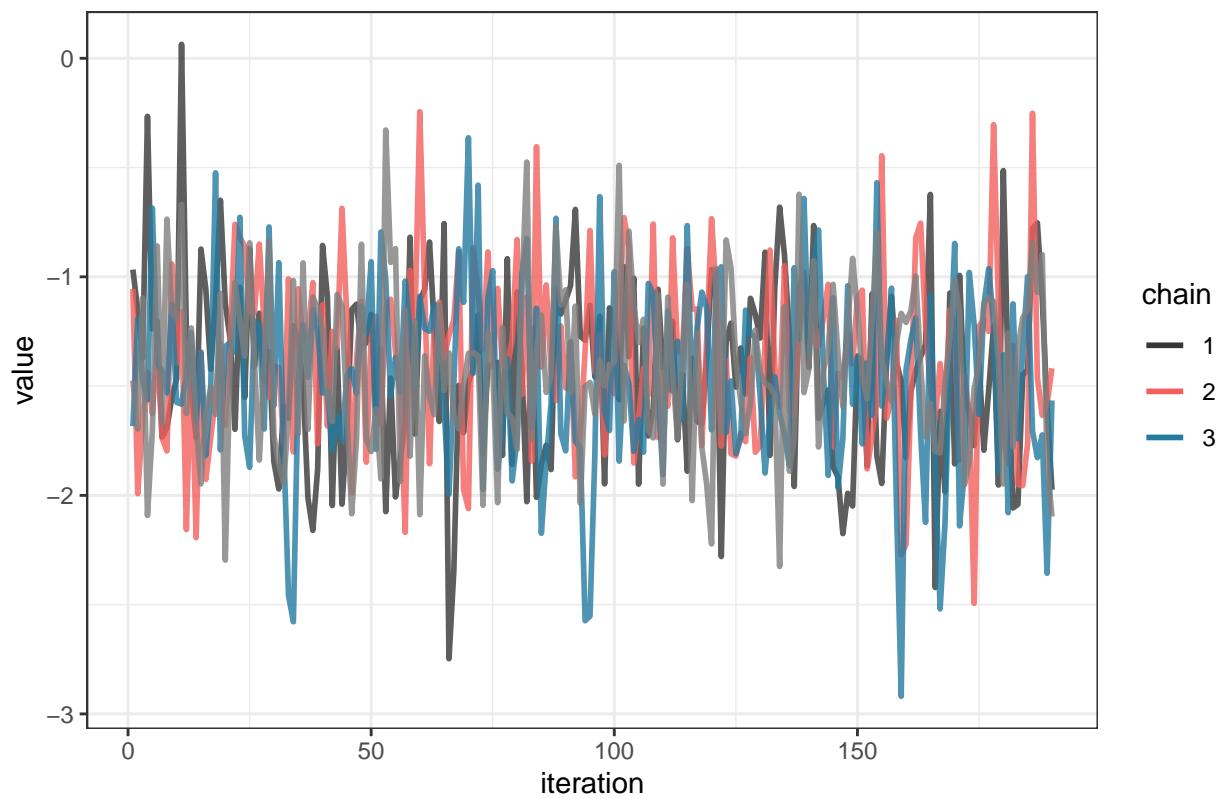
Traceplot of black



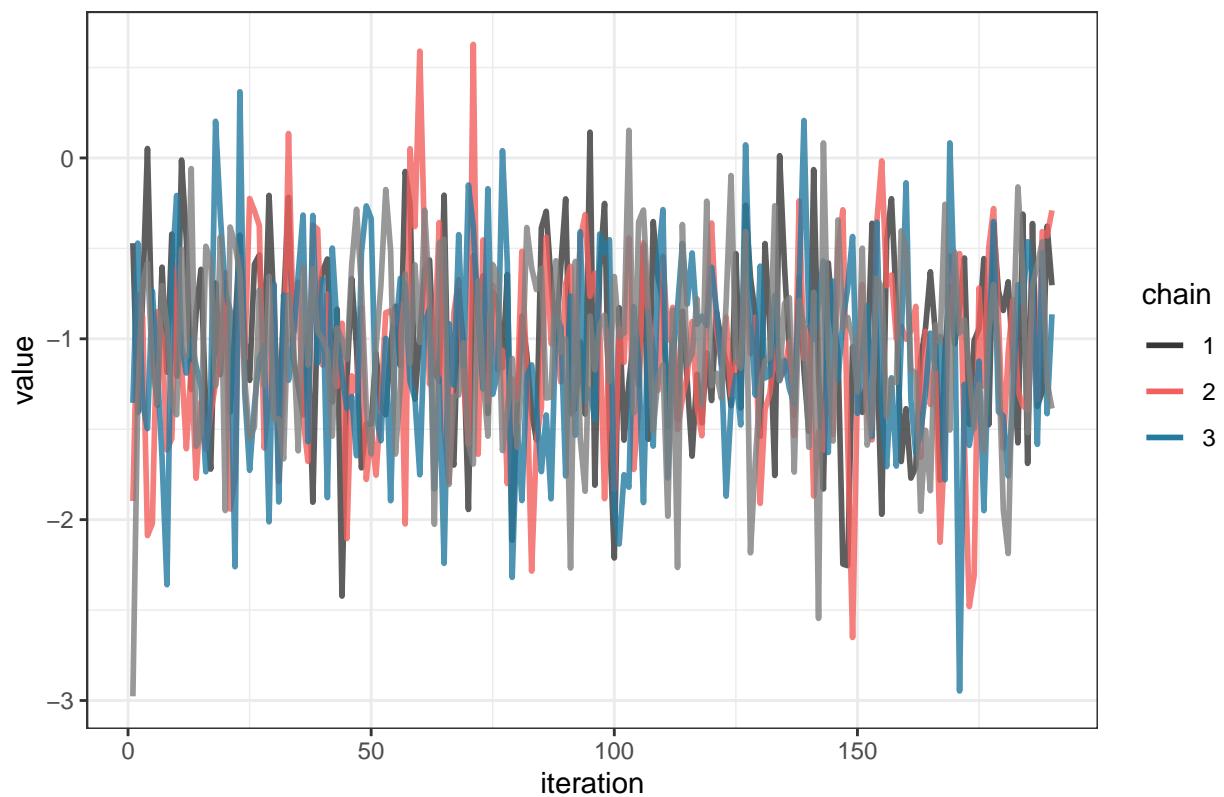
Traceplot of hypertension



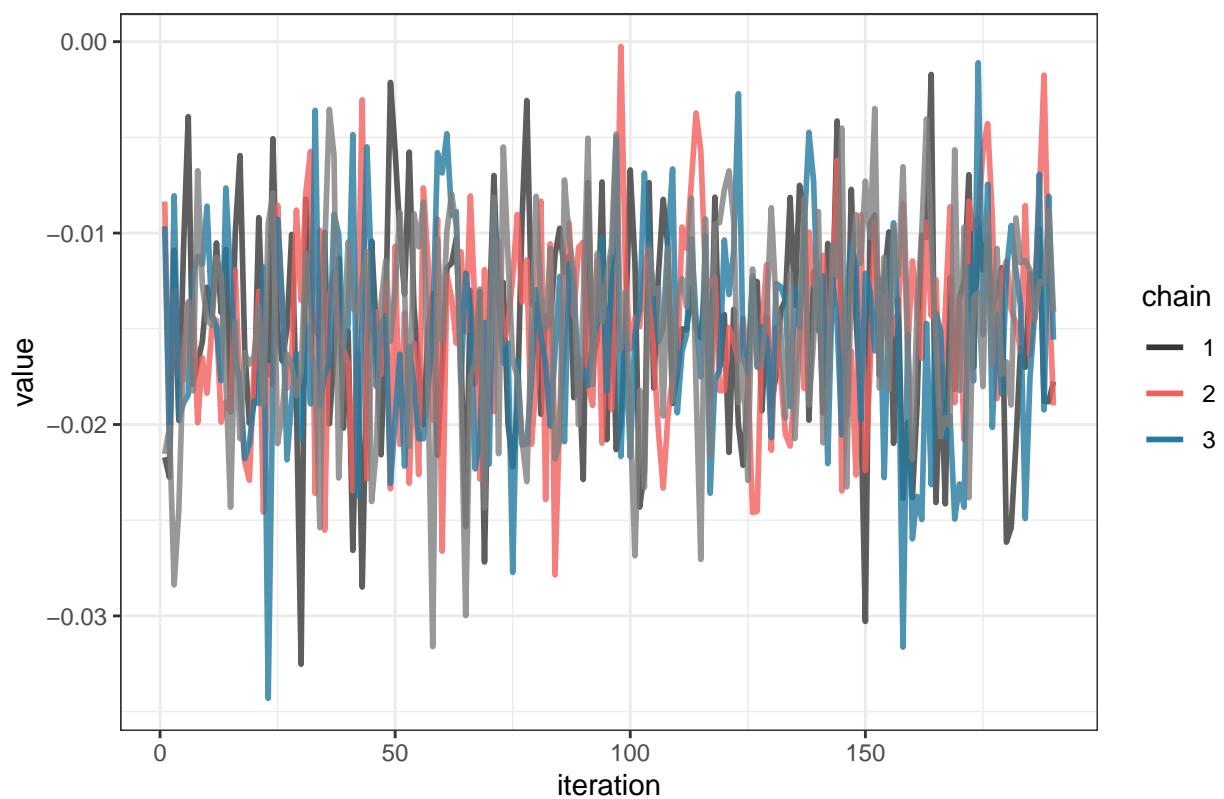
Traceplot of mmf



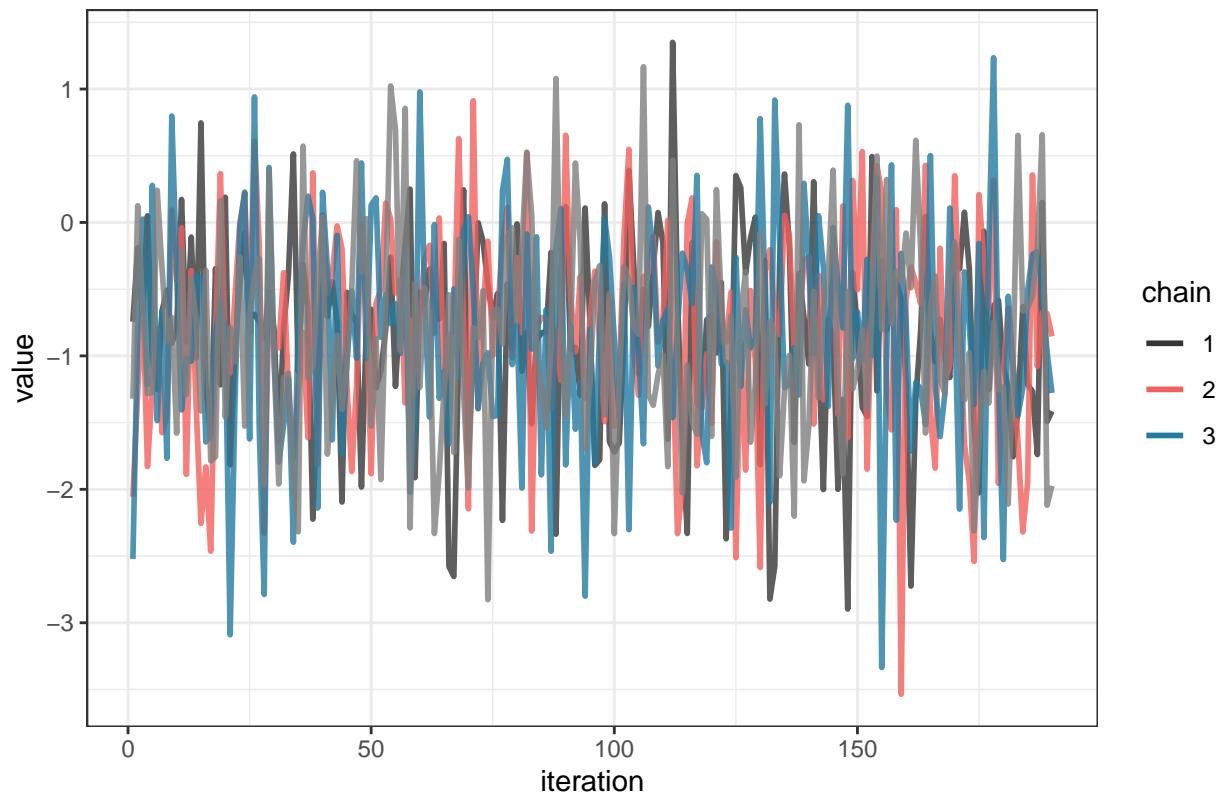
Traceplot of cyc



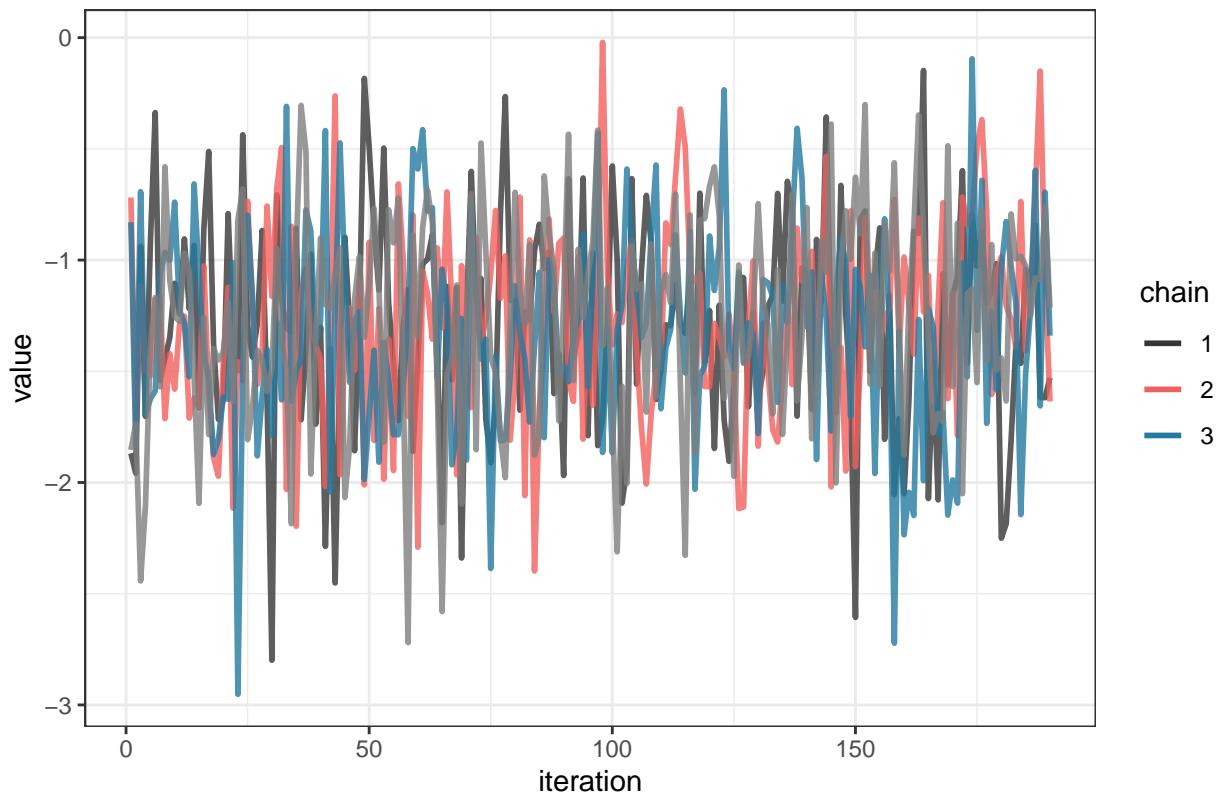
Traceplot of area(eGFR)



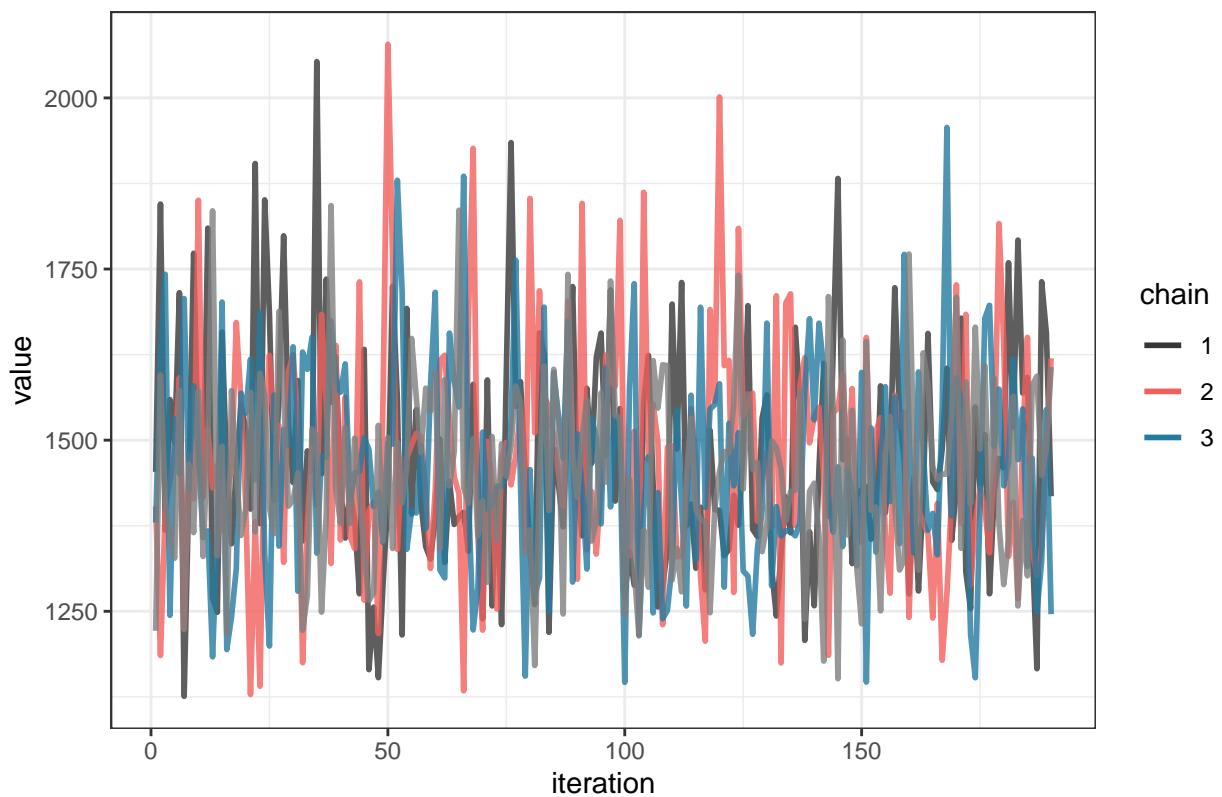
Traceplot of



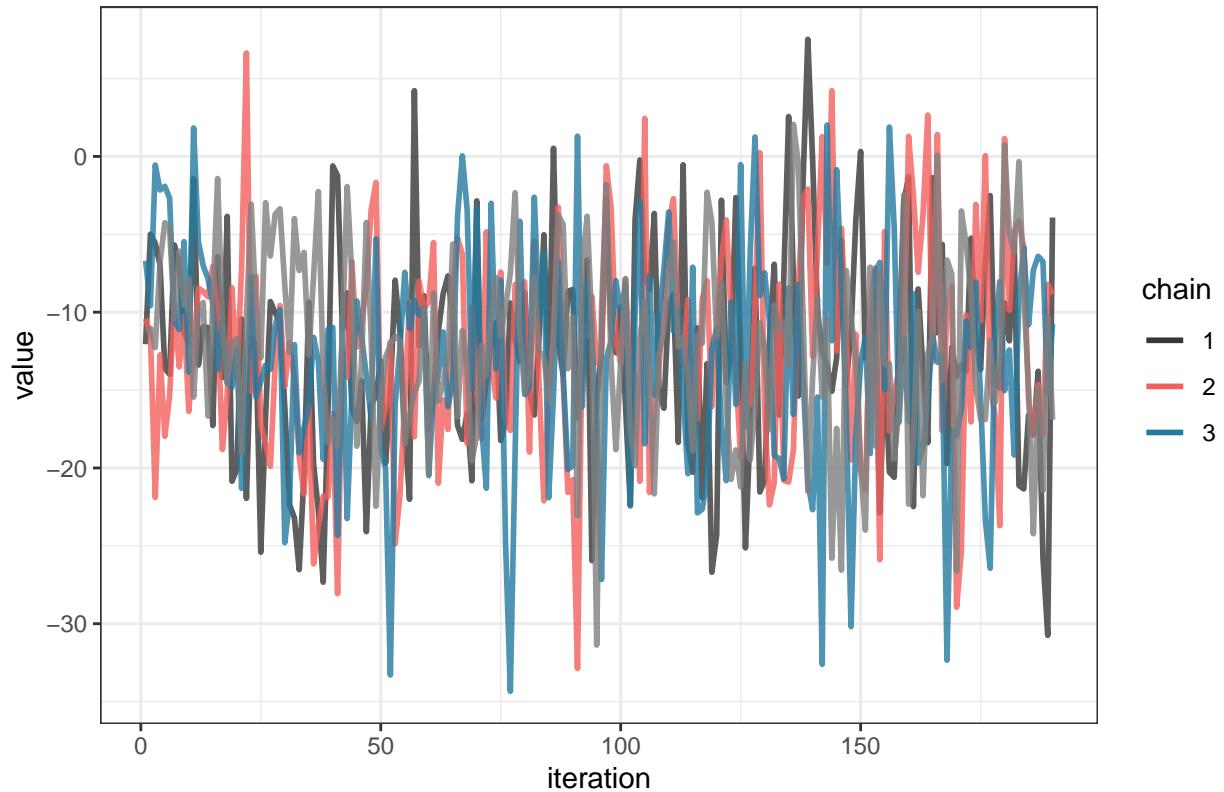
Traceplot of .1



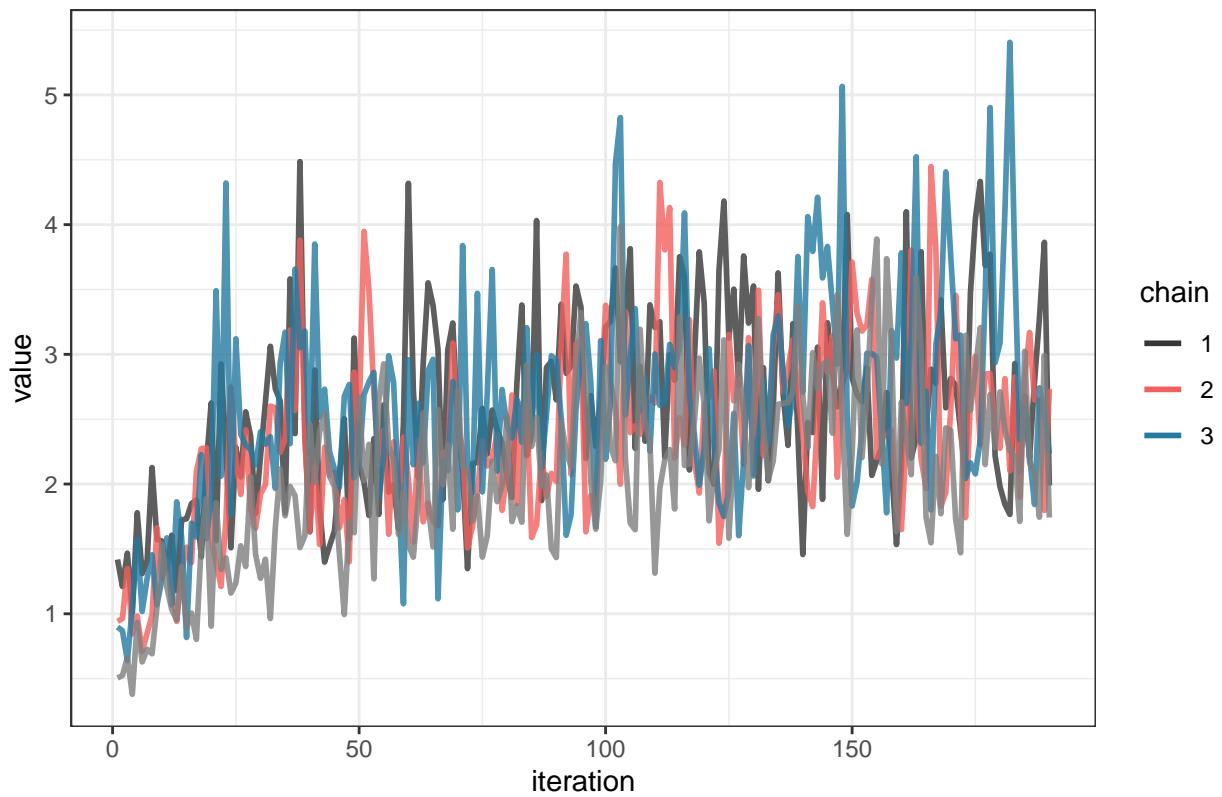
Traceplot of $D[1, 1]$



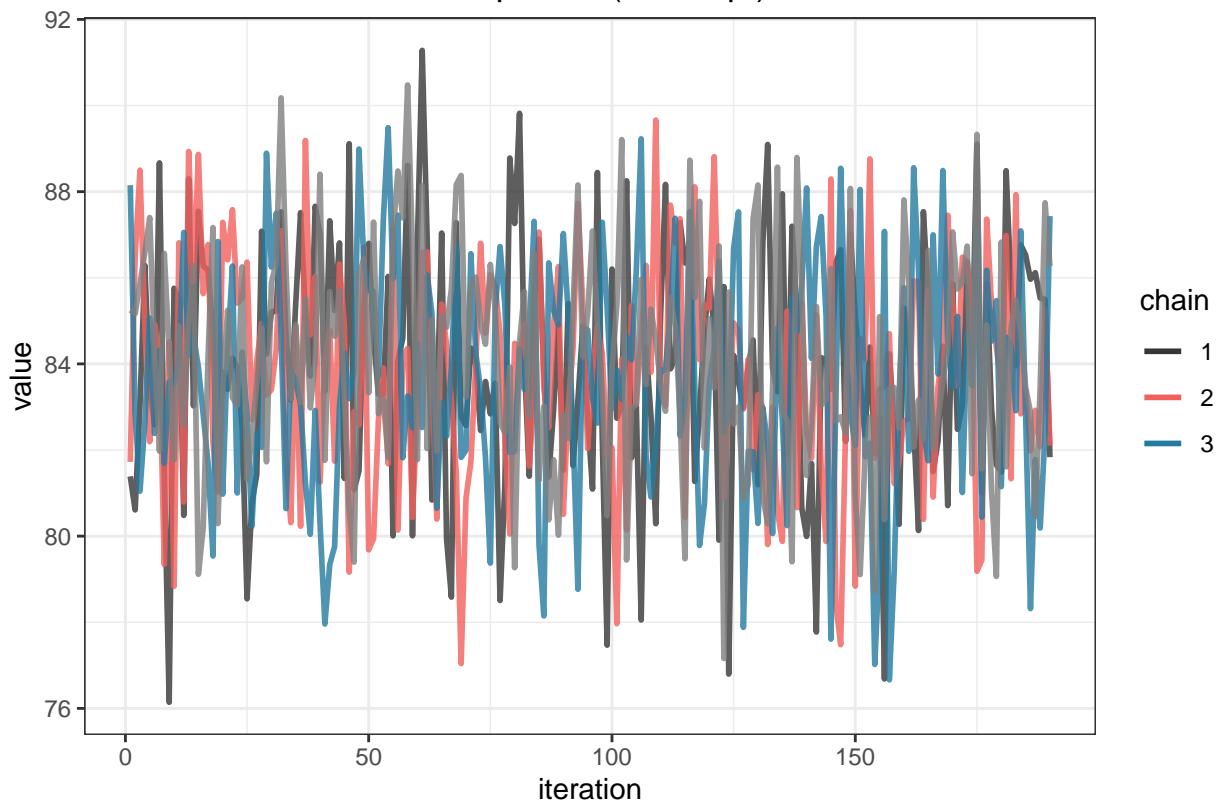
Traceplot of $D[2, 1]$



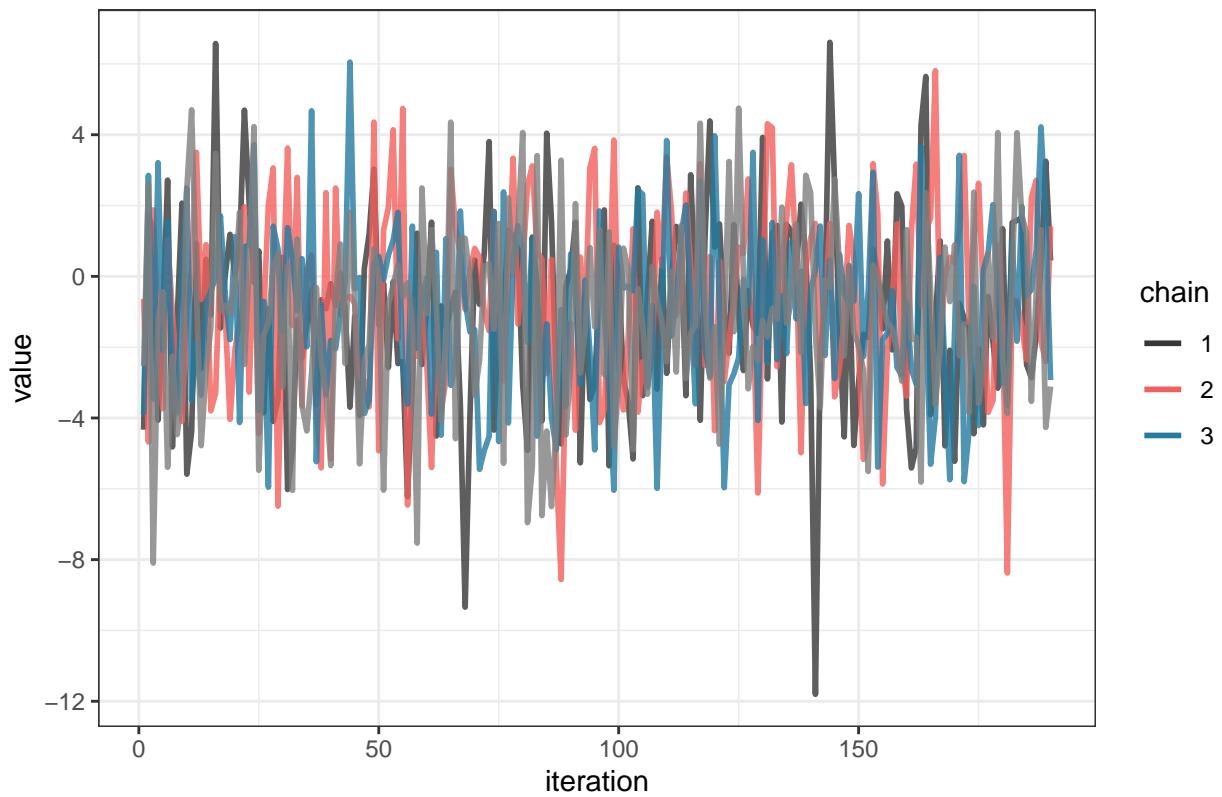
Traceplot of $D[2, 2]$



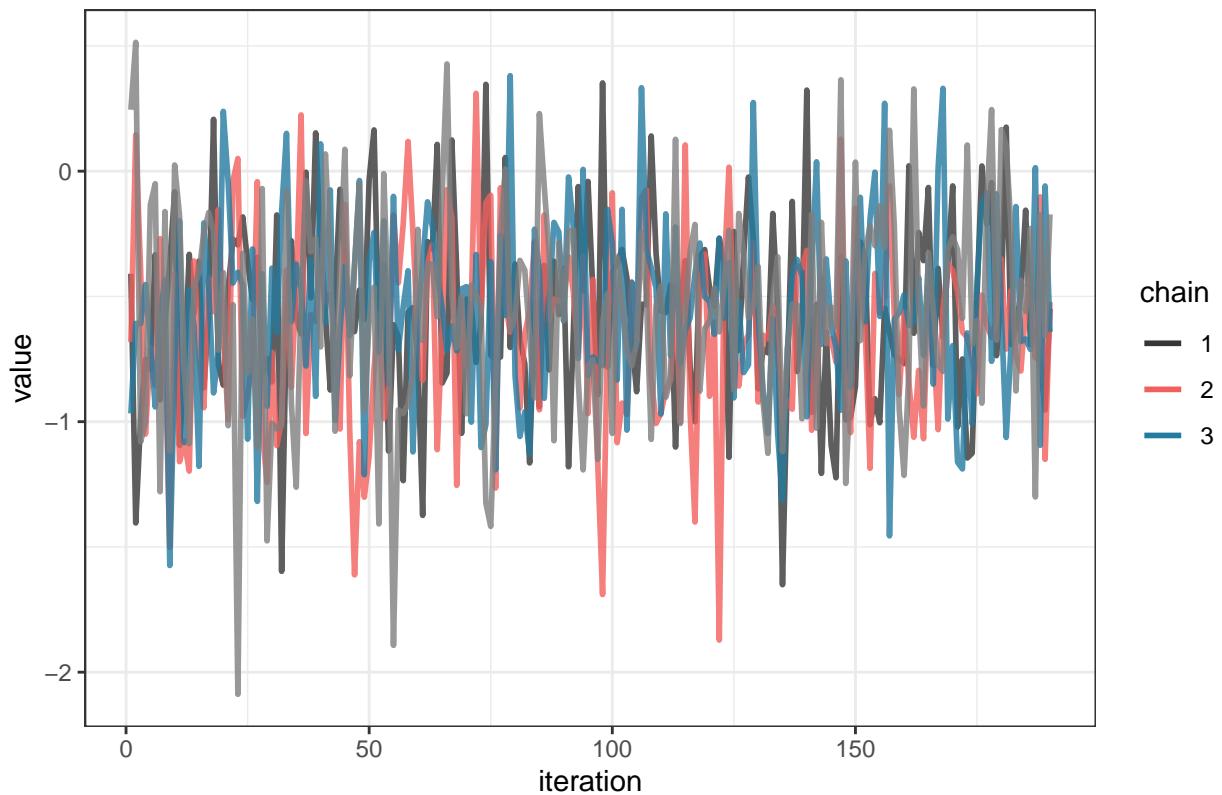
Traceplot of (Intercept)



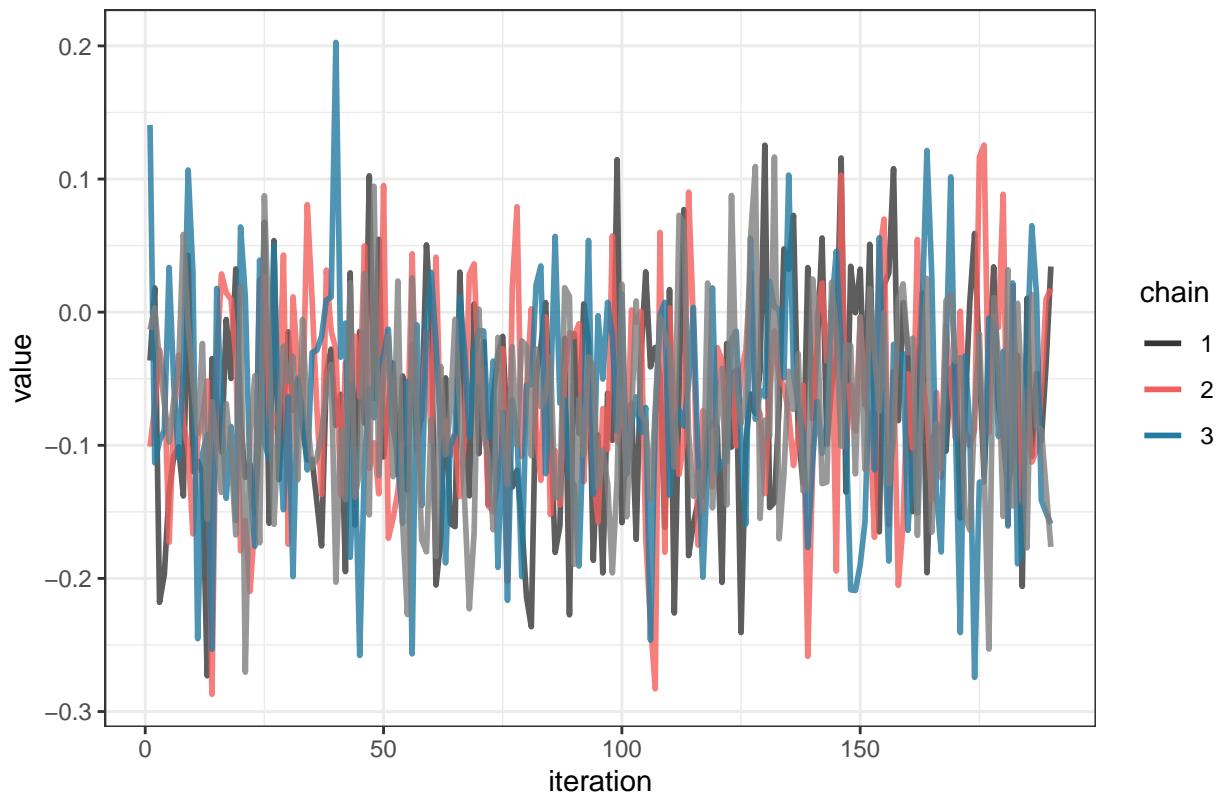
Traceplot of LOWC31.1



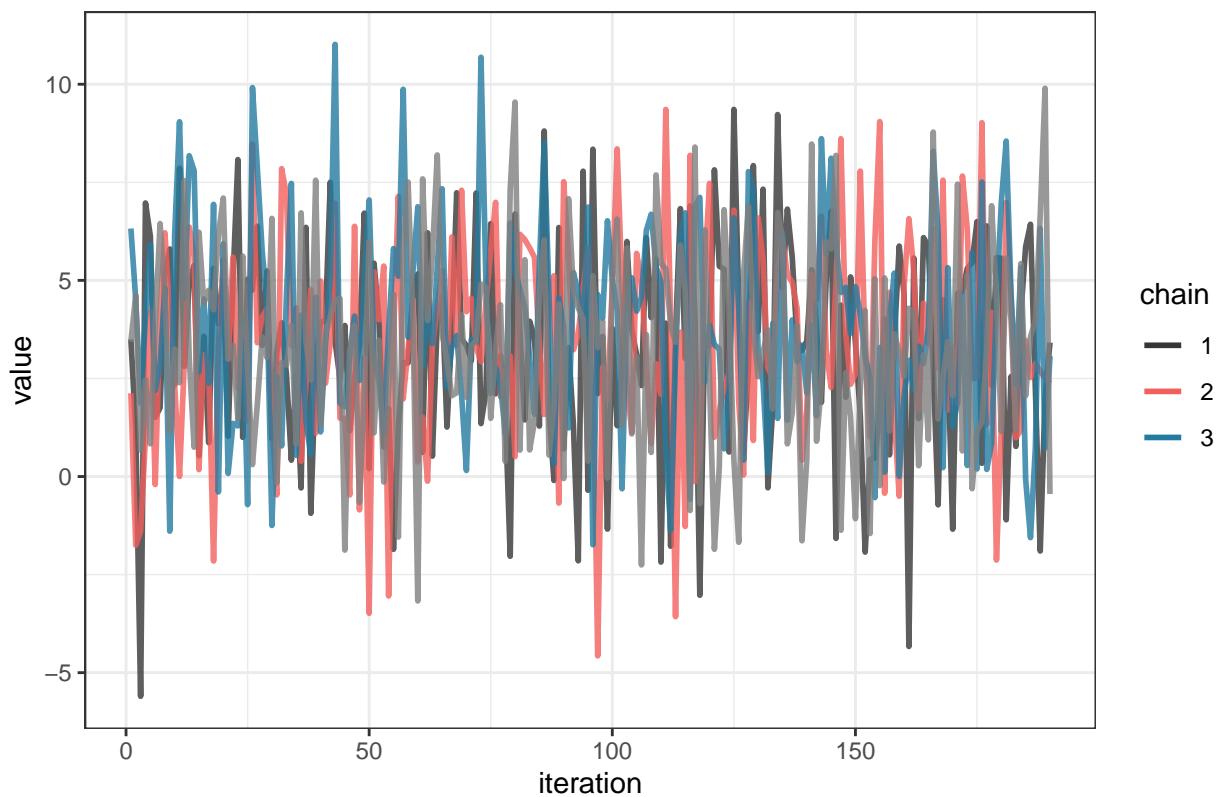
Traceplot of time



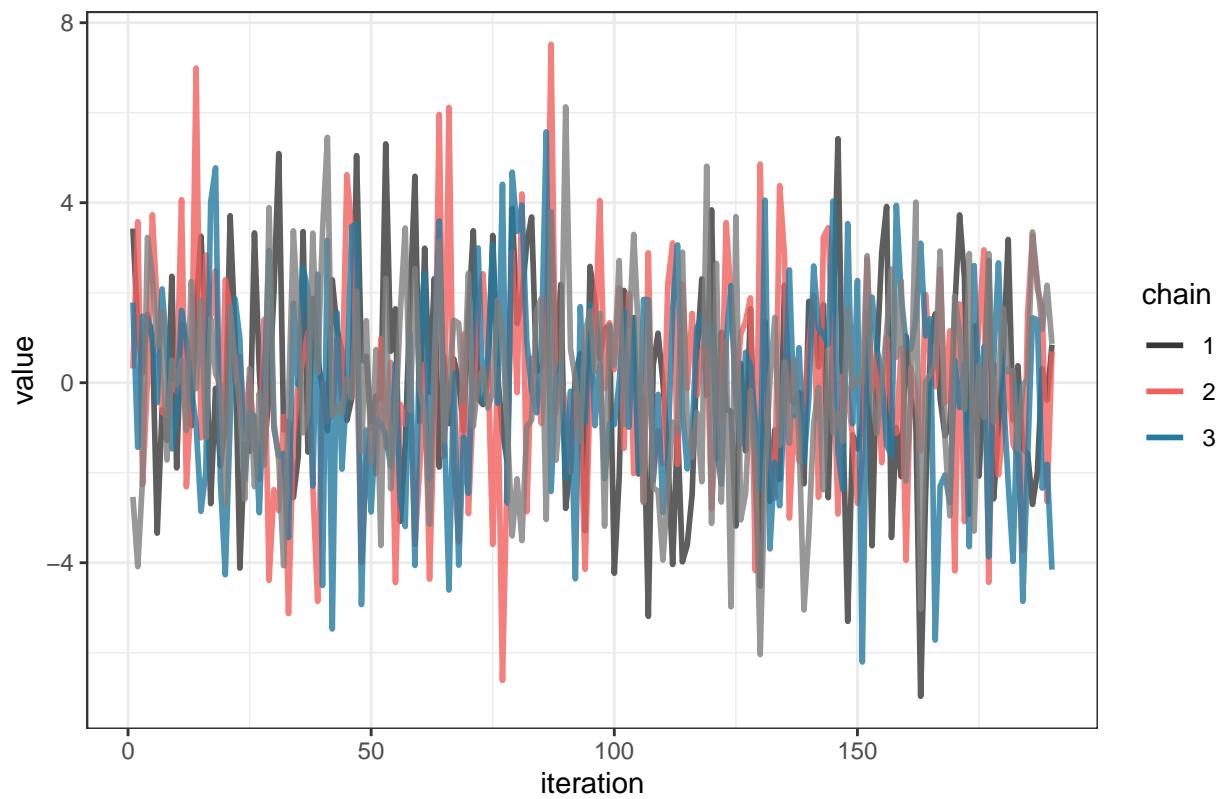
Traceplot of ageatbiopsy.1



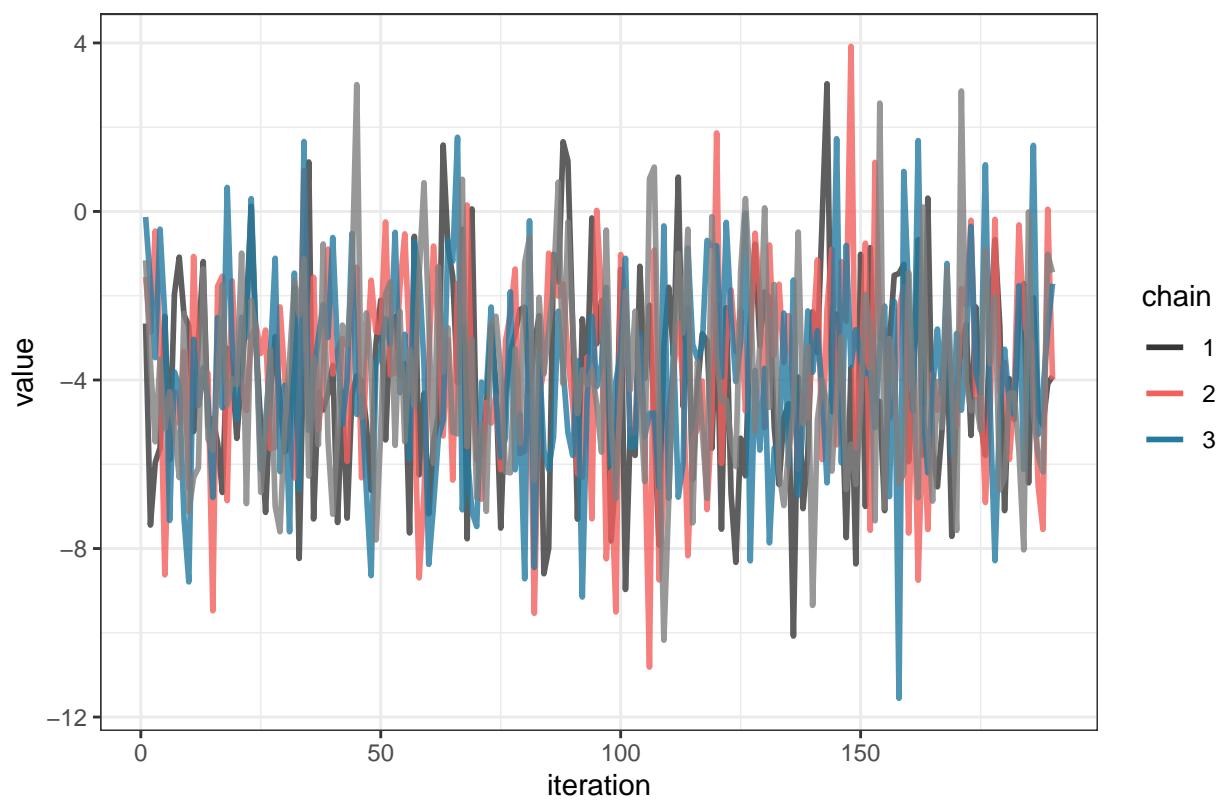
Traceplot of sex.1



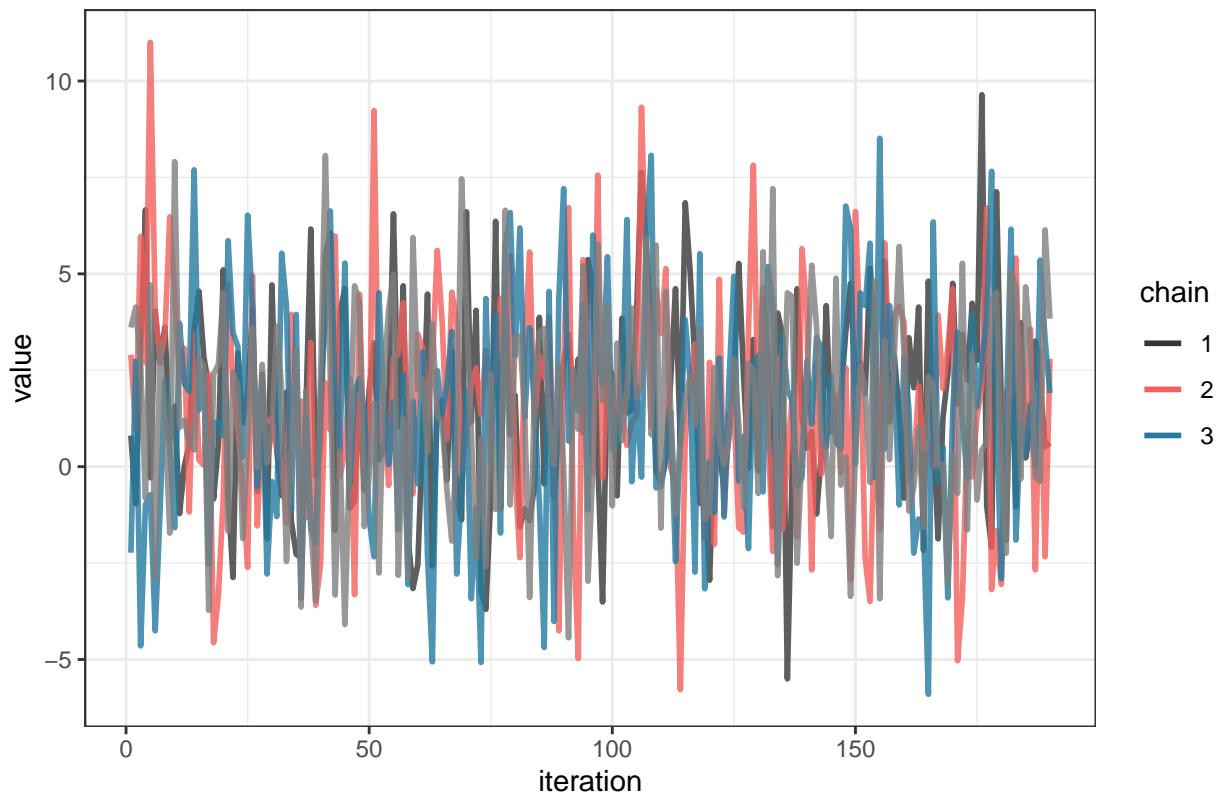
Traceplot of black.1



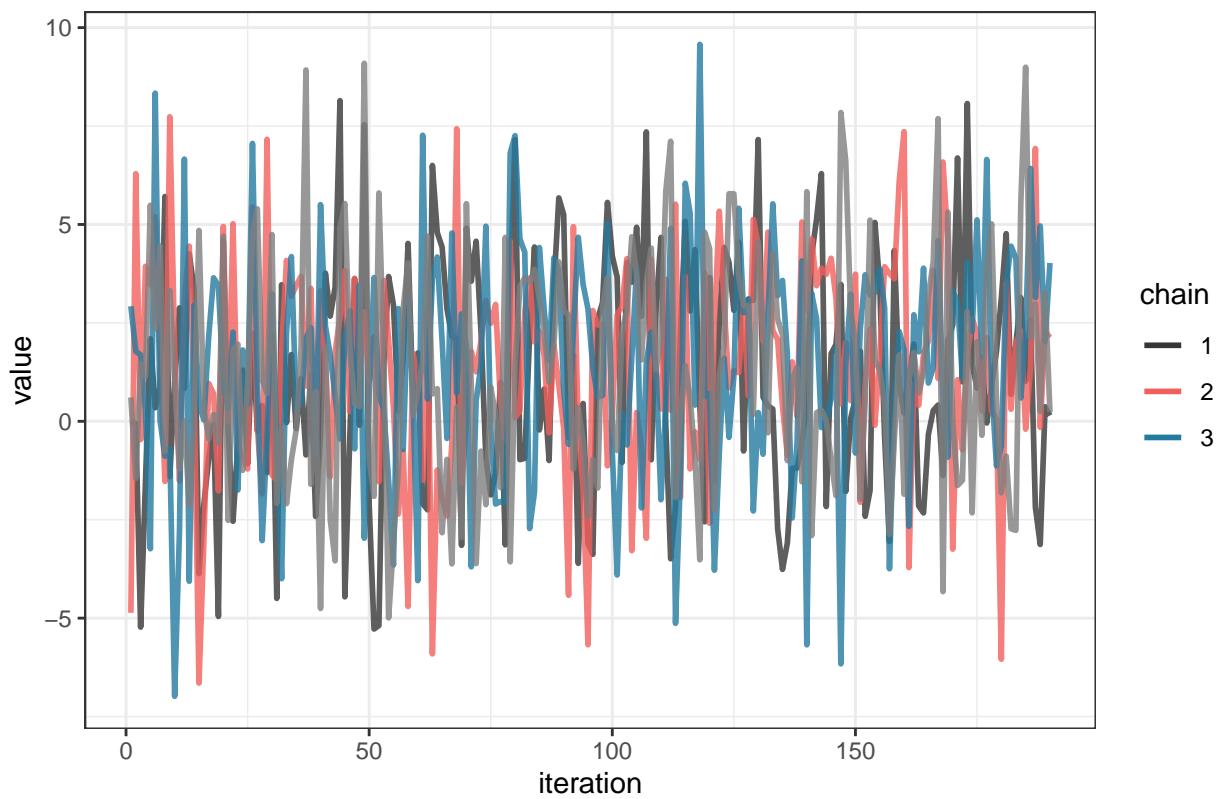
Traceplot of hypertension.1



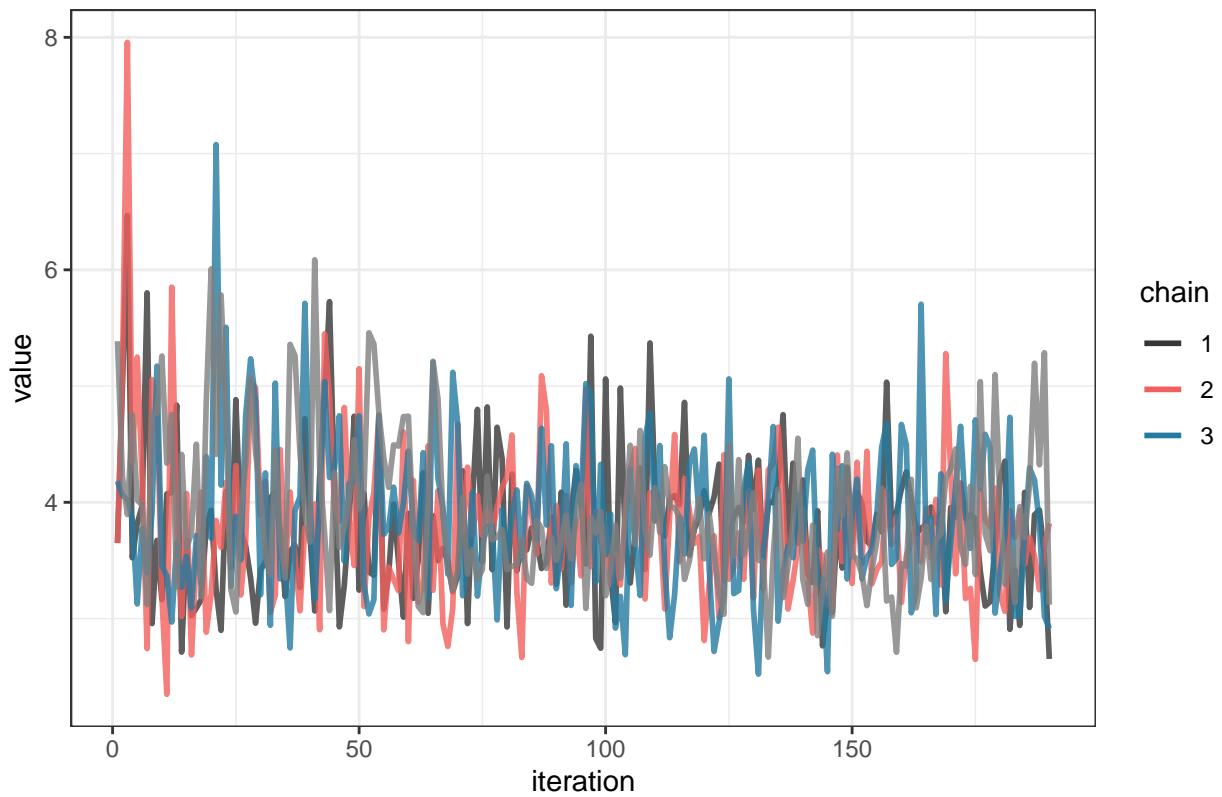
Traceplot of mmf.1



Traceplot of cyc.1

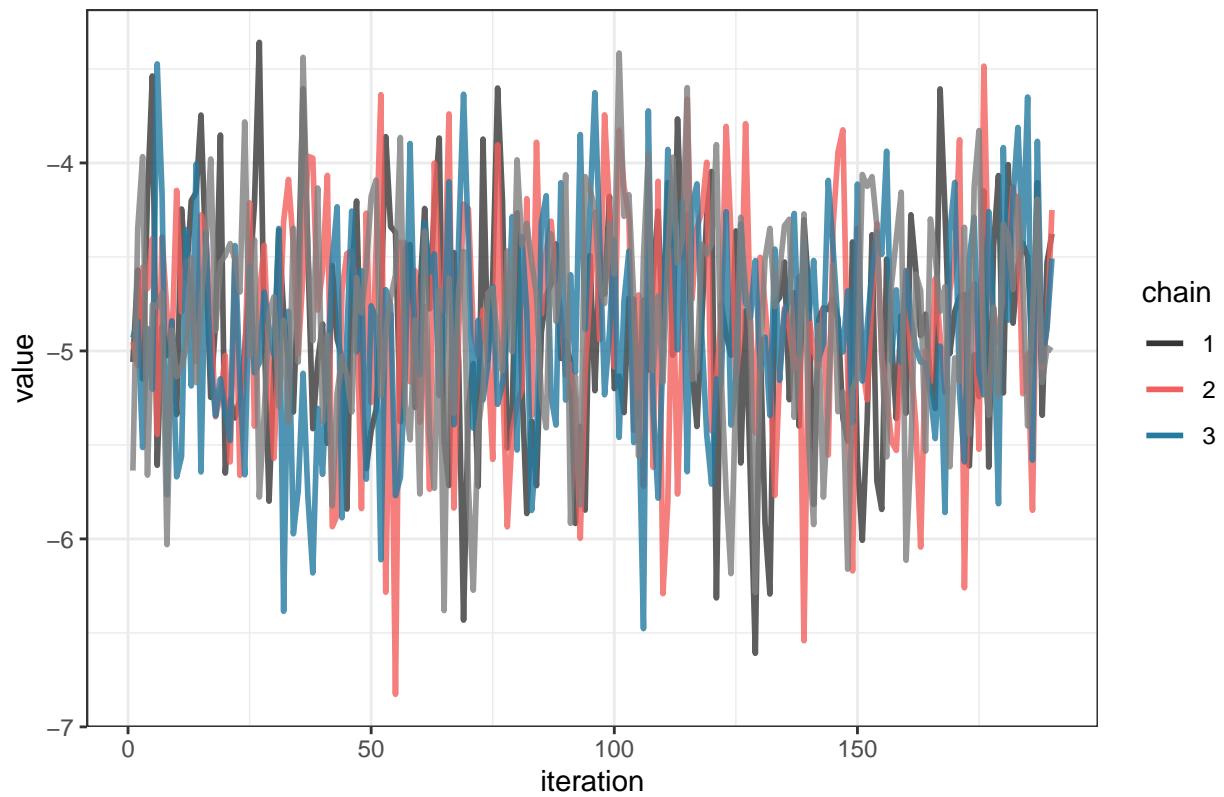


Traceplot of sigmas_1

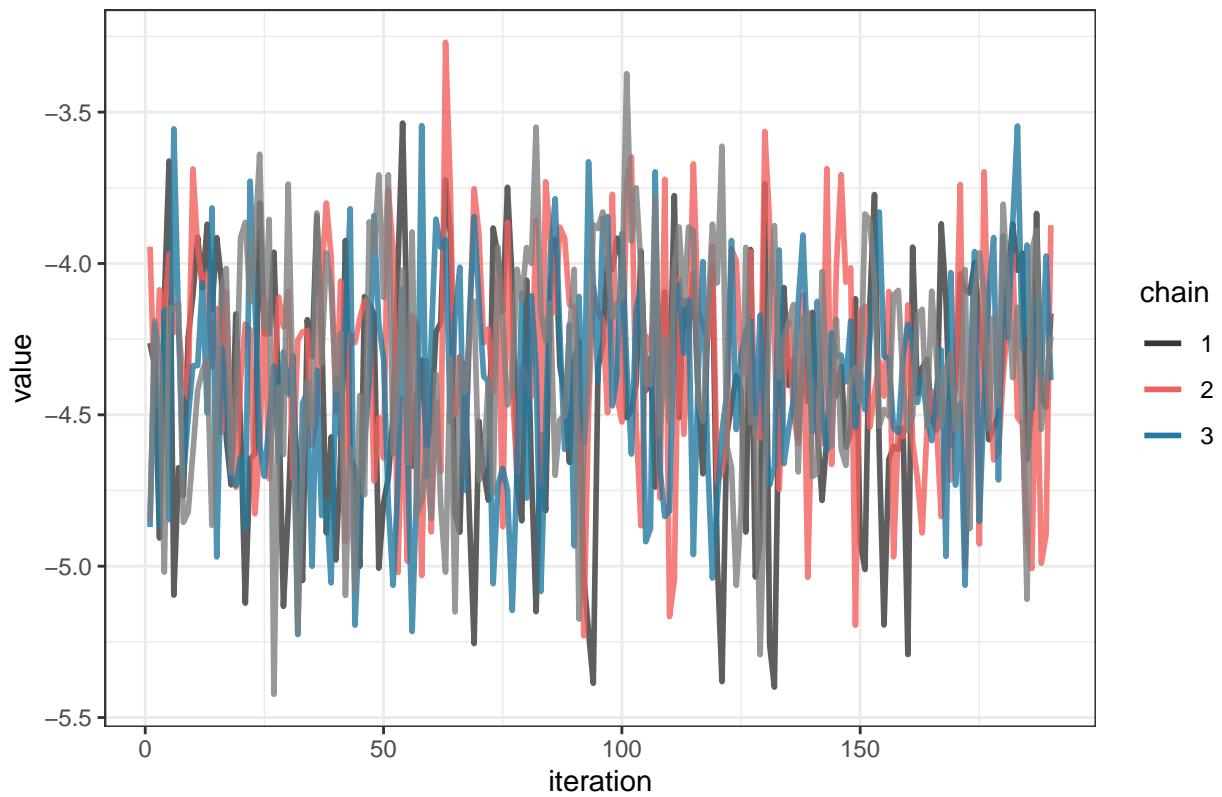


```
## ADJUSTED
traceplt
## NULL
traceplt1
## NULL
traceplt2
## NULL
##CRUDE
traceCplt <- ggtraceplot(jointCFit)
```

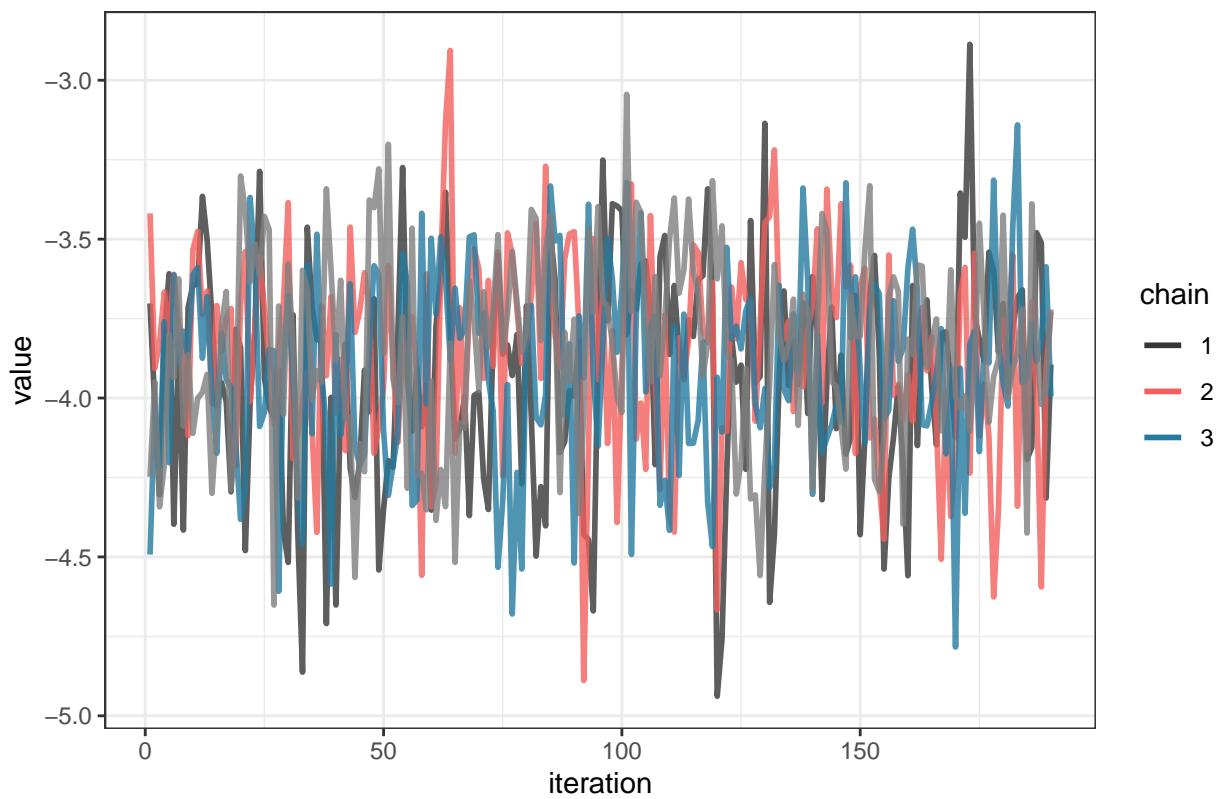
Traceplot of bs_gammas_1



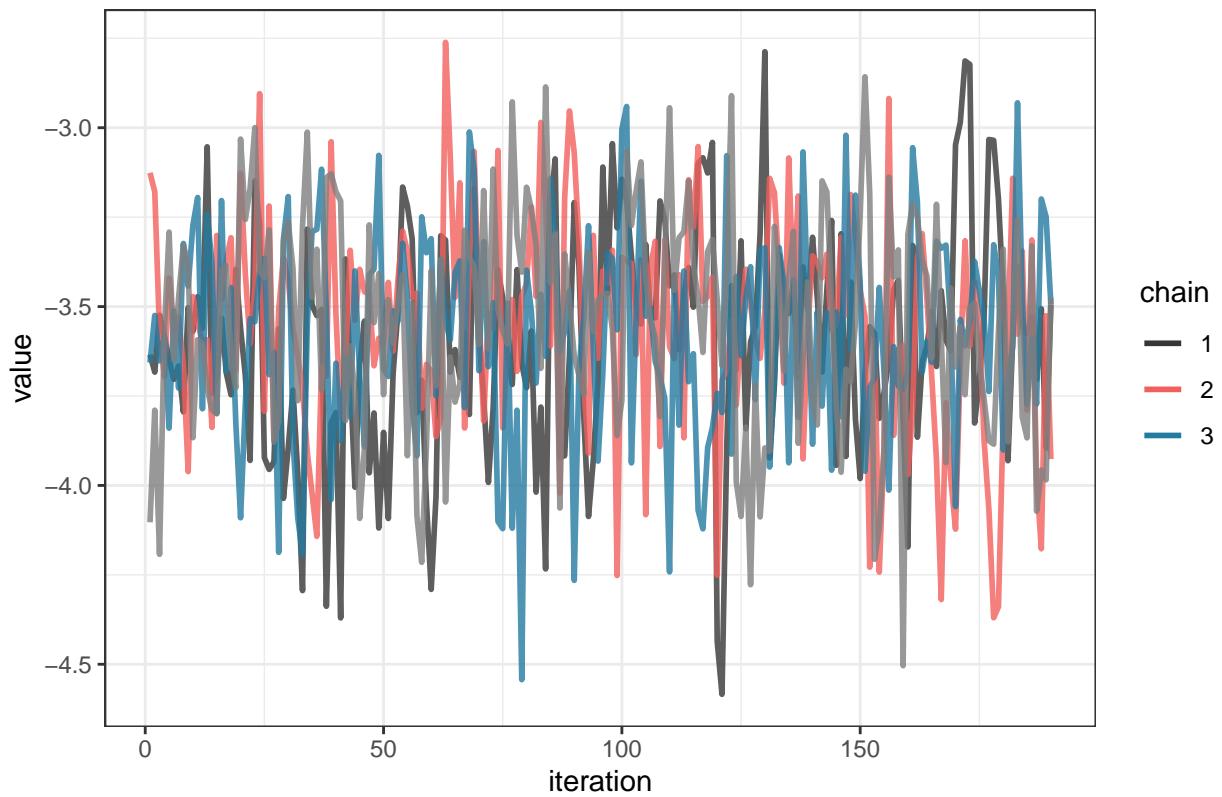
Traceplot of bs_gammas_2



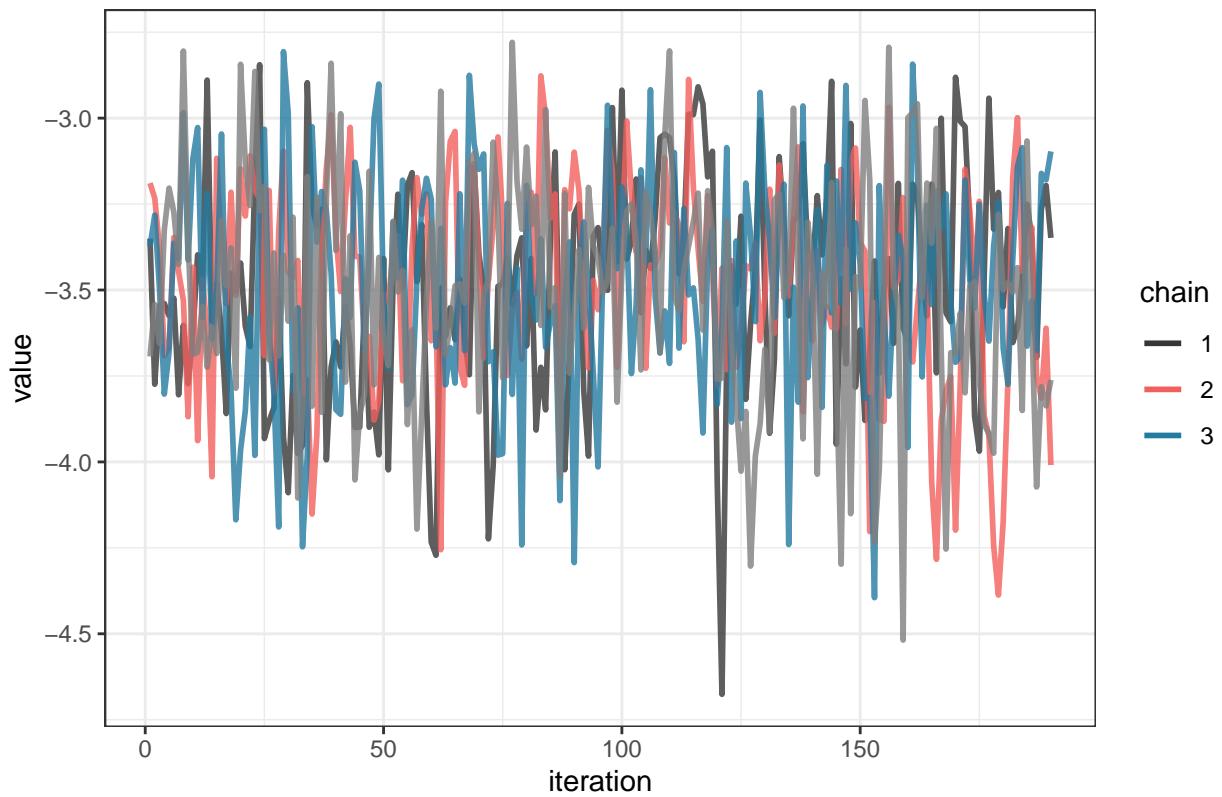
Traceplot of bs_gammas_3



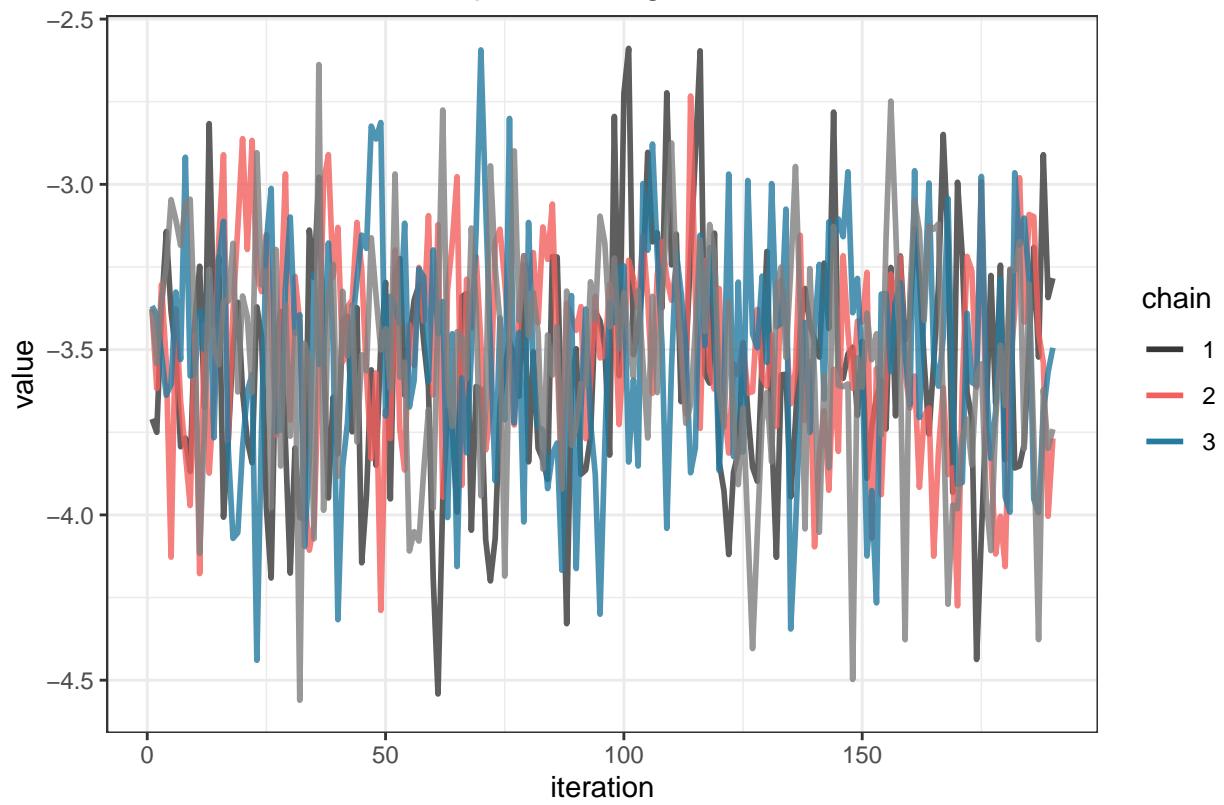
Traceplot of bs_gammas_4



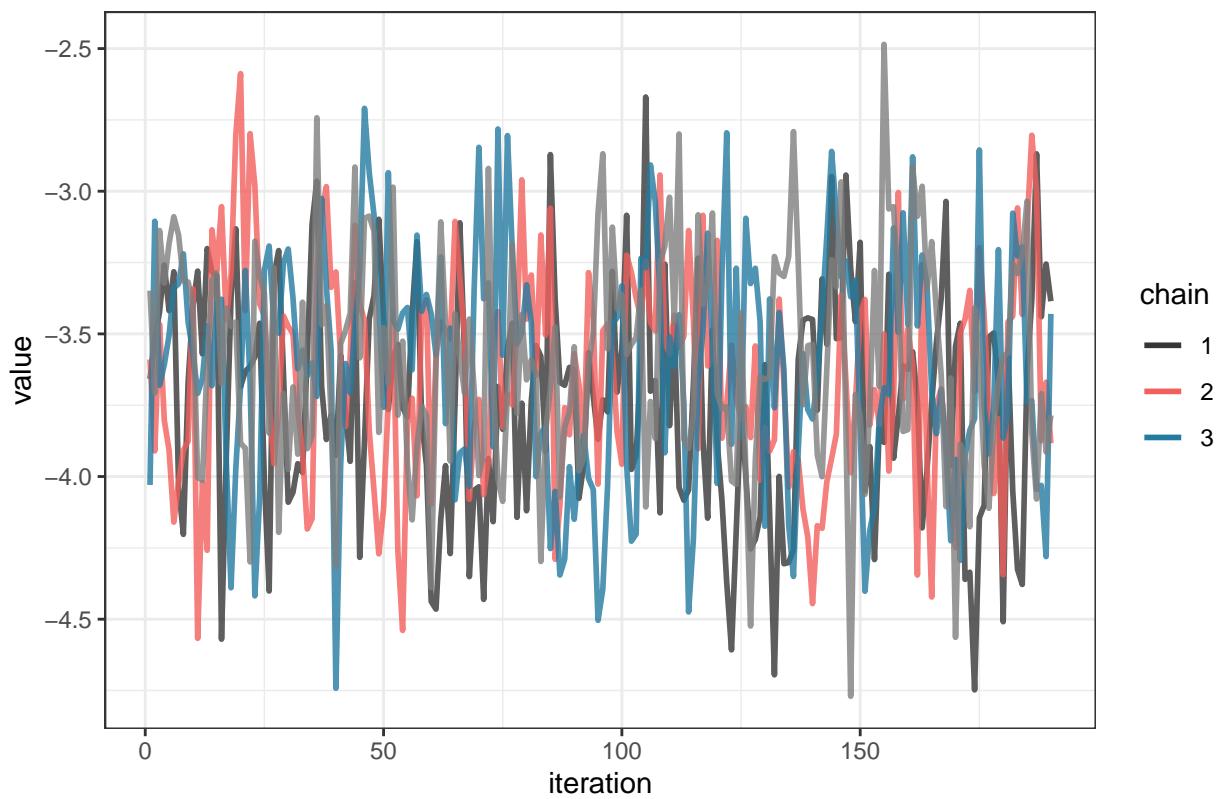
Traceplot of bs_gammas_5



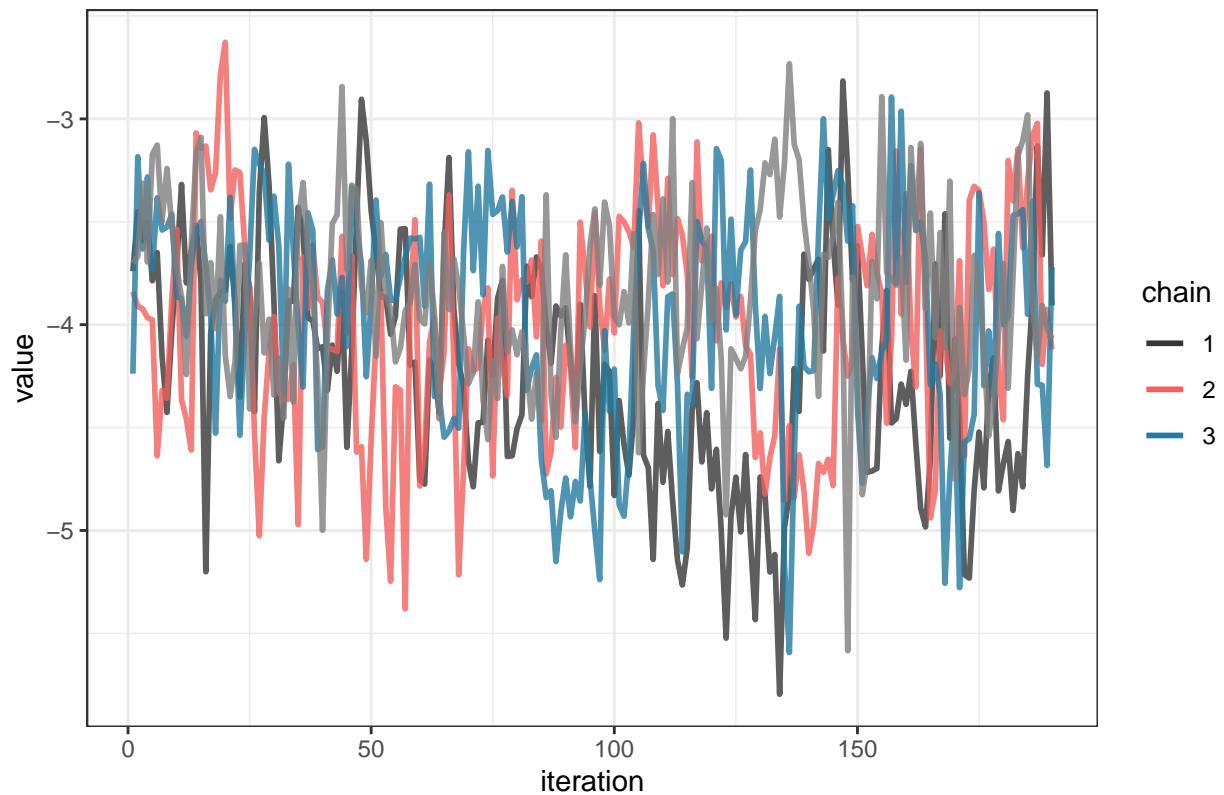
Traceplot of bs_gammas_6



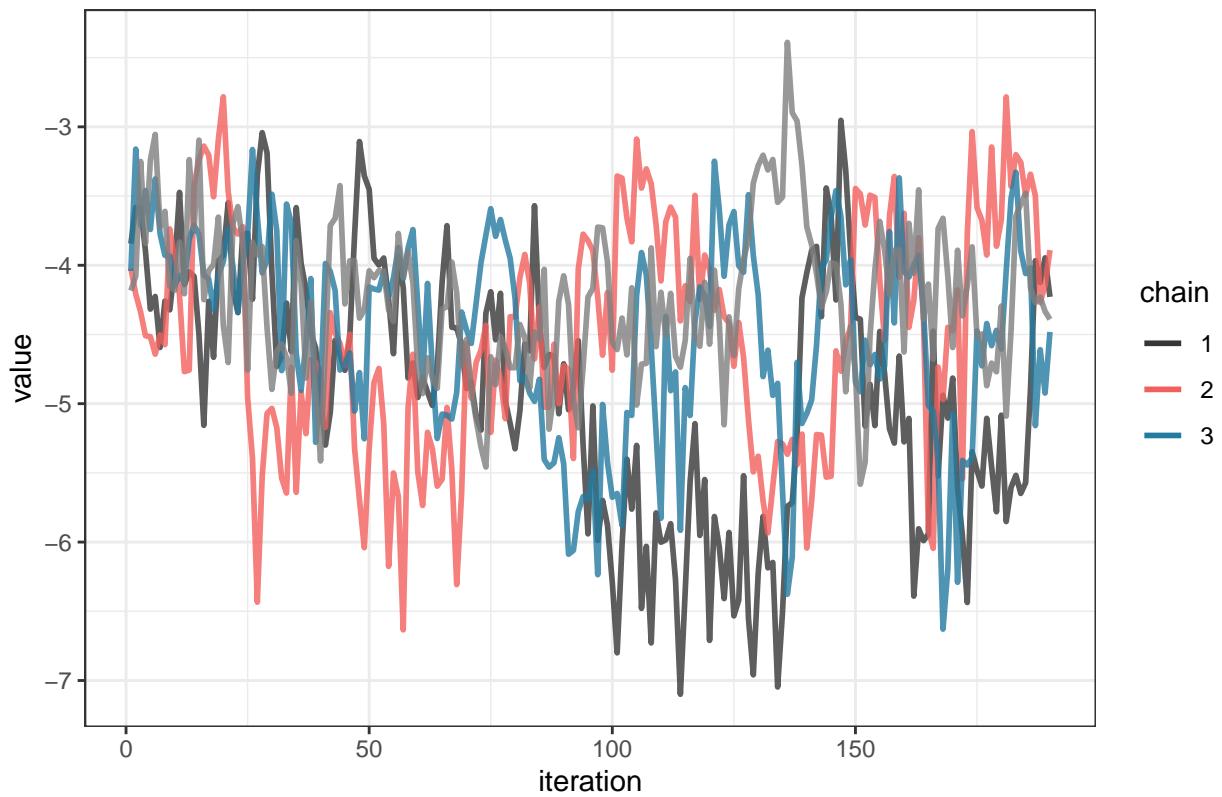
Traceplot of bs_gammas_7



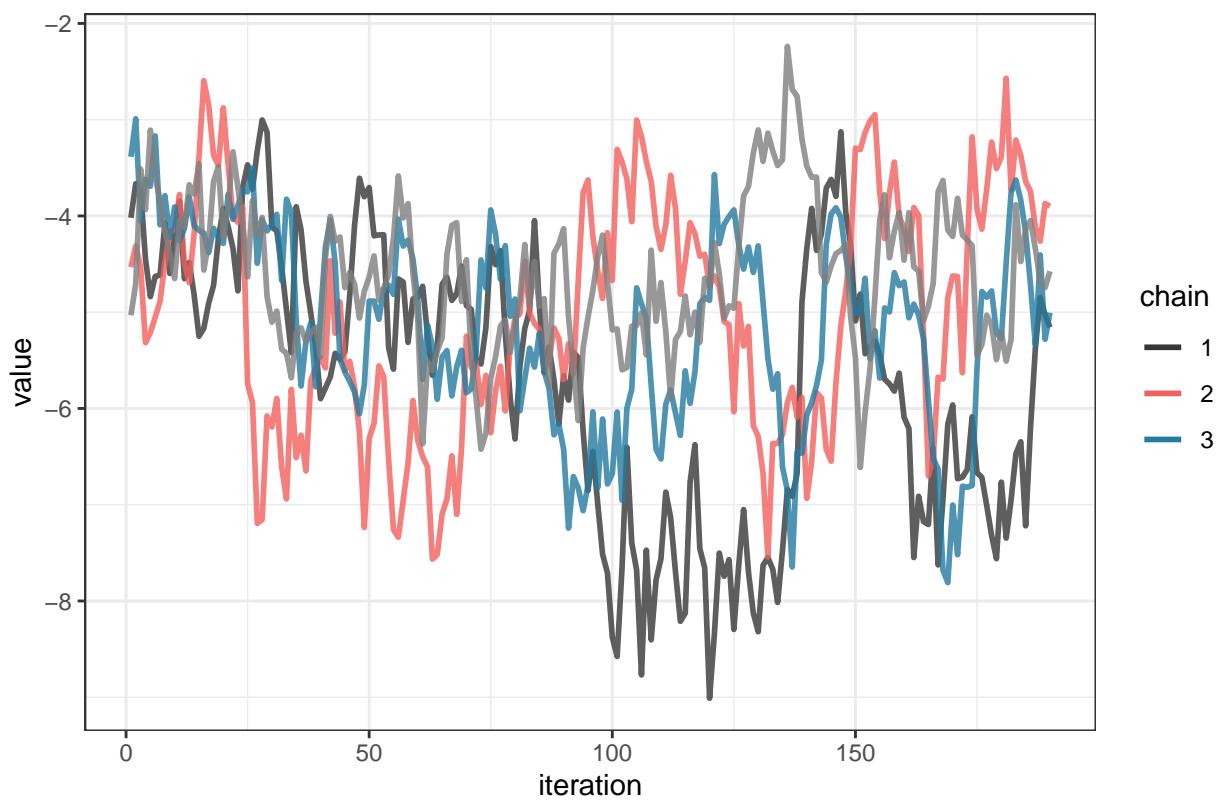
Traceplot of bs_gammas_8



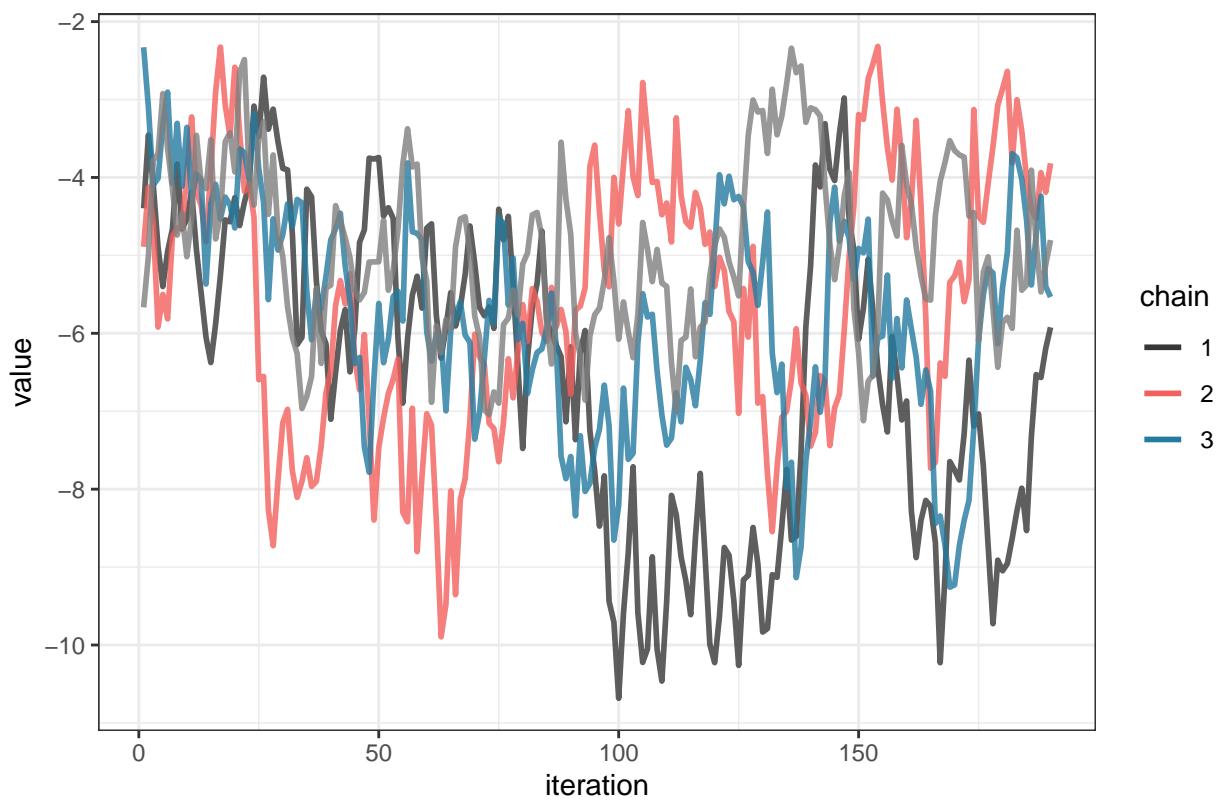
Traceplot of bs_gammas_9



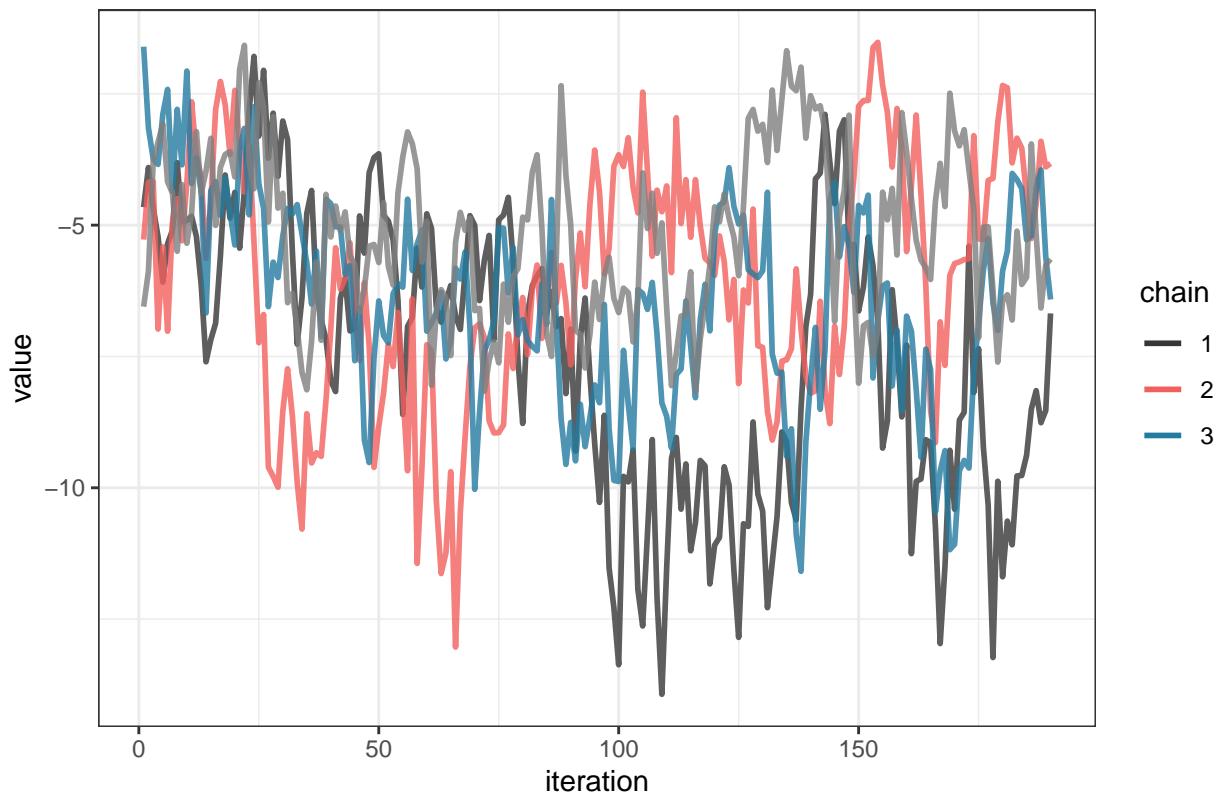
Traceplot of bs_gammas_10



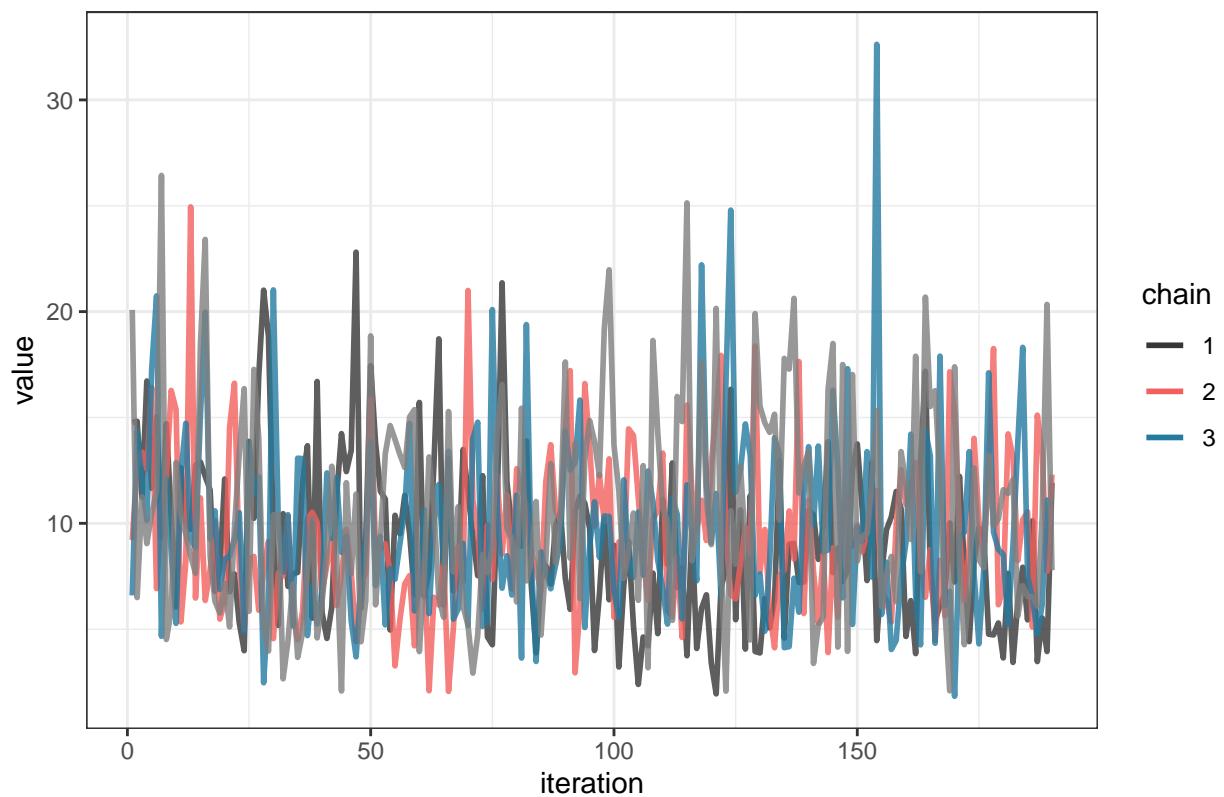
Traceplot of bs_gammas_11



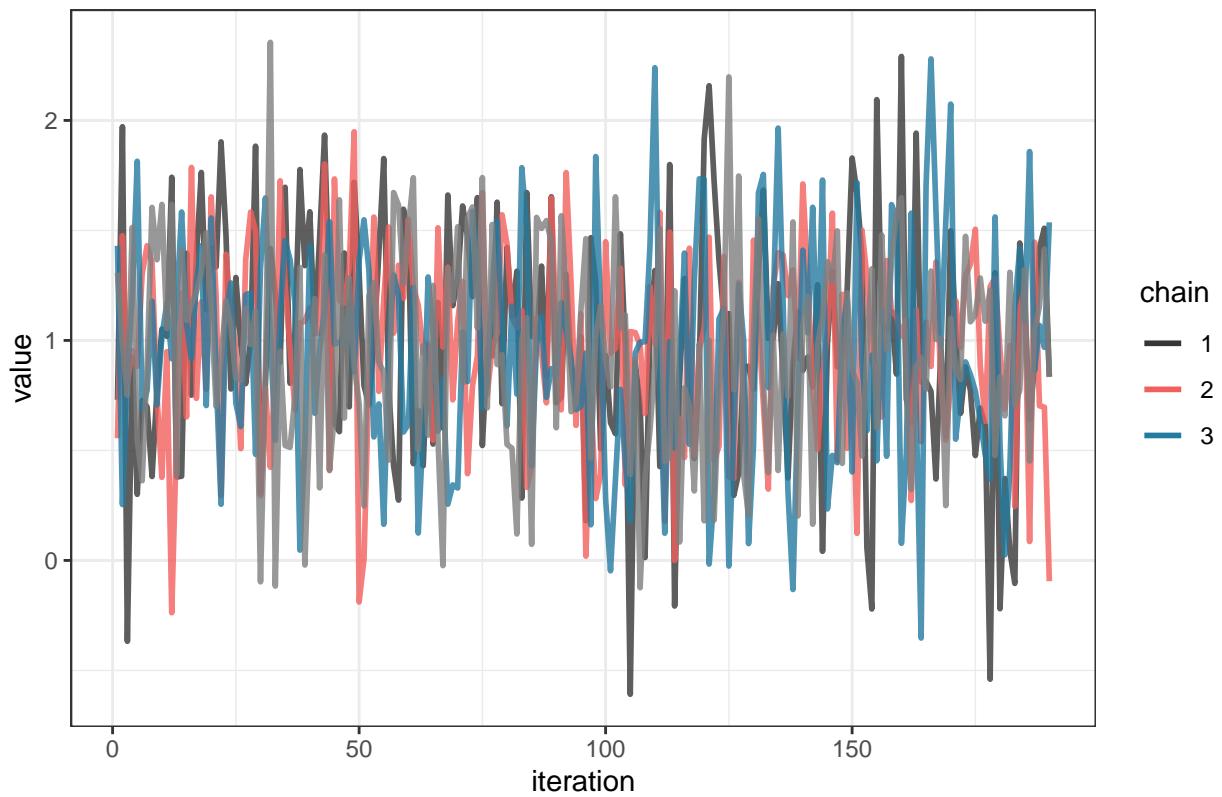
Traceplot of bs_gammas_12



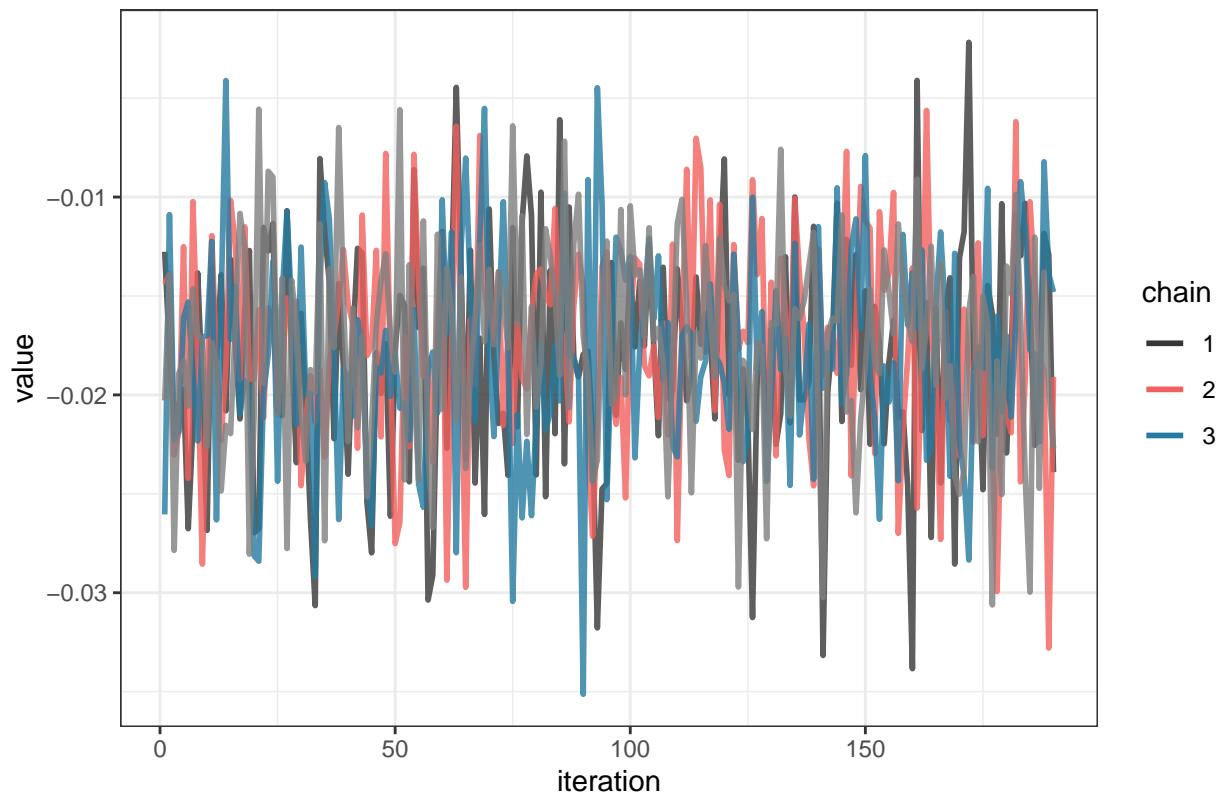
Traceplot of tau_bs_gammas



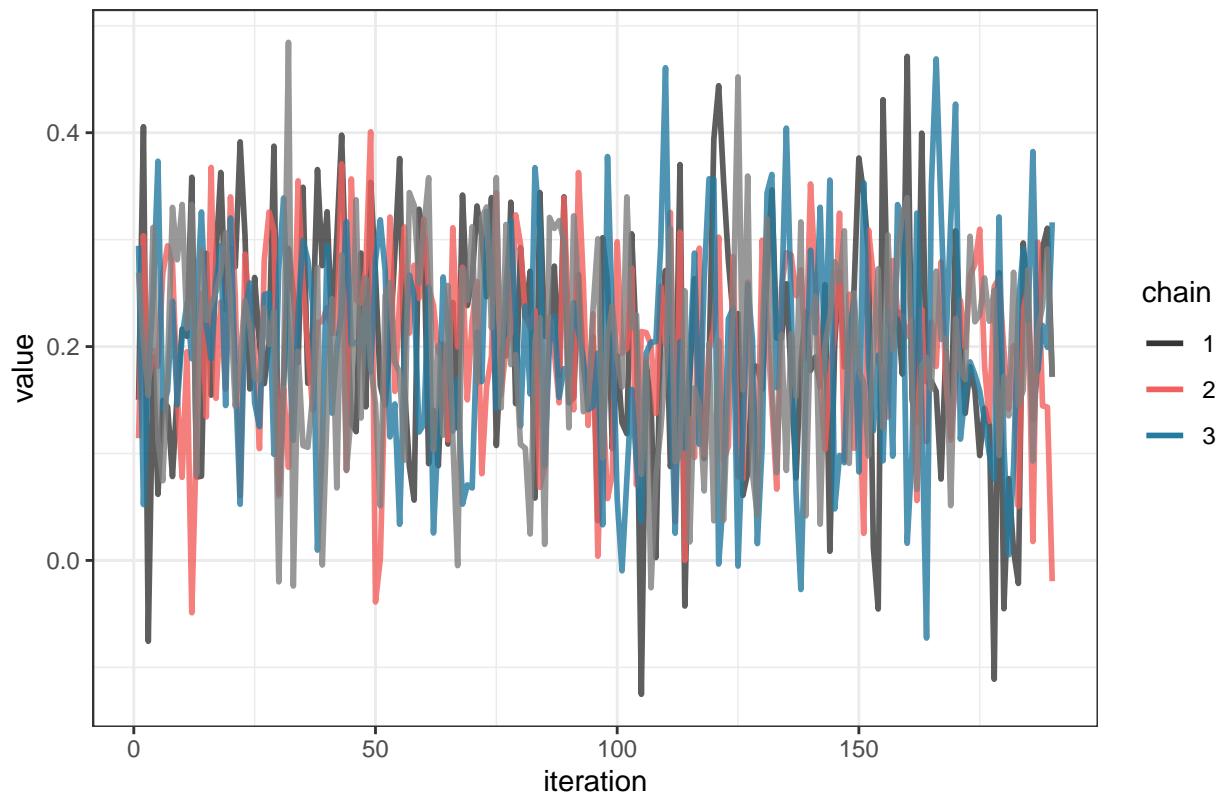
Traceplot of LOWC31



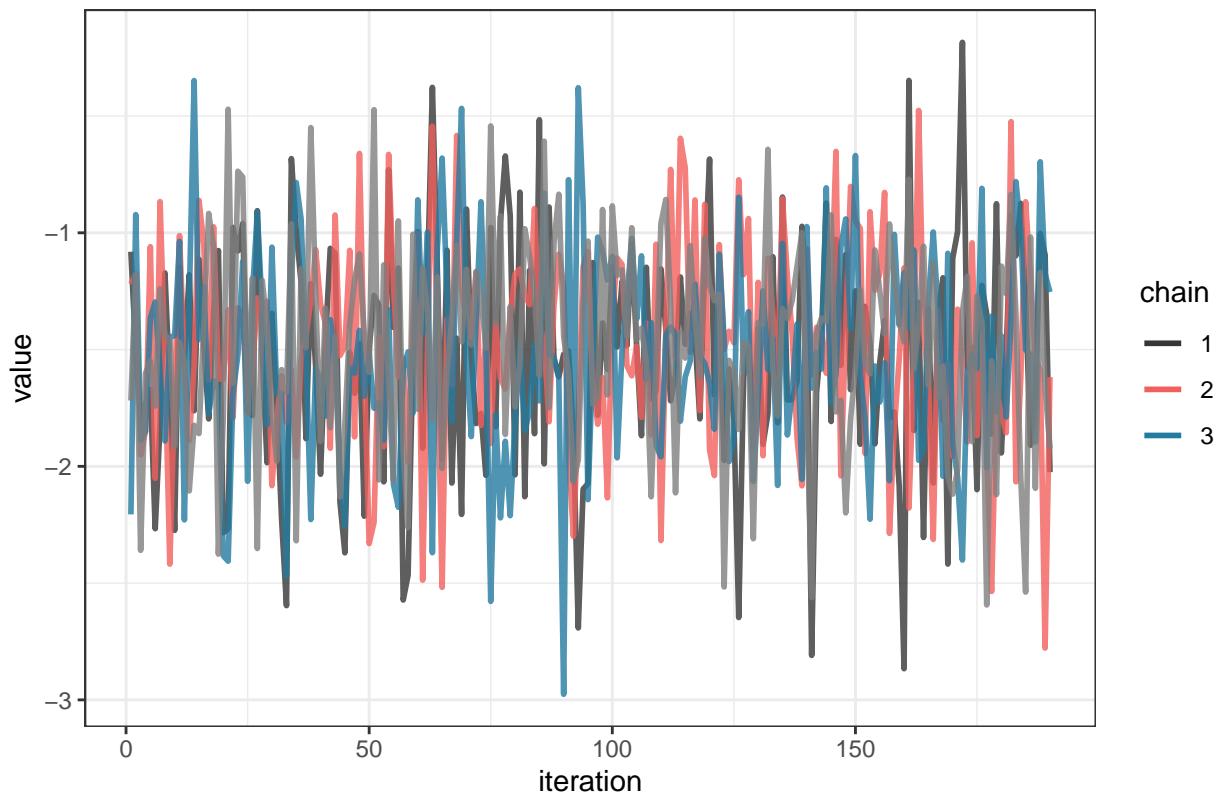
Traceplot of value(eGFR)



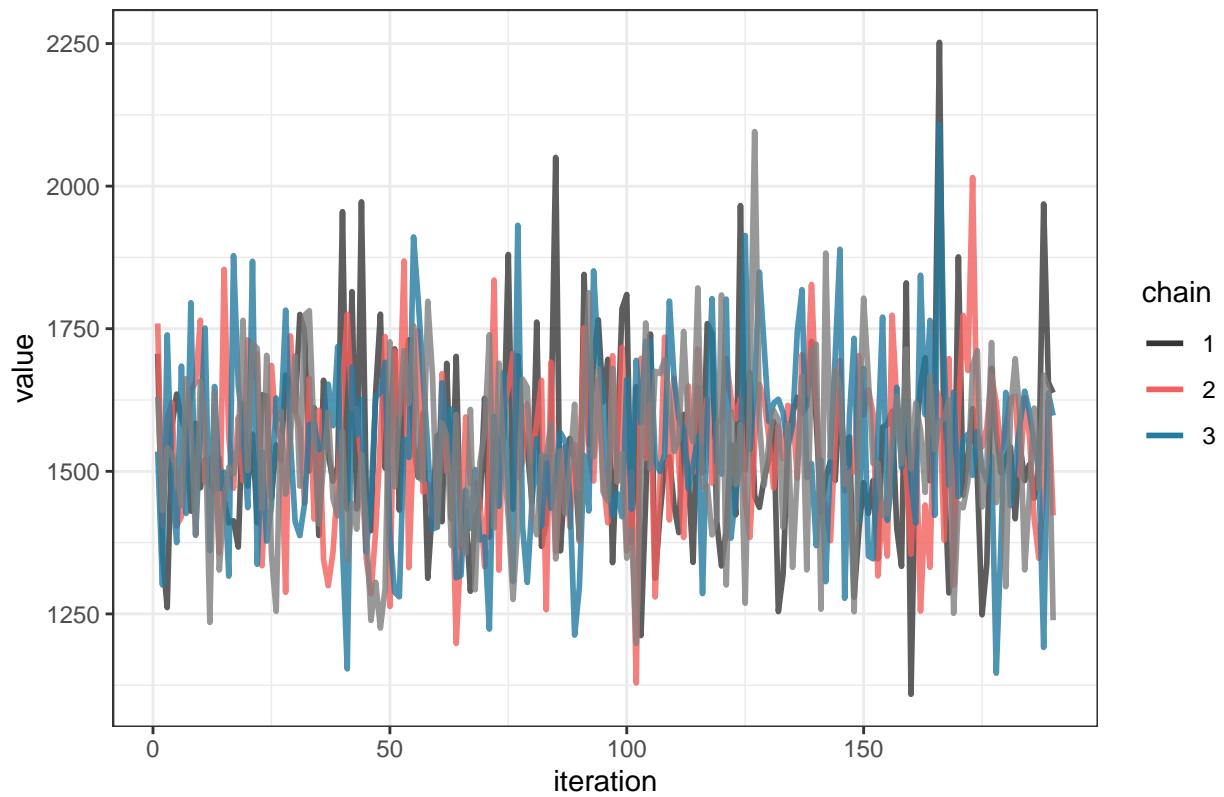
Traceplot of



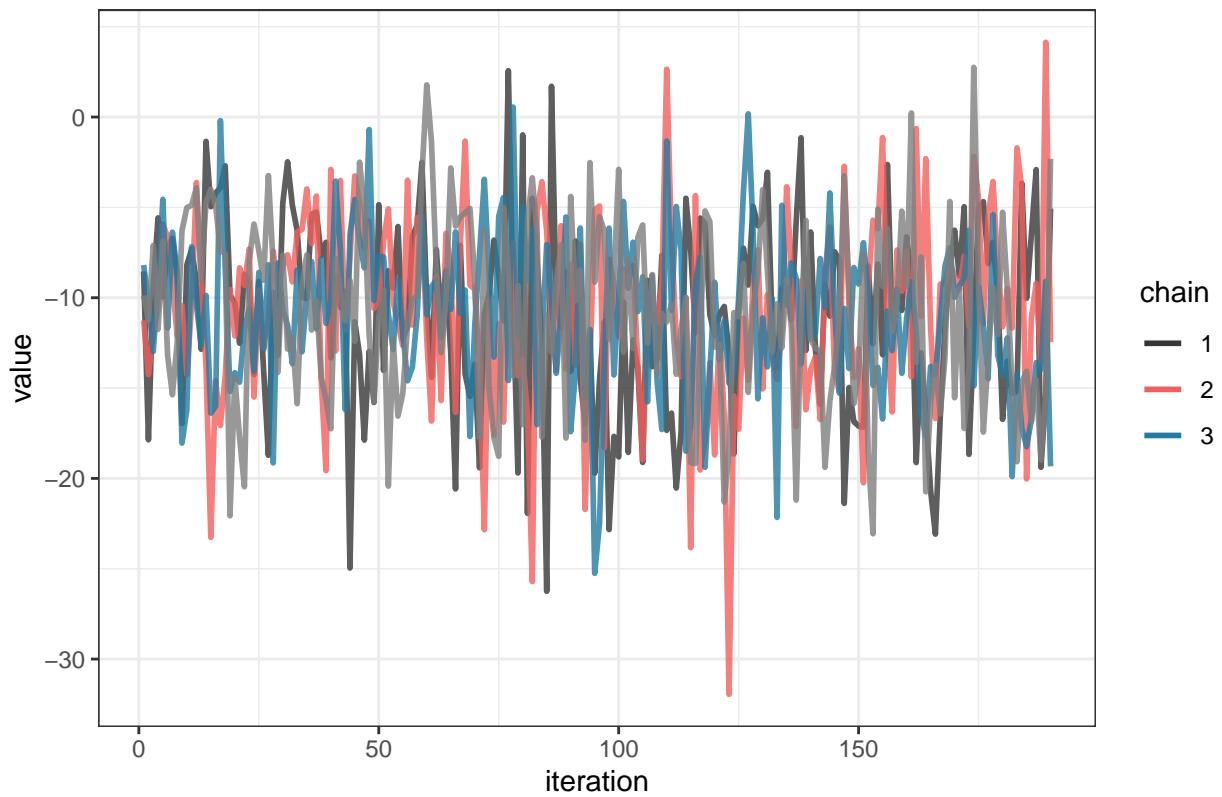
Traceplot of .1



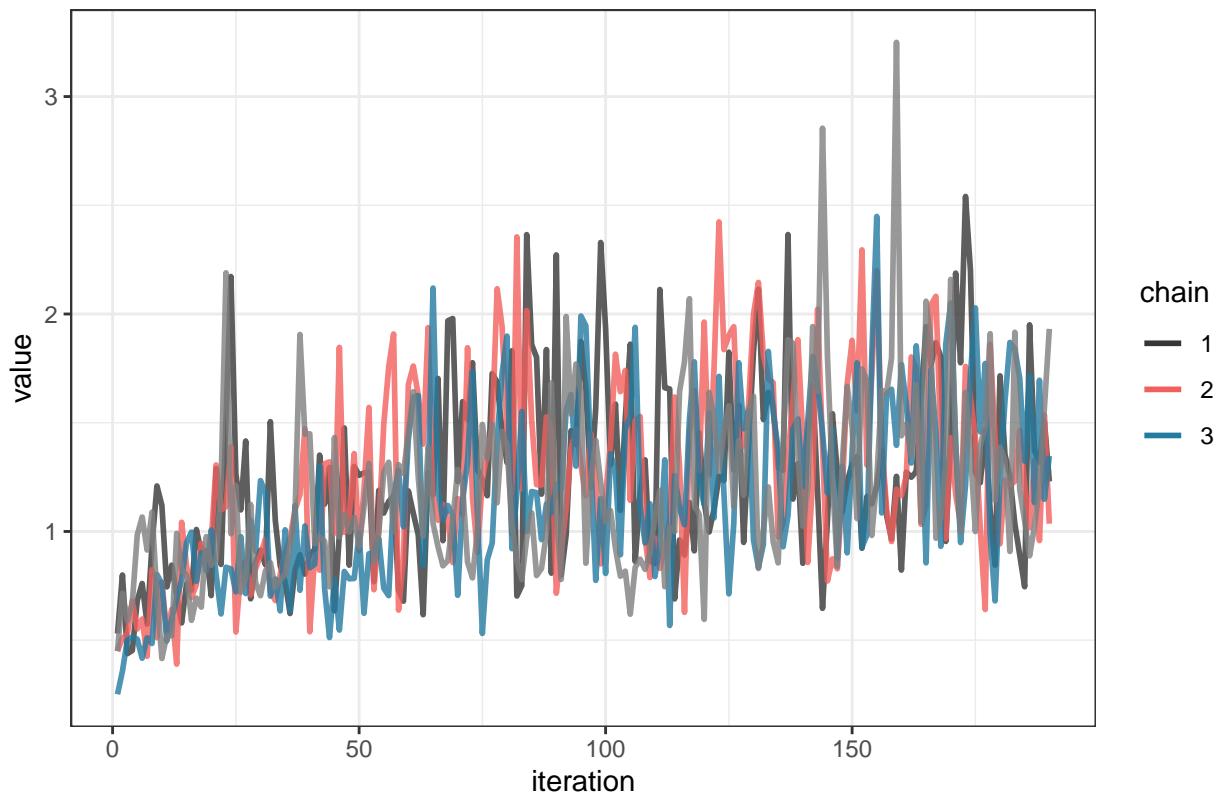
Traceplot of $D[1, 1]$



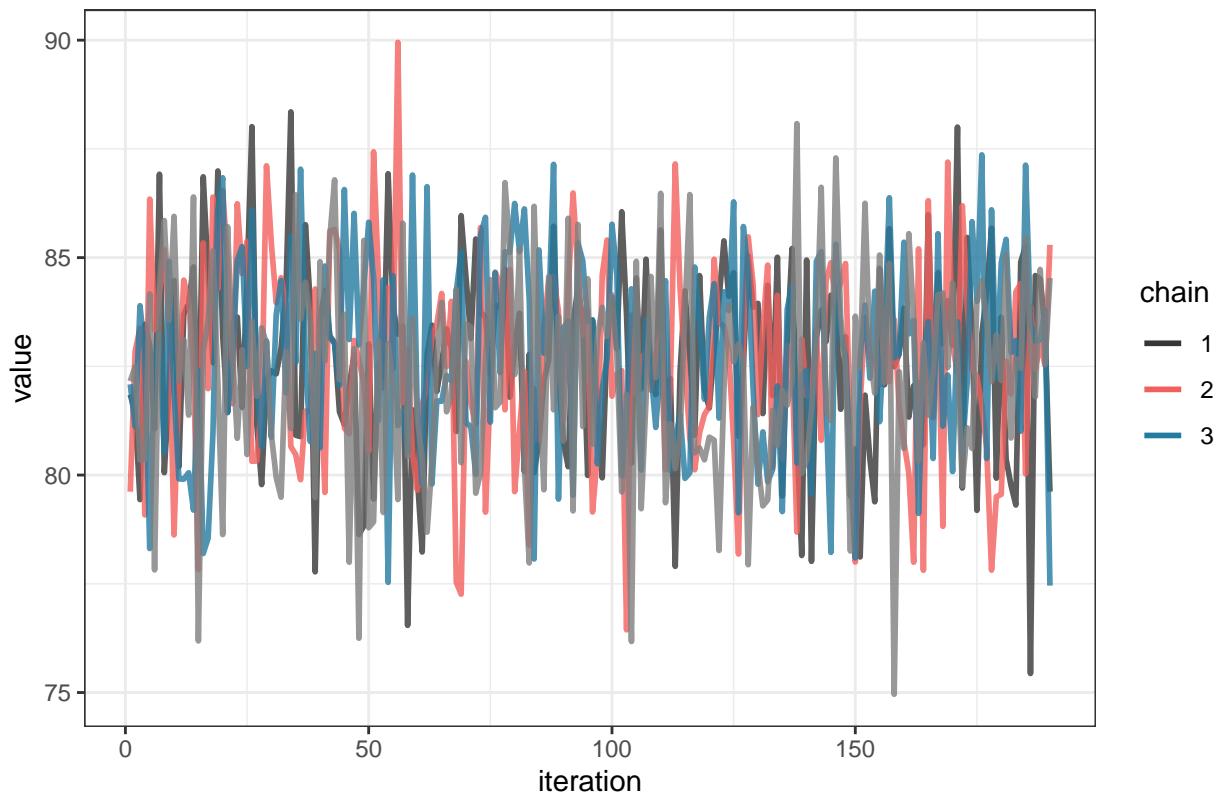
Traceplot of $D[2, 1]$



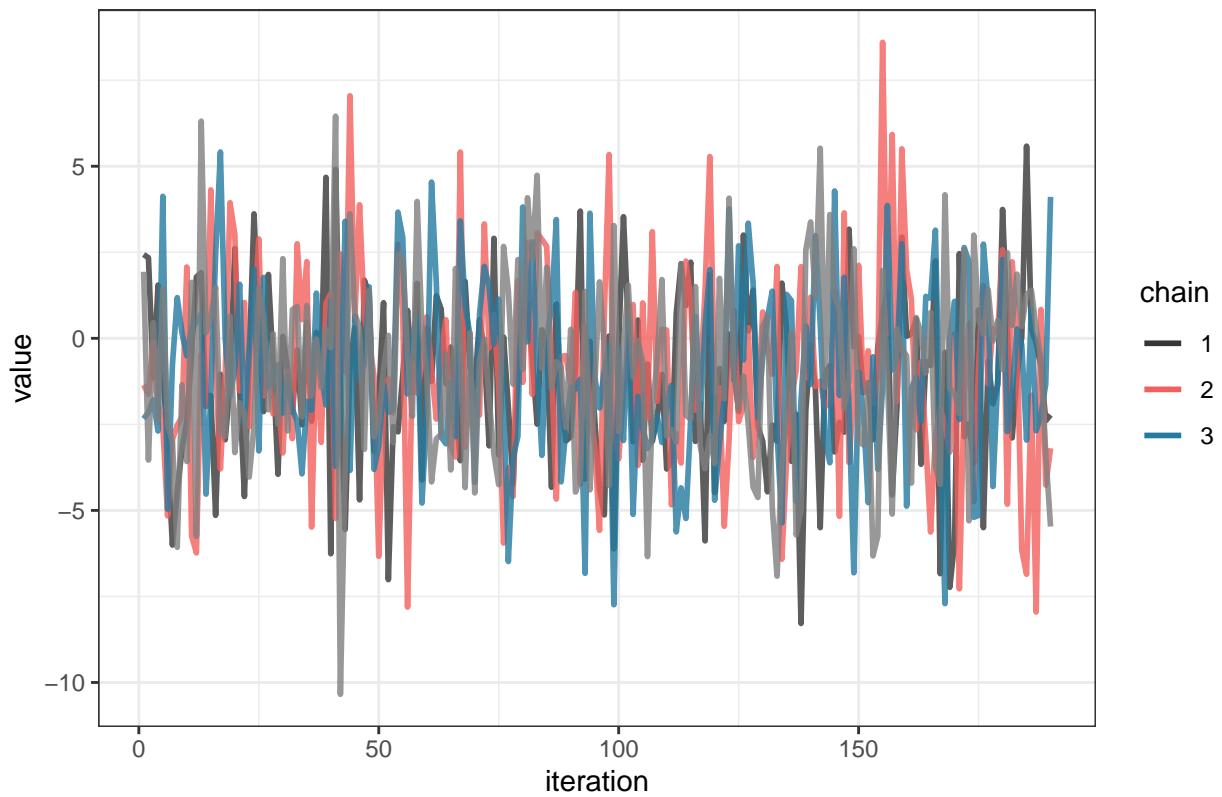
Traceplot of $D[2, 2]$



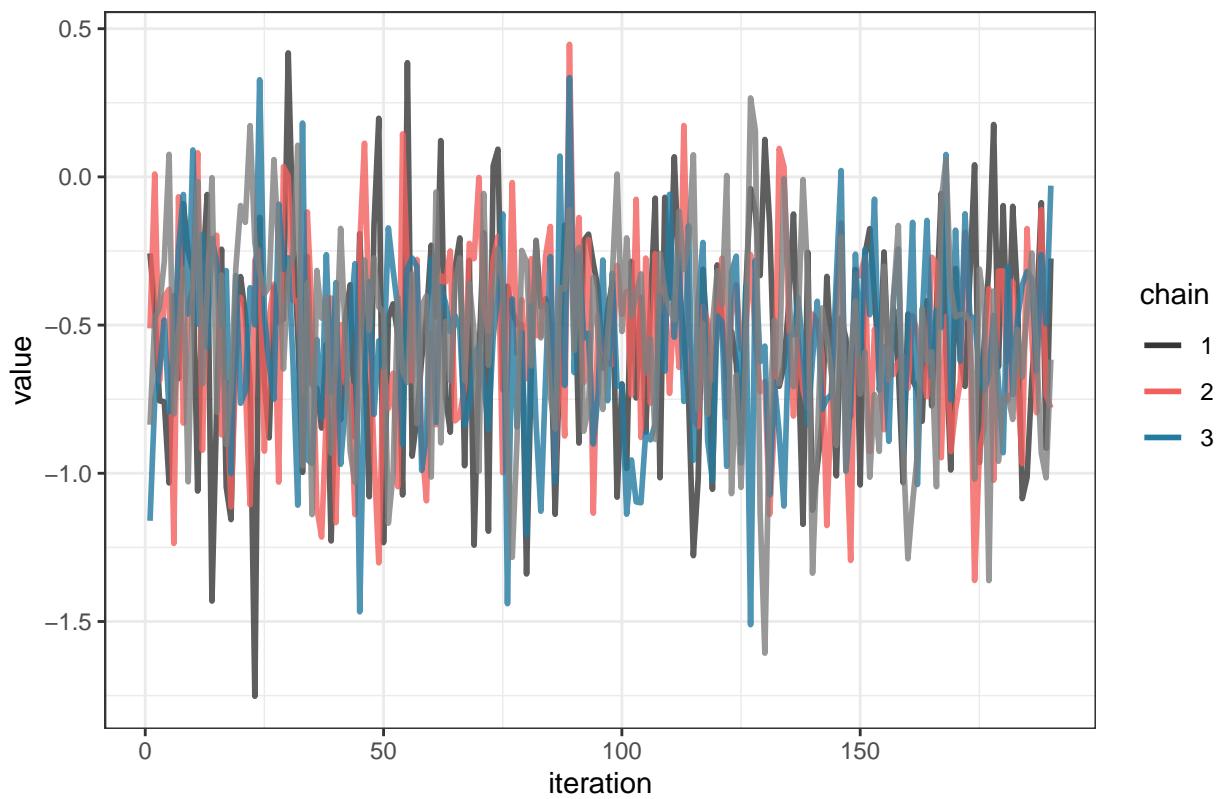
Traceplot of (Intercept)



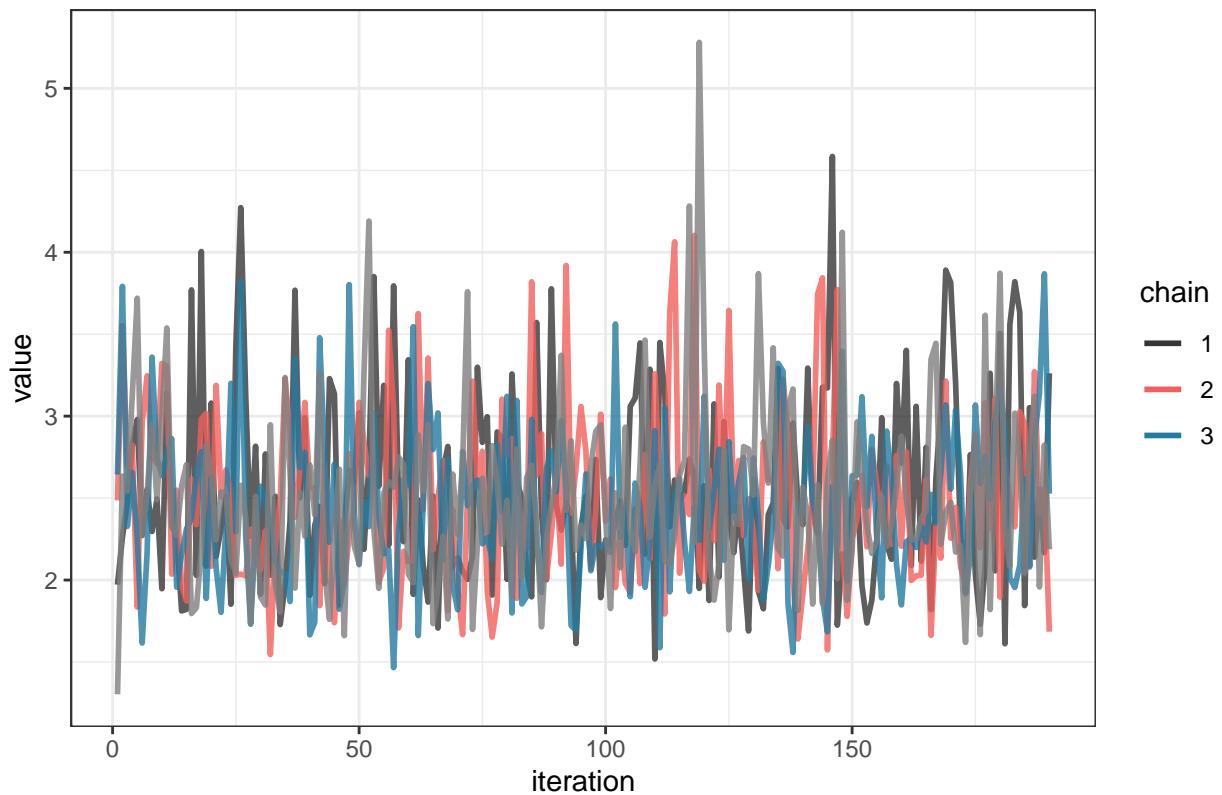
Traceplot of LOWC31.1



Traceplot of time

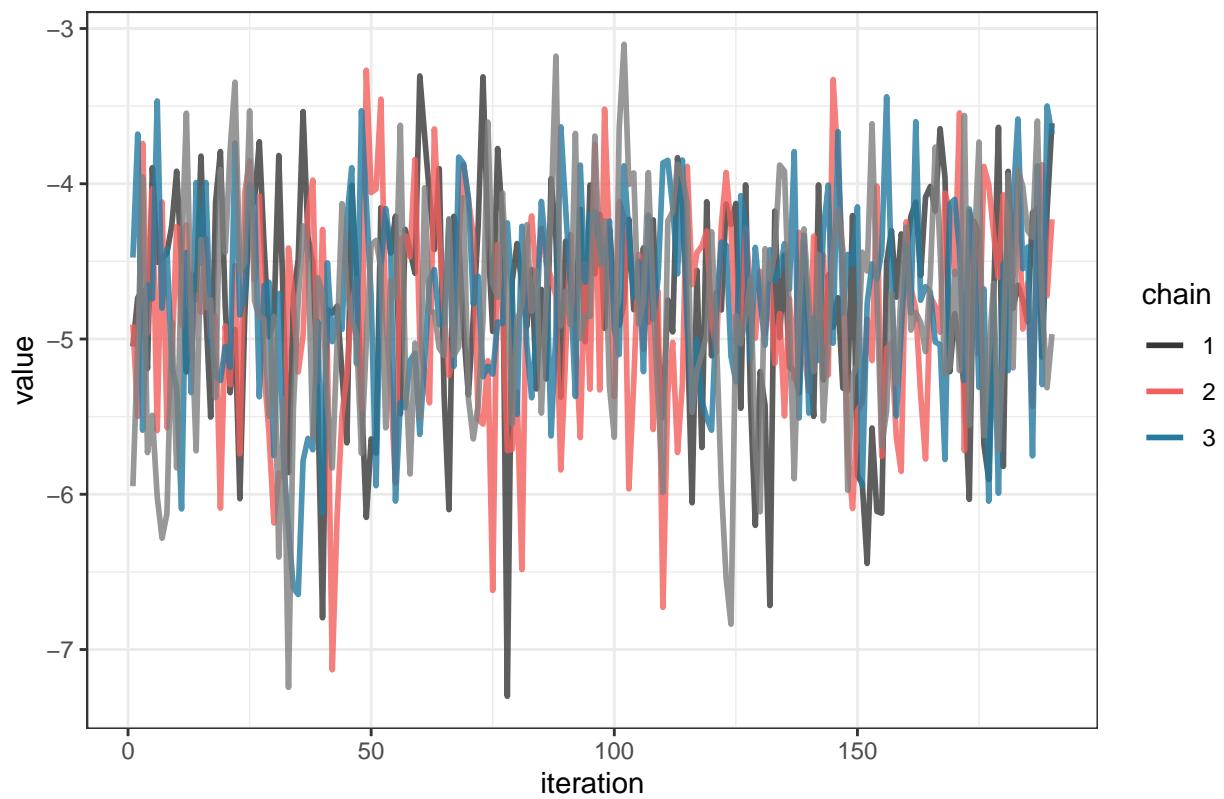


Traceplot of sigmas_1

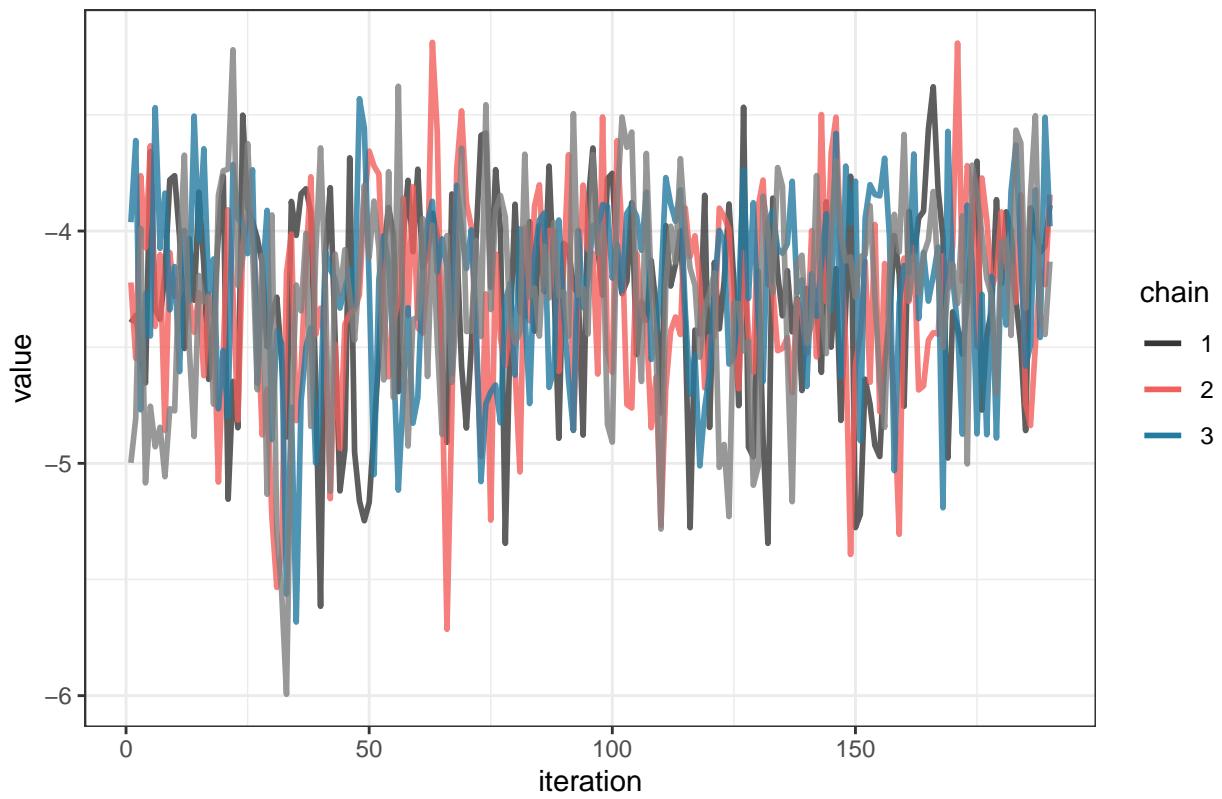


```
traceCplt1 <- ggtraceplot(jointCFit1)
```

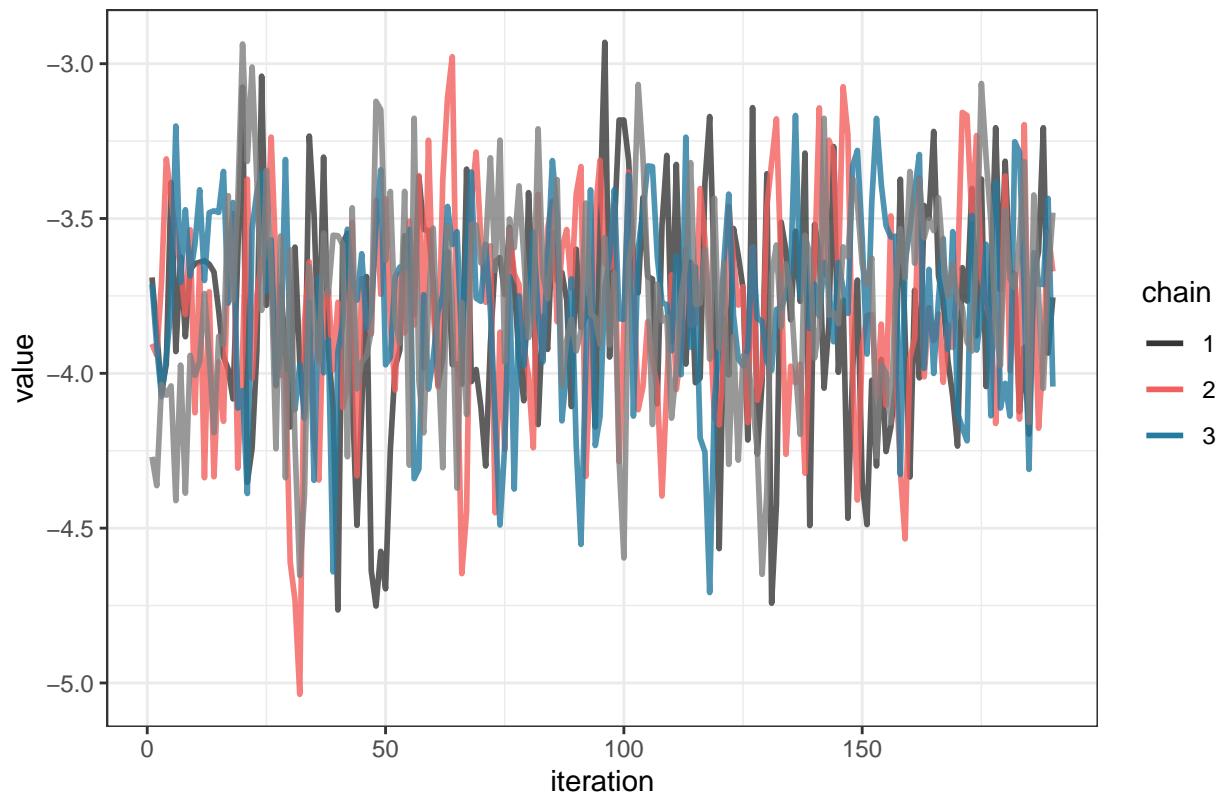
Traceplot of bs_gammas_1



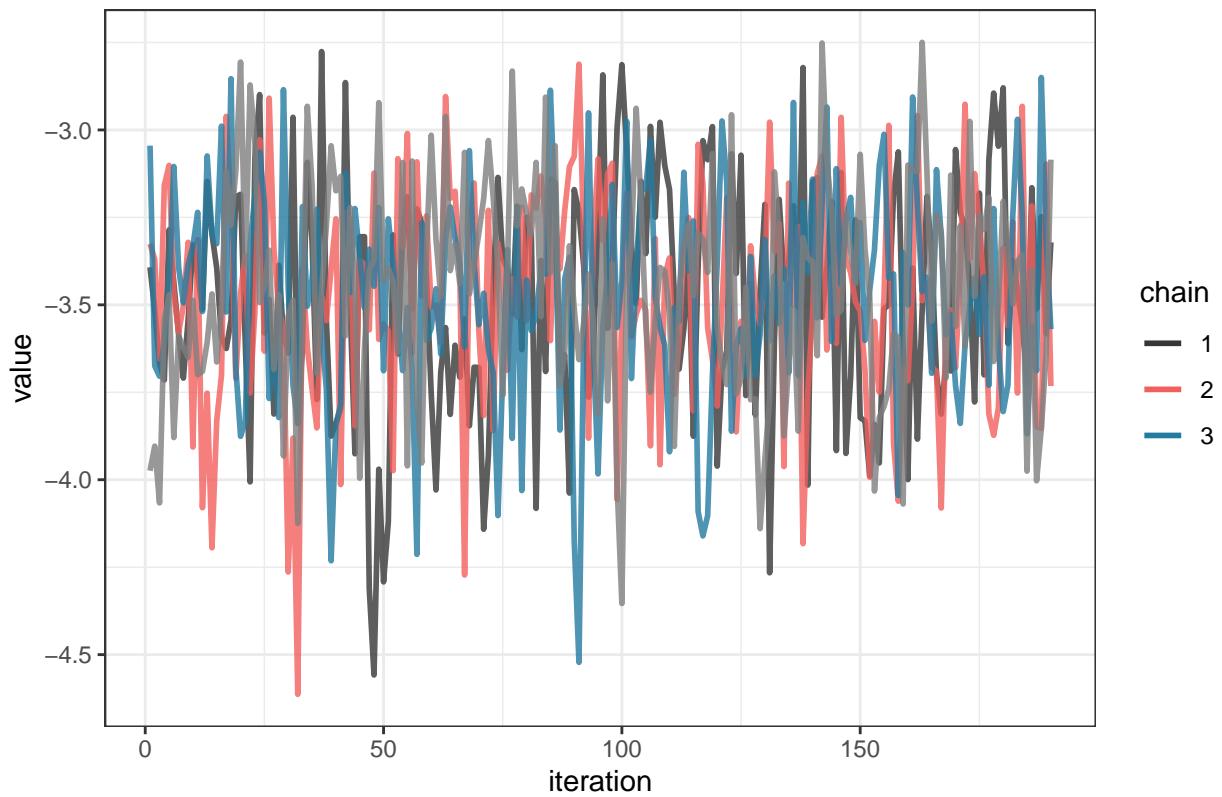
Traceplot of bs_gammas_2



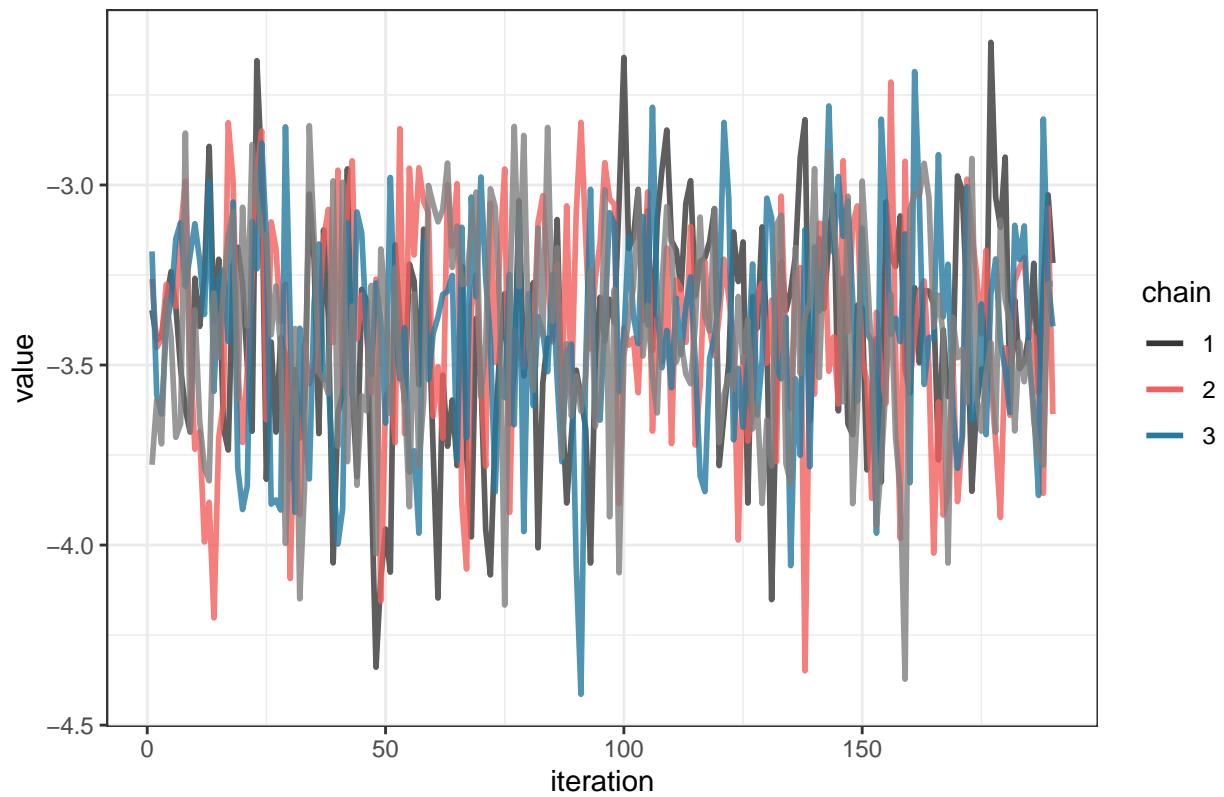
Traceplot of bs_gammas_3



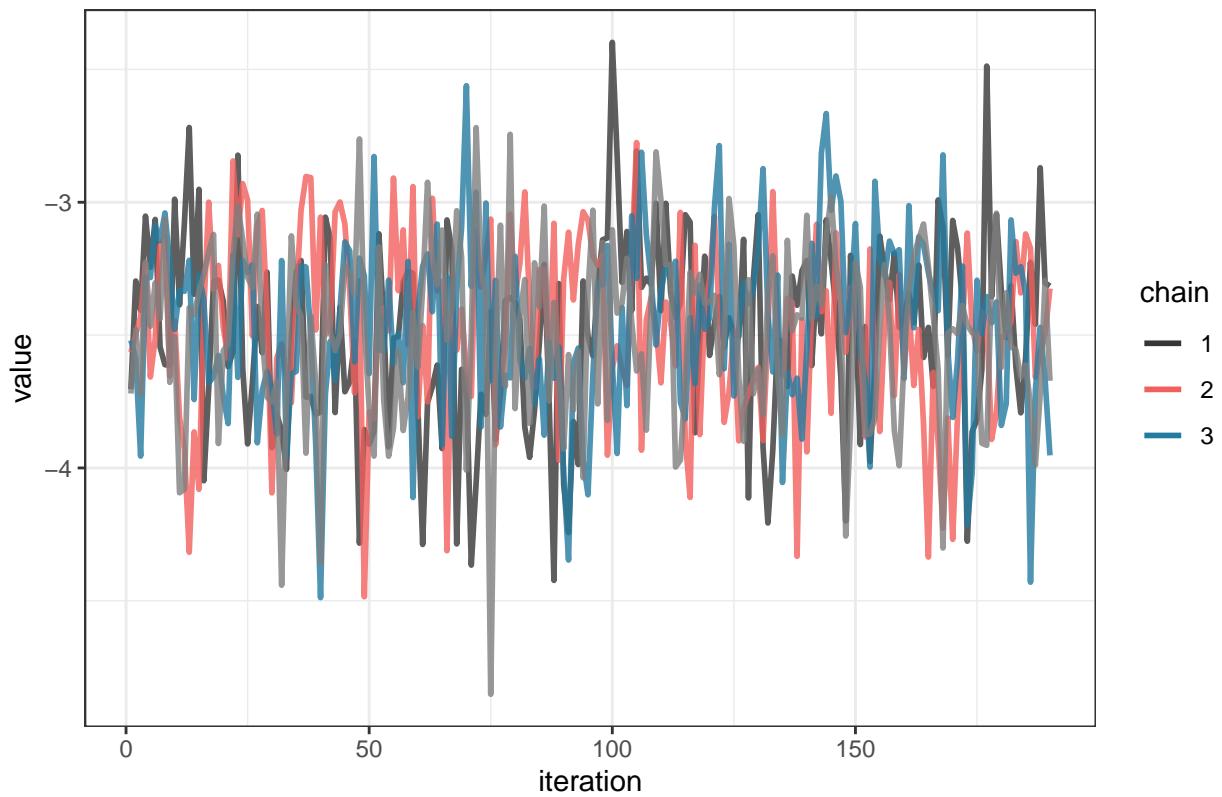
Traceplot of bs_gammas_4



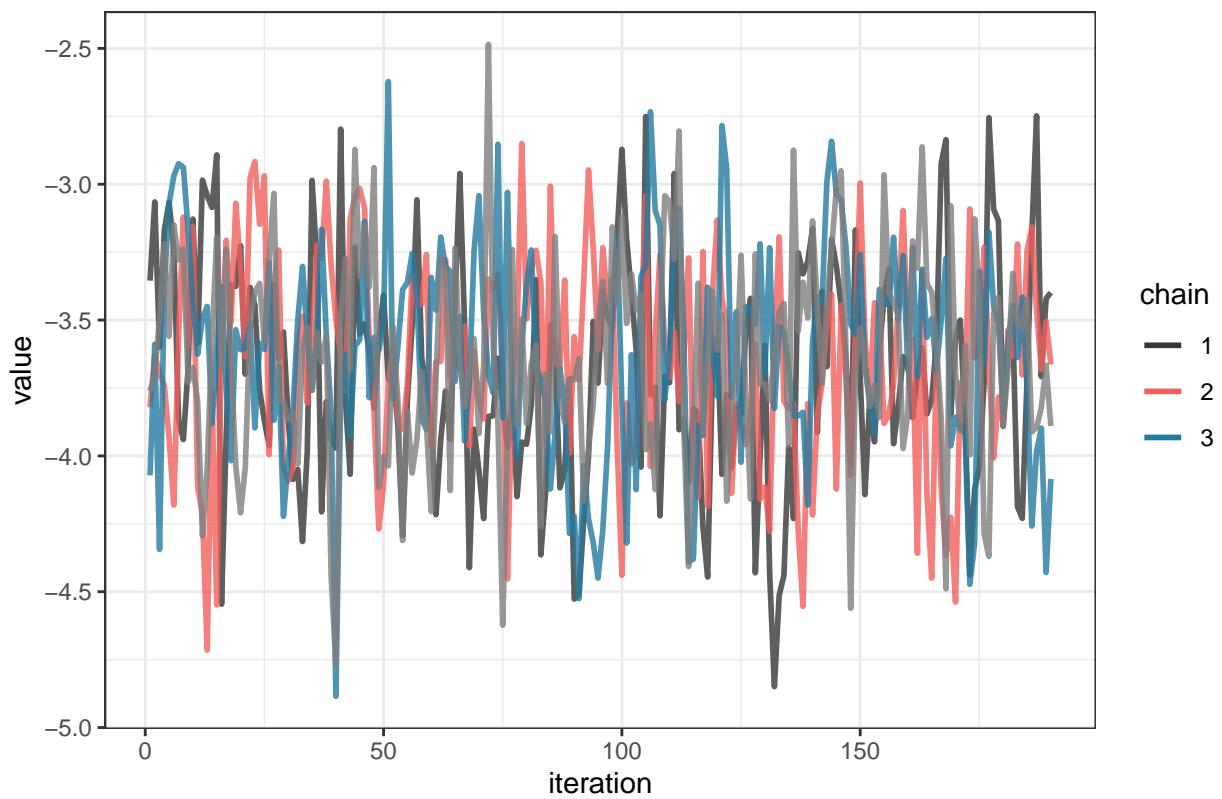
Traceplot of bs_gammas_5



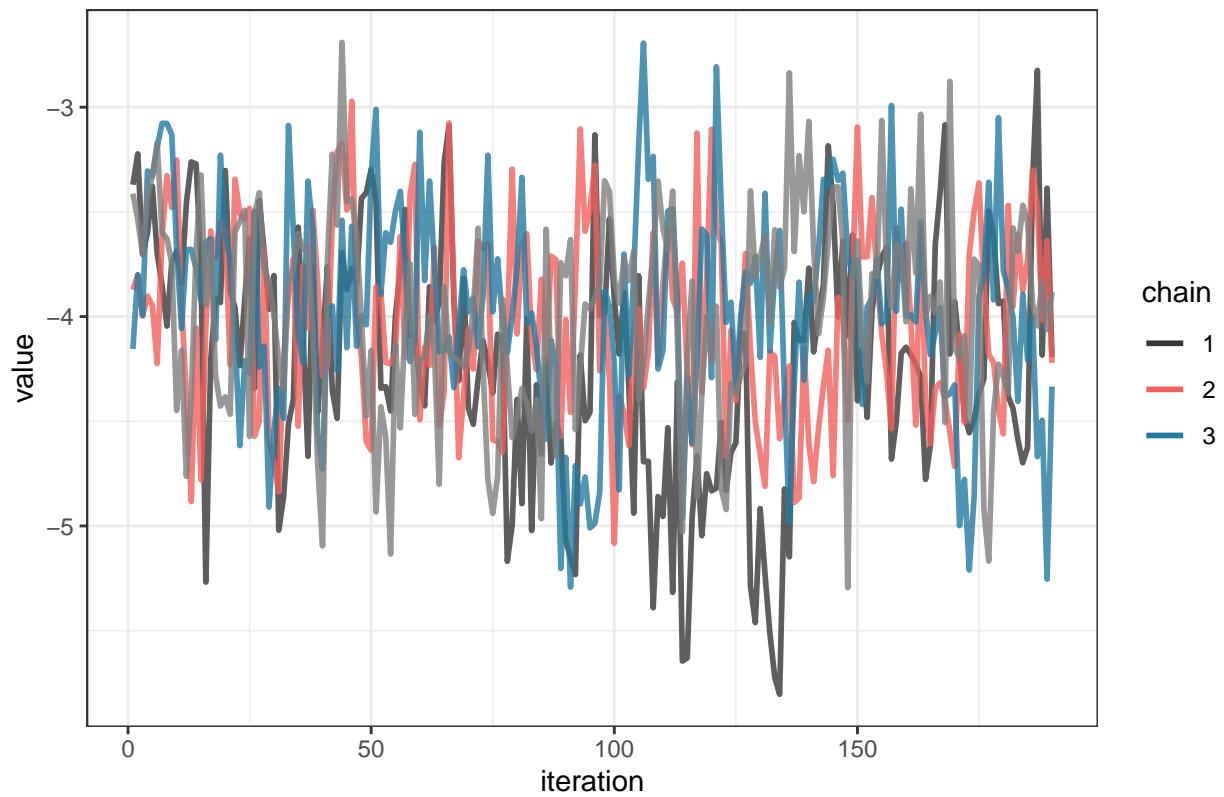
Traceplot of bs_gammas_6



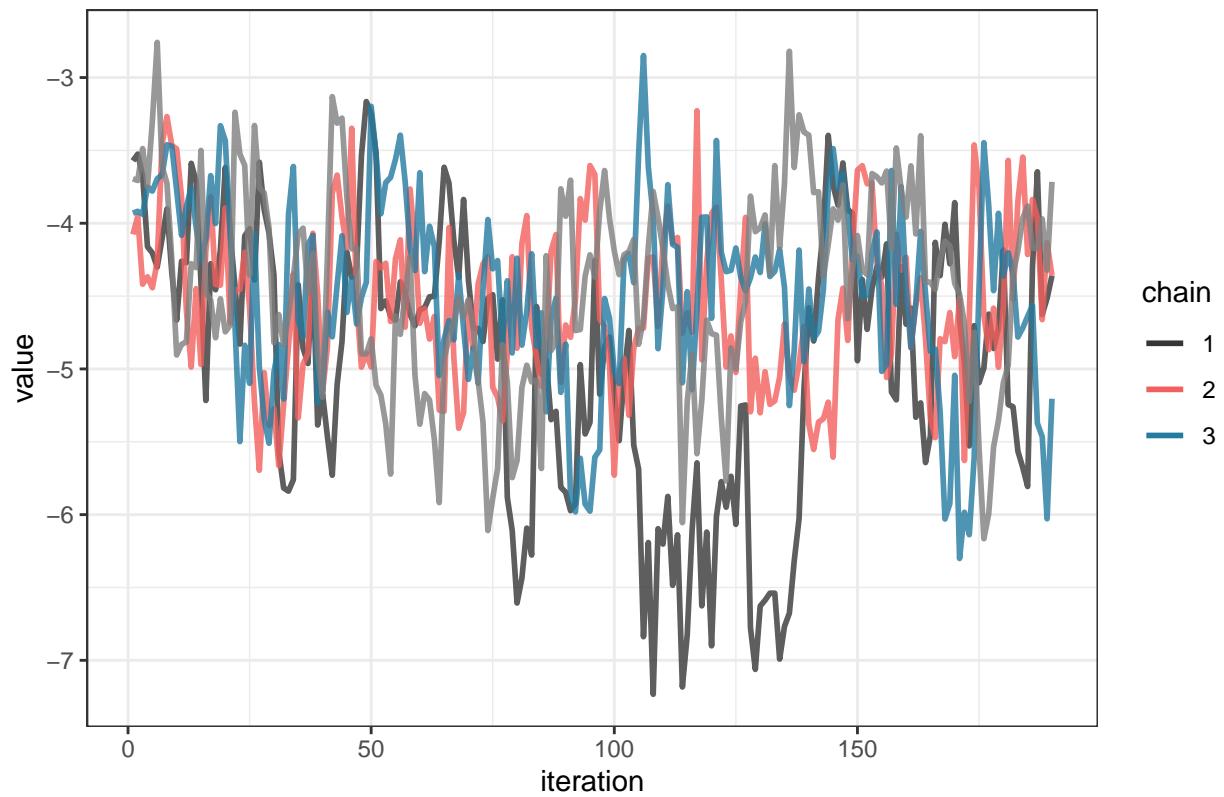
Traceplot of bs_gammas_7



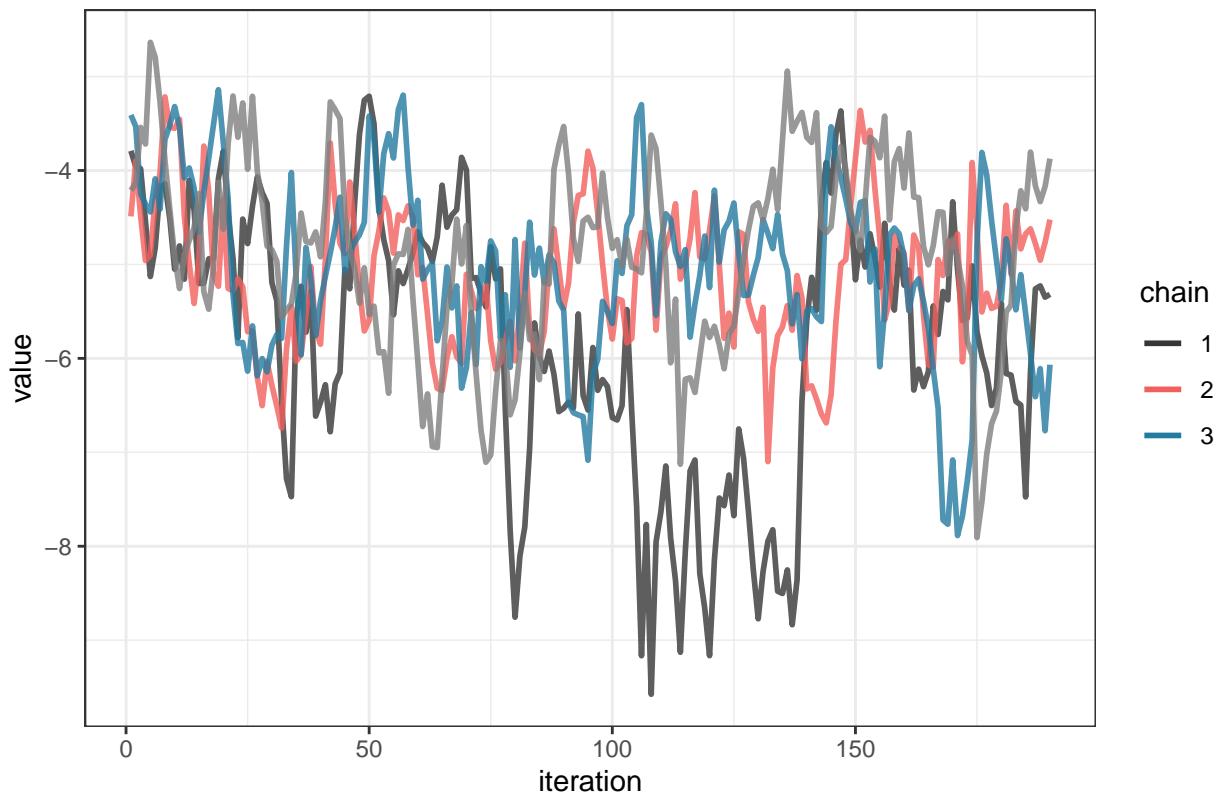
Traceplot of bs_gammas_8



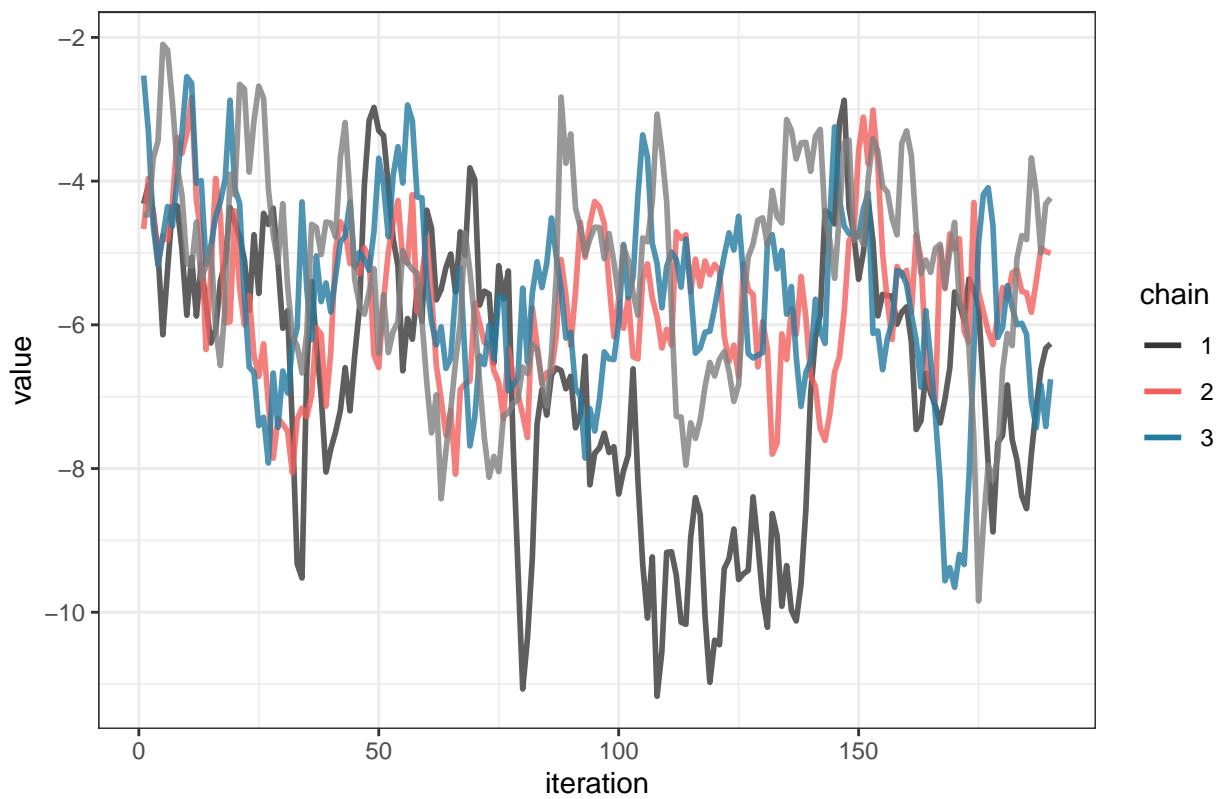
Traceplot of bs_gammas_9



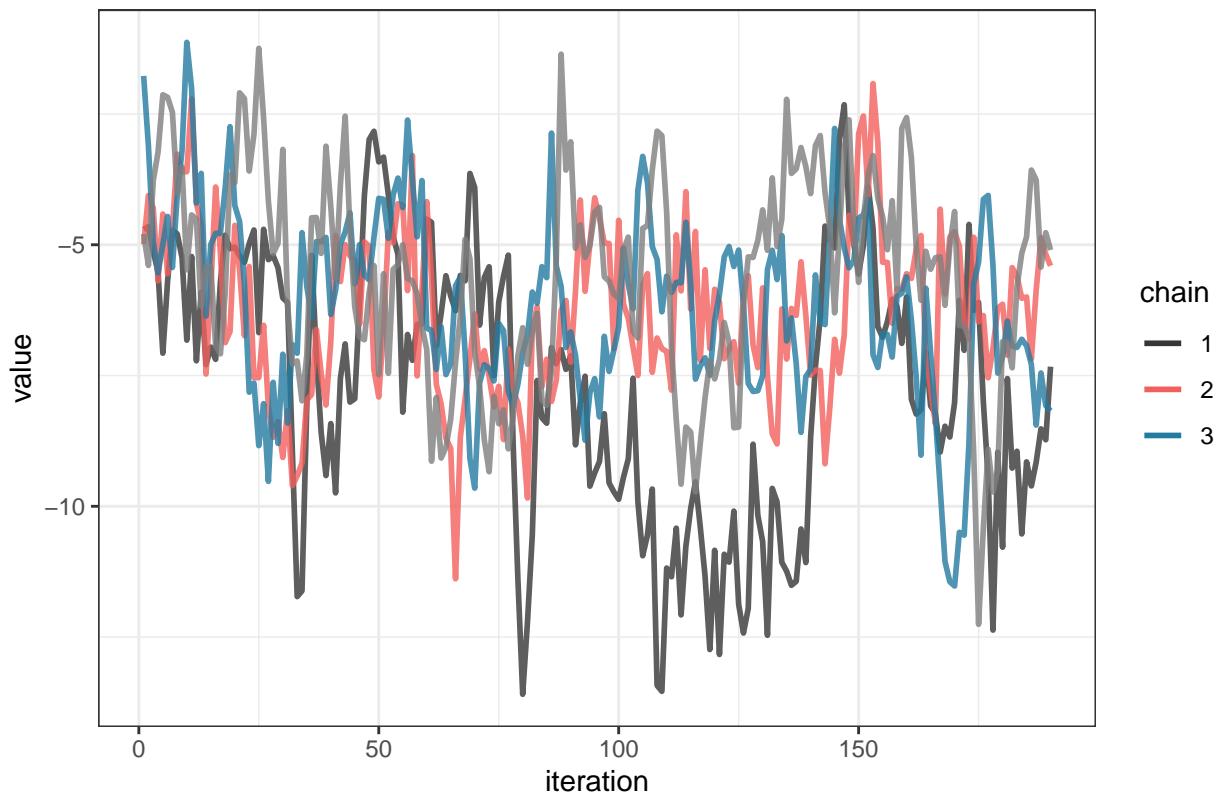
Traceplot of bs_gammas_10



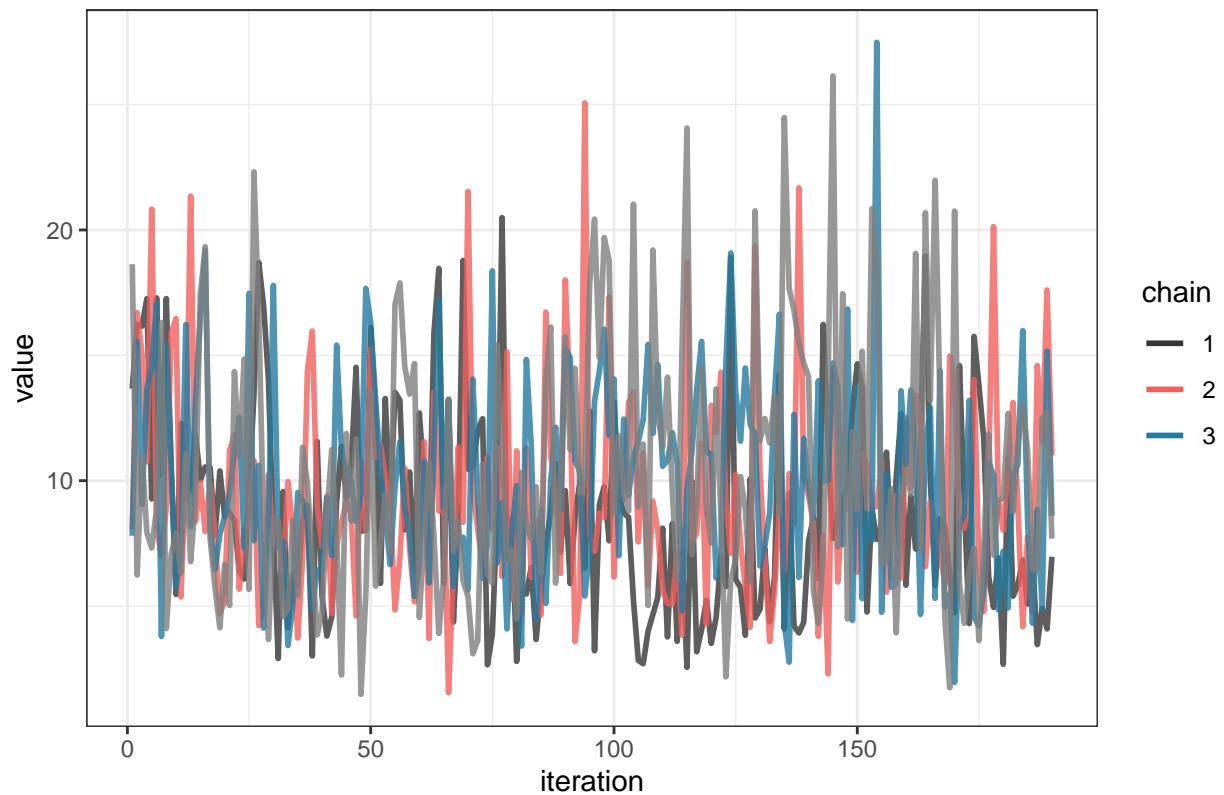
Traceplot of bs_gammas_11



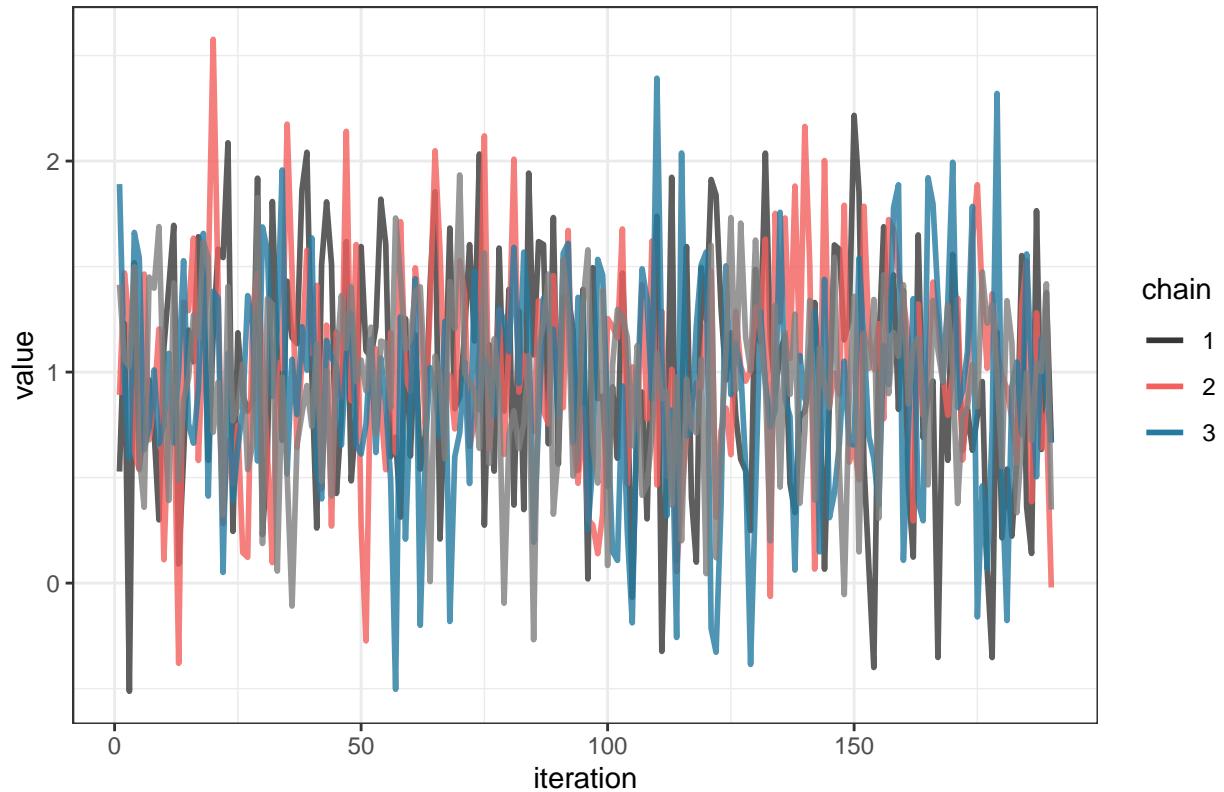
Traceplot of bs_gammas_12



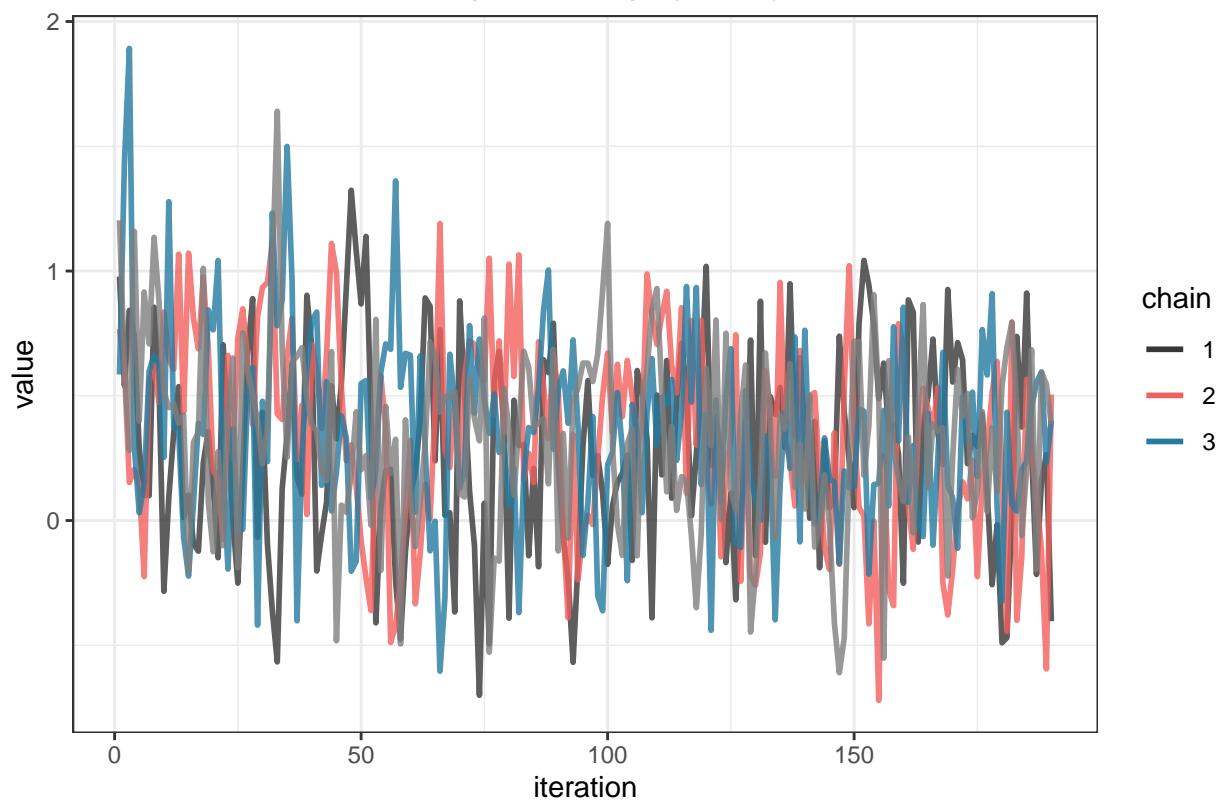
Traceplot of tau_bs_gammas



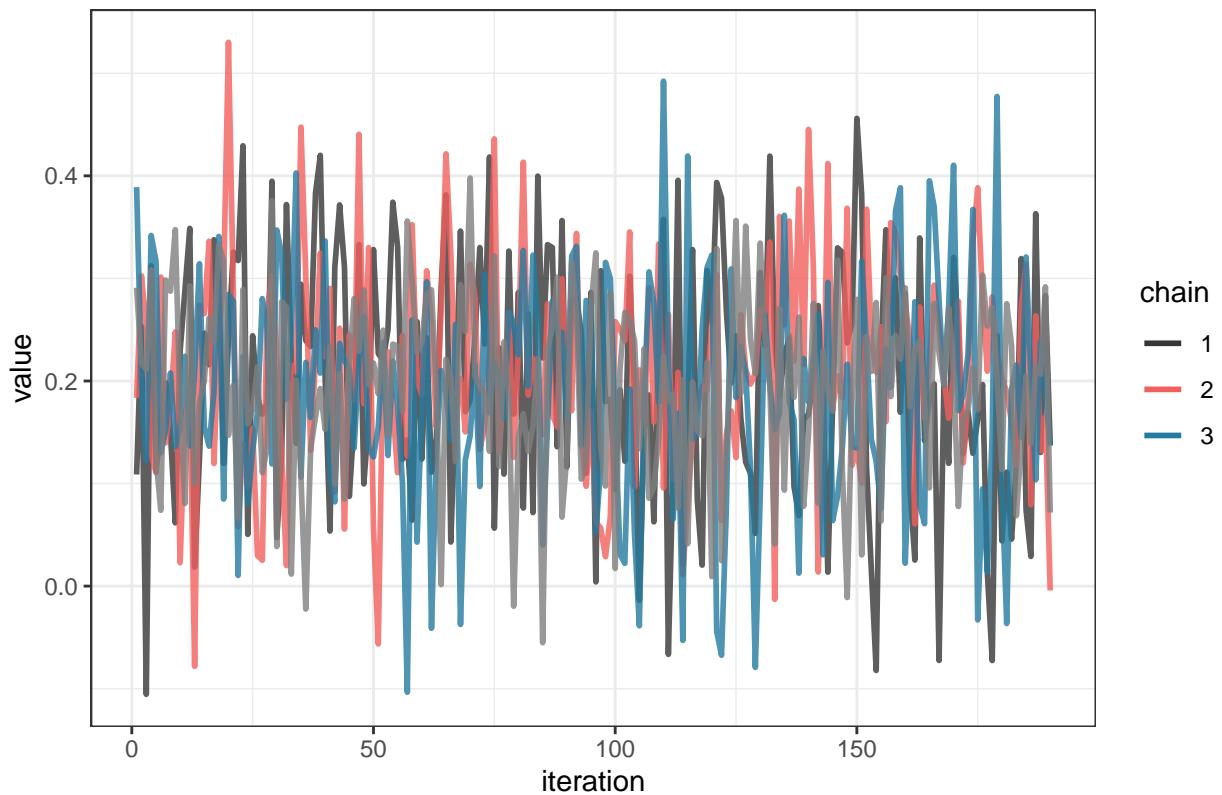
Traceplot of LOWC31



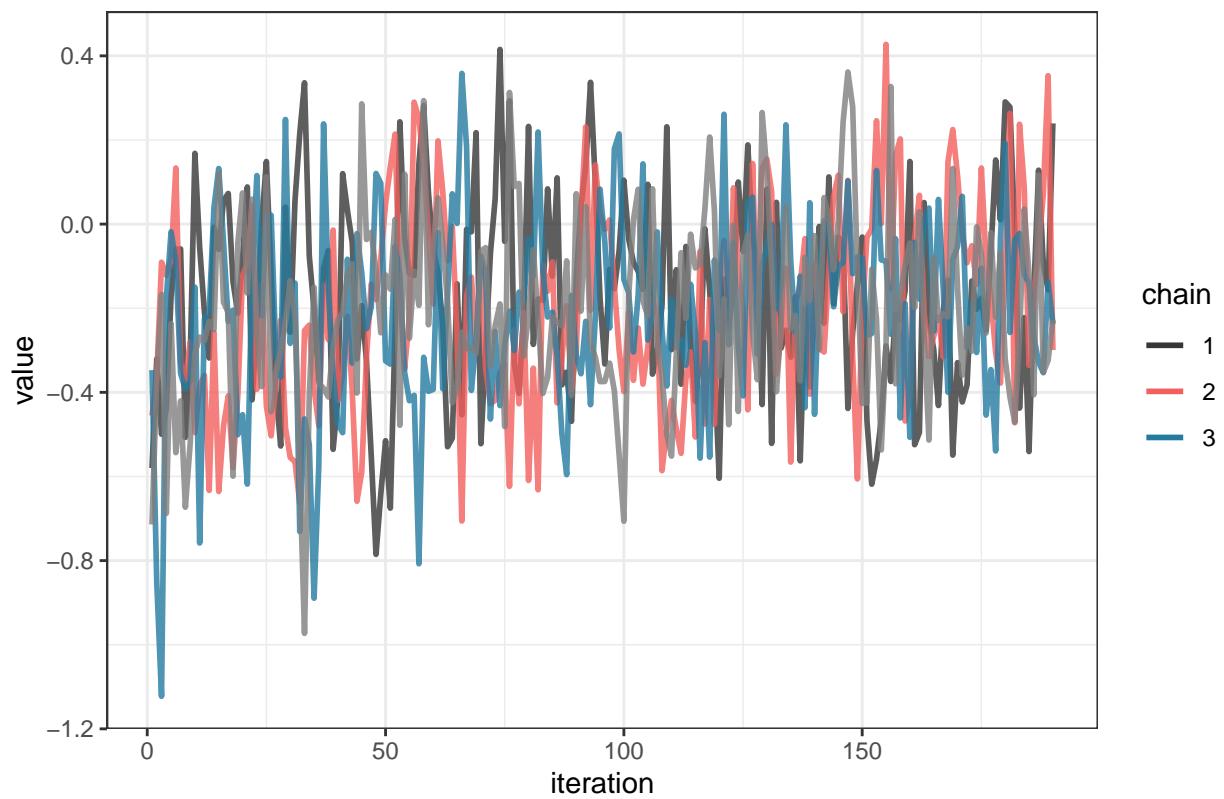
Traceplot of slope(eGFR)



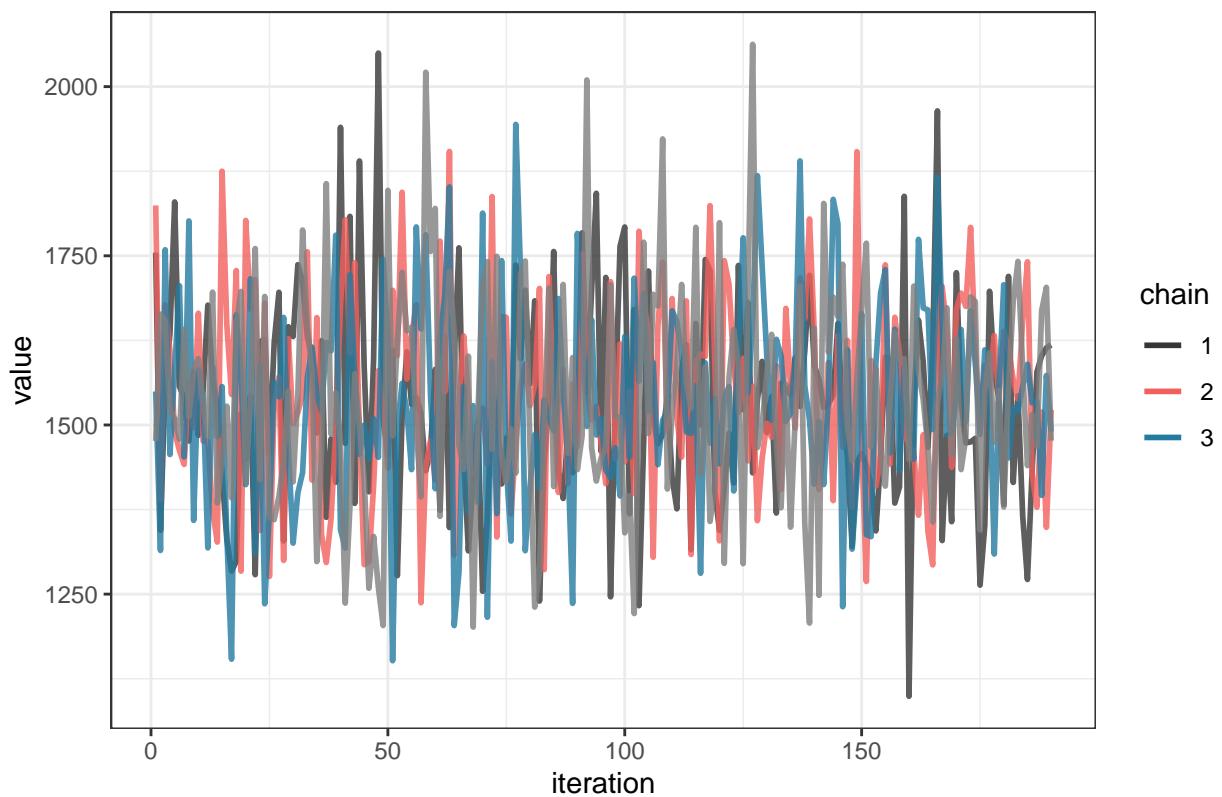
Traceplot of



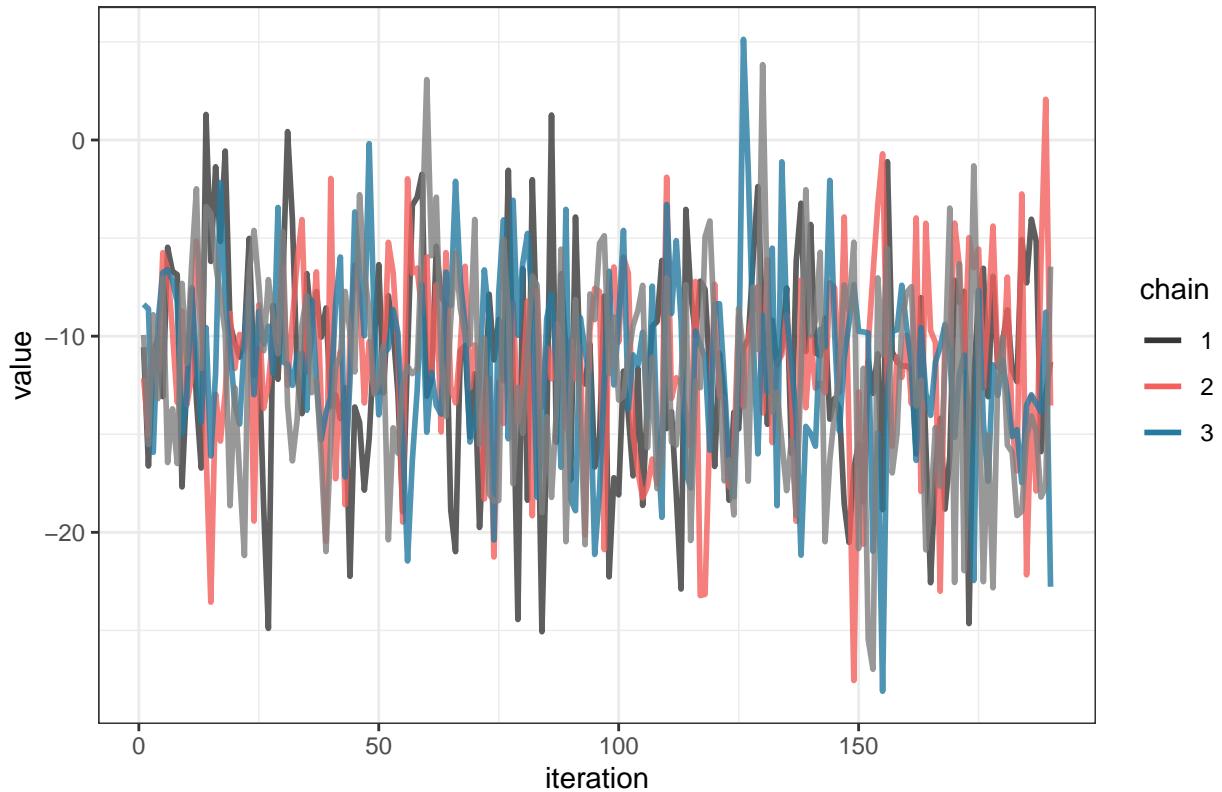
Traceplot of .1



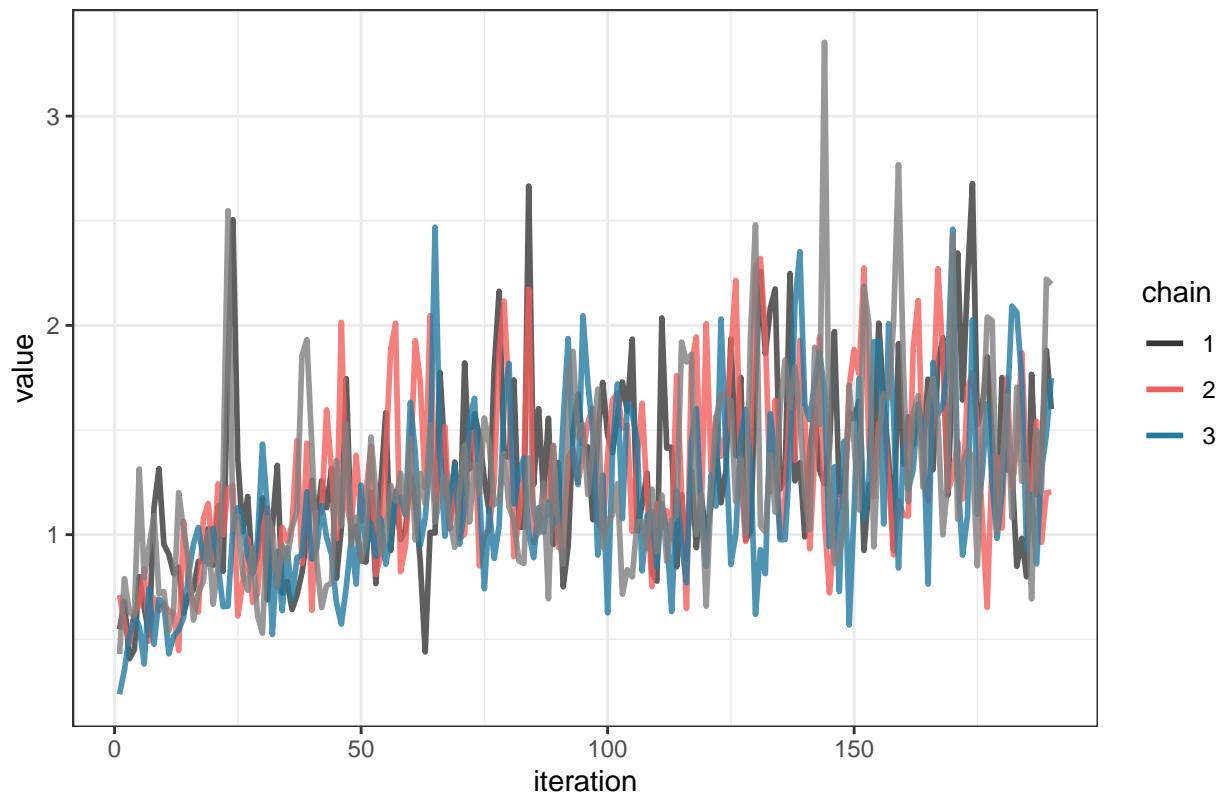
Traceplot of $D[1, 1]$



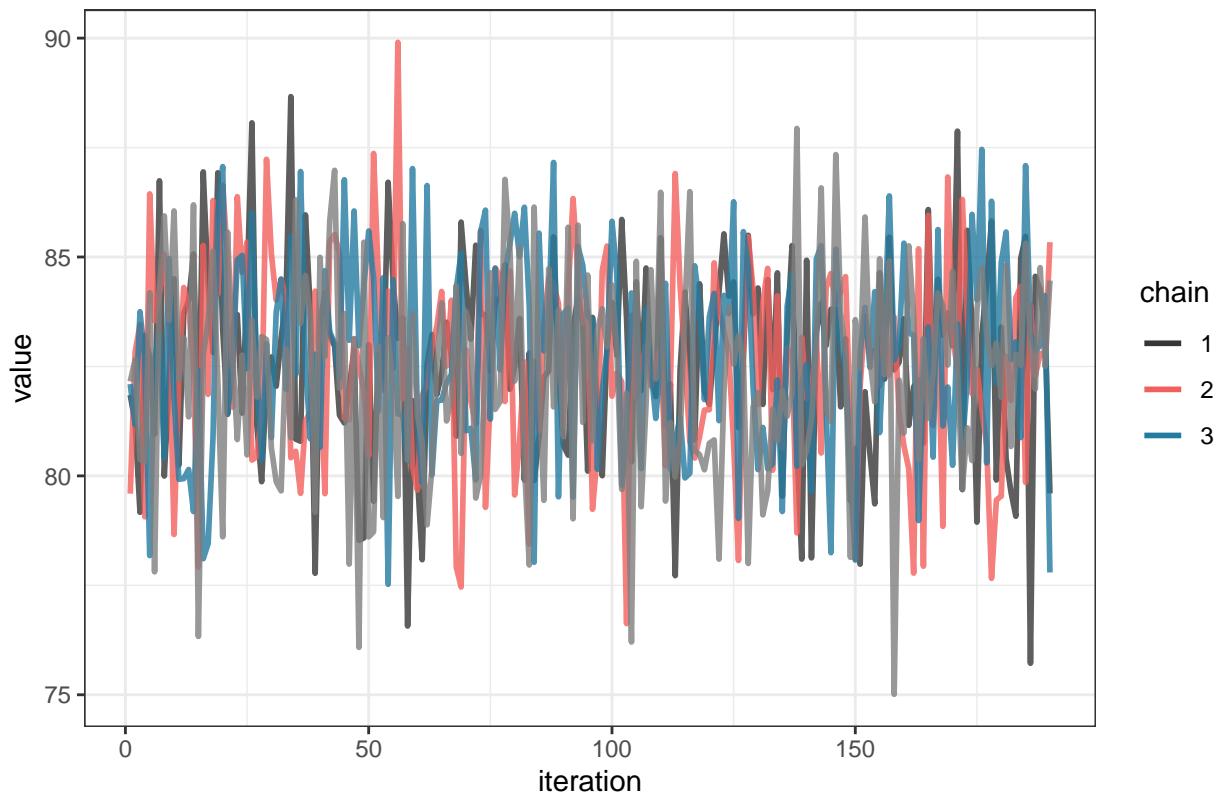
Traceplot of $D[2, 1]$



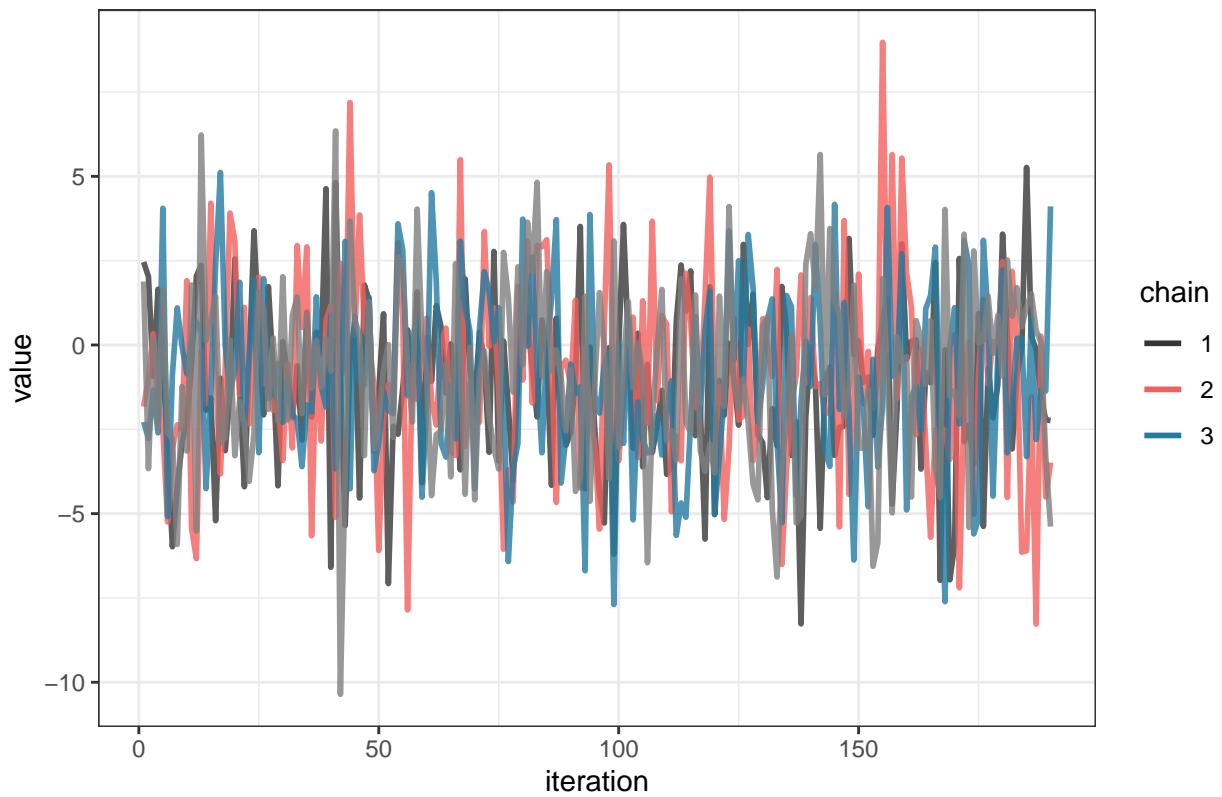
Traceplot of $D[2, 2]$



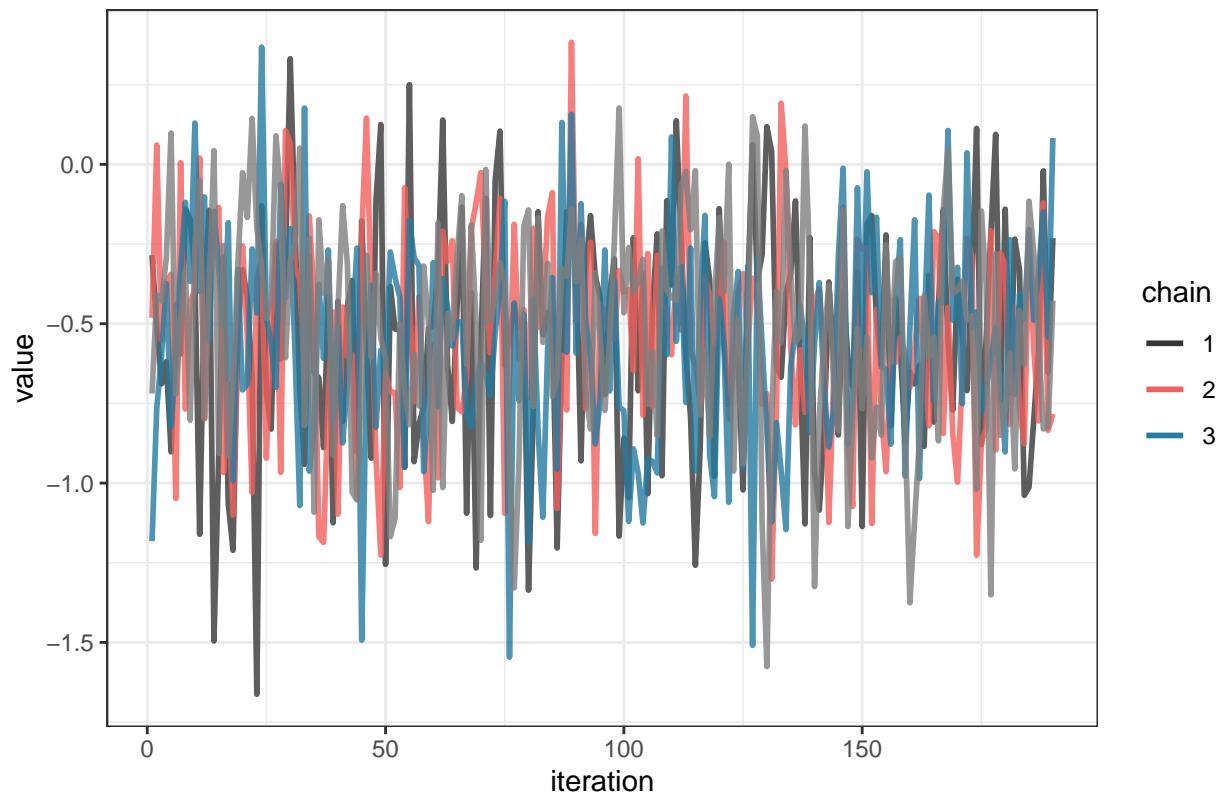
Traceplot of (Intercept)



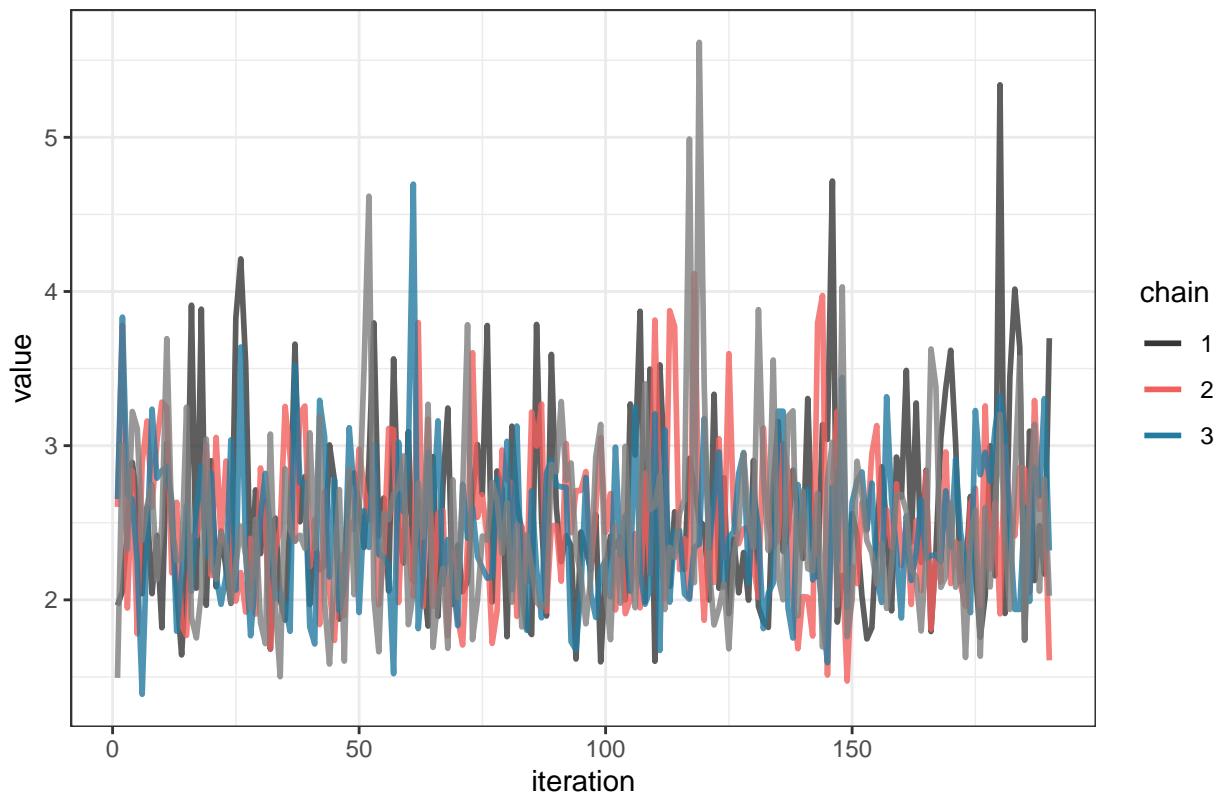
Traceplot of LOWC31.1



Traceplot of time

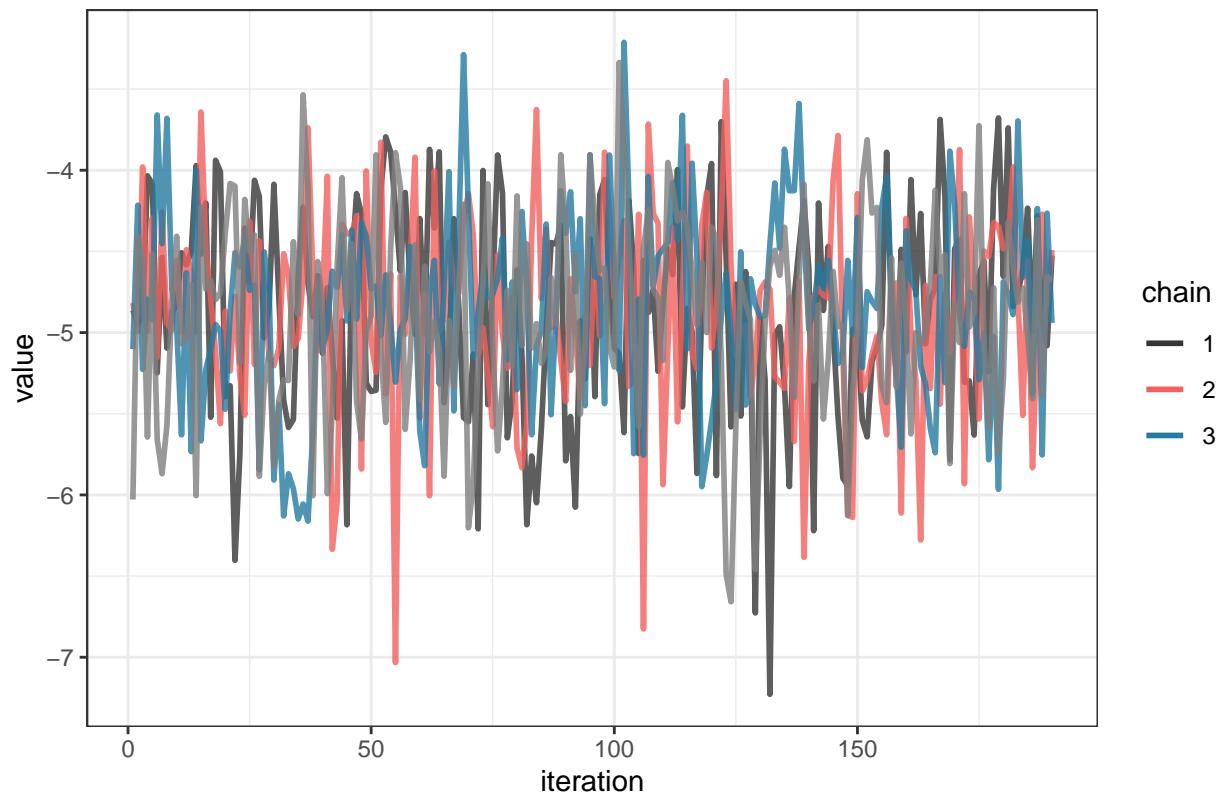


Traceplot of sigmas_1

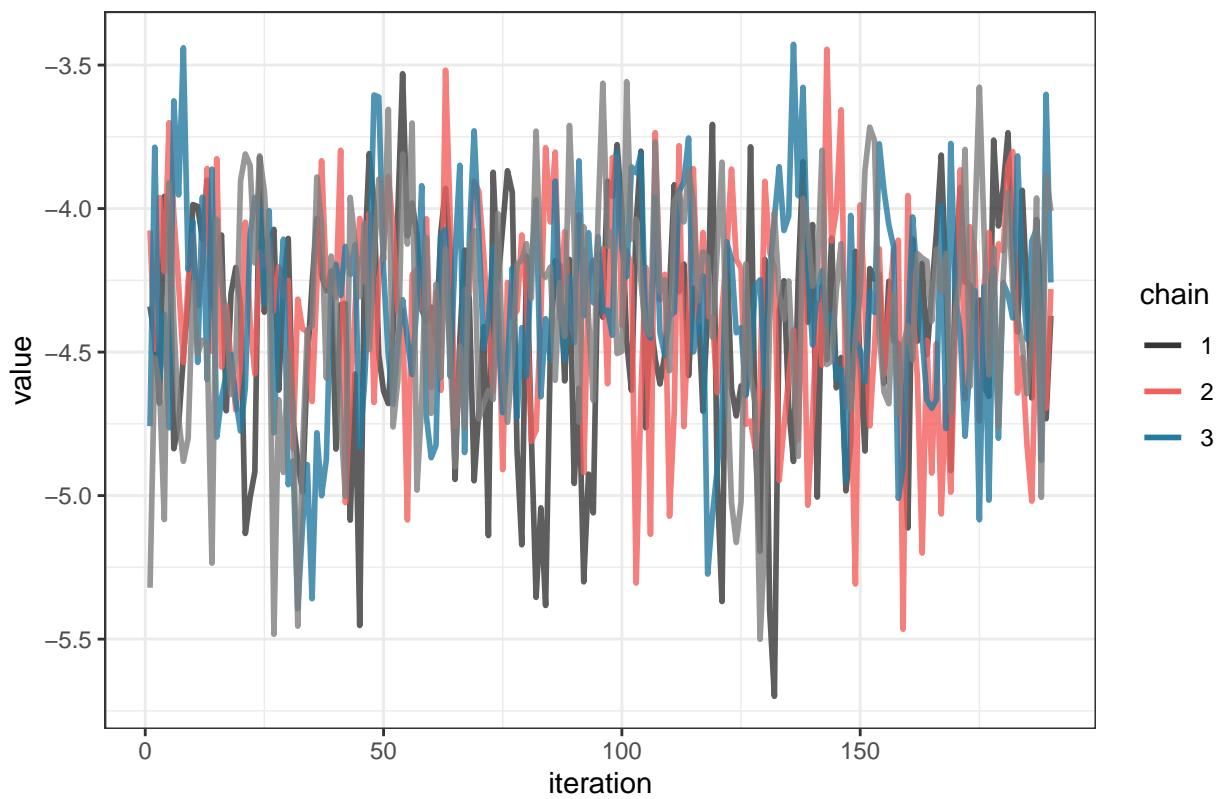


```
traceCplt2 <- ggtraceplot(jointCFit2)
```

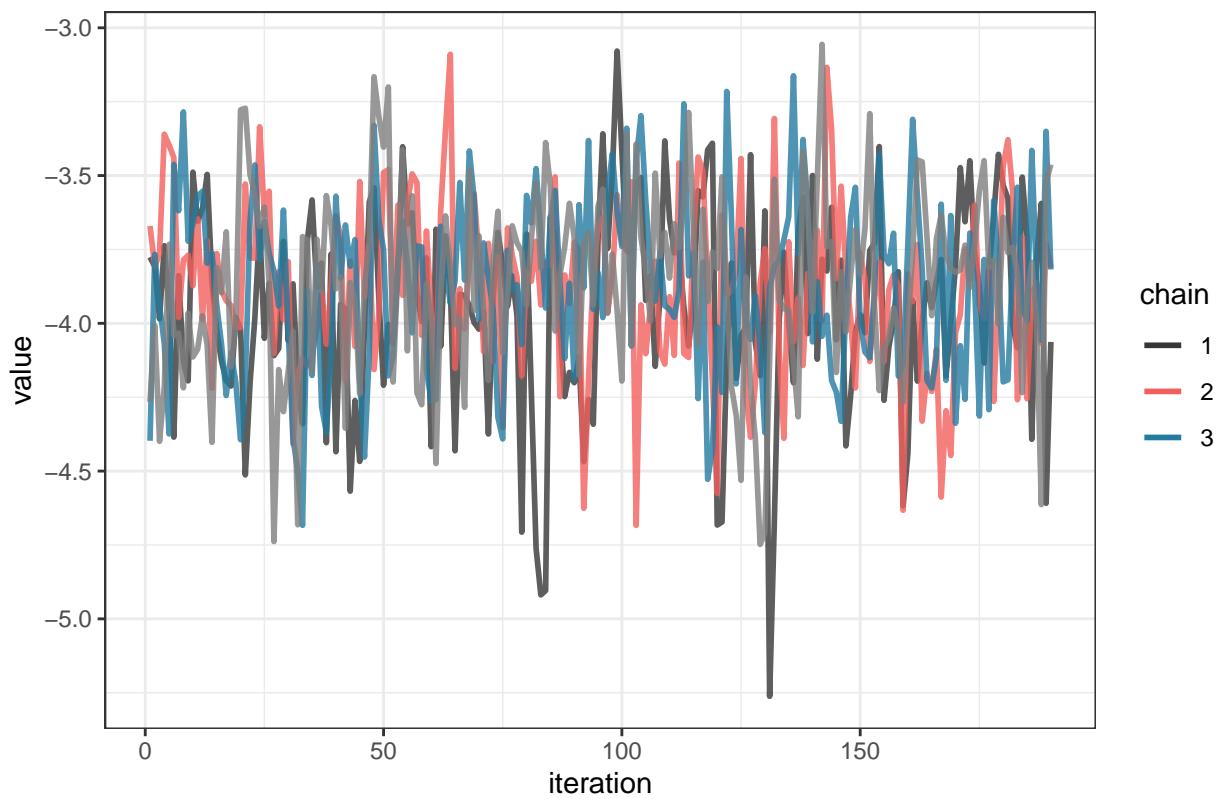
Traceplot of bs_gammas_1



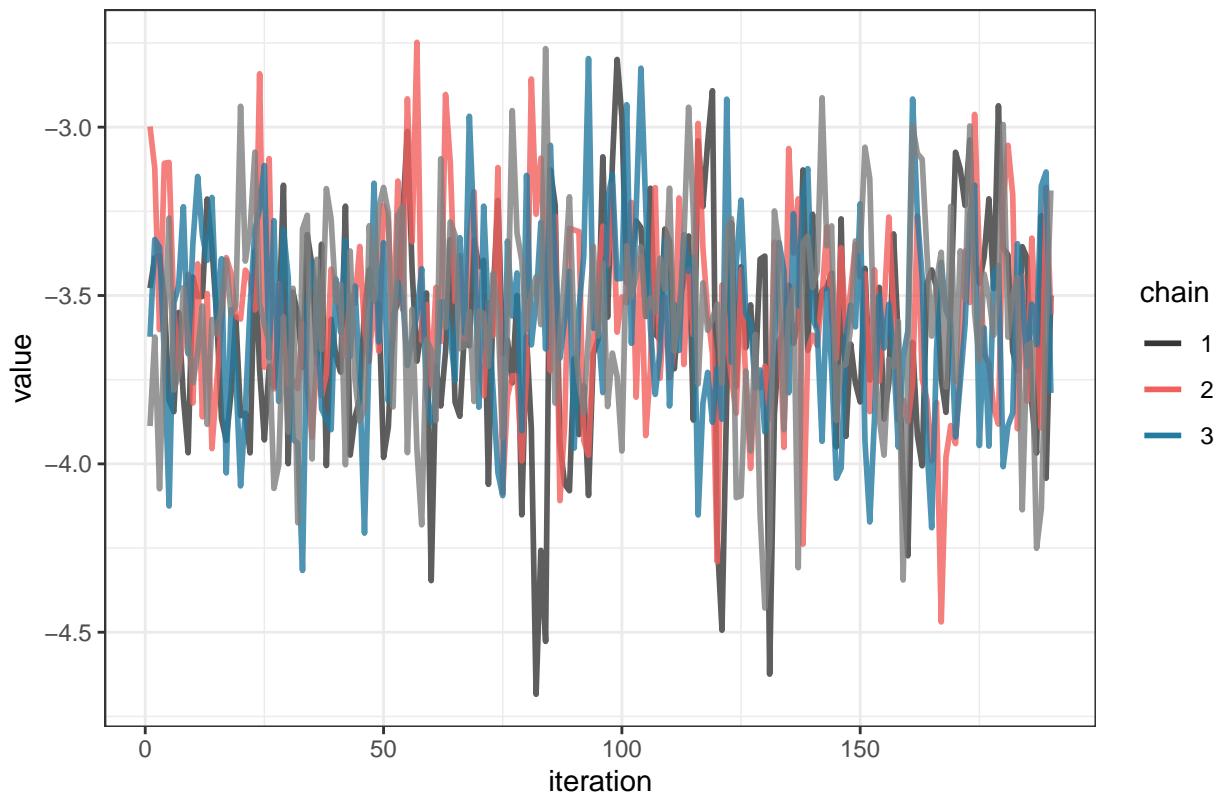
Traceplot of bs_gammas_2



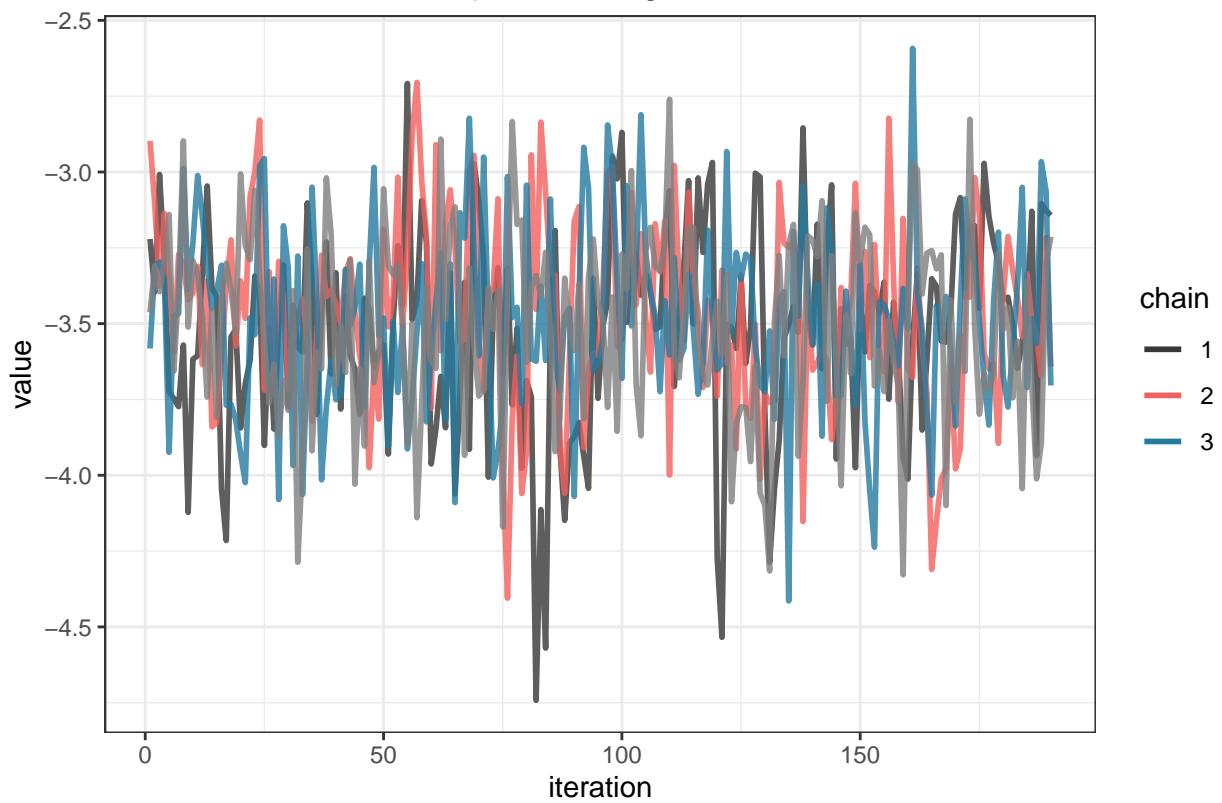
Traceplot of bs_gammas_3



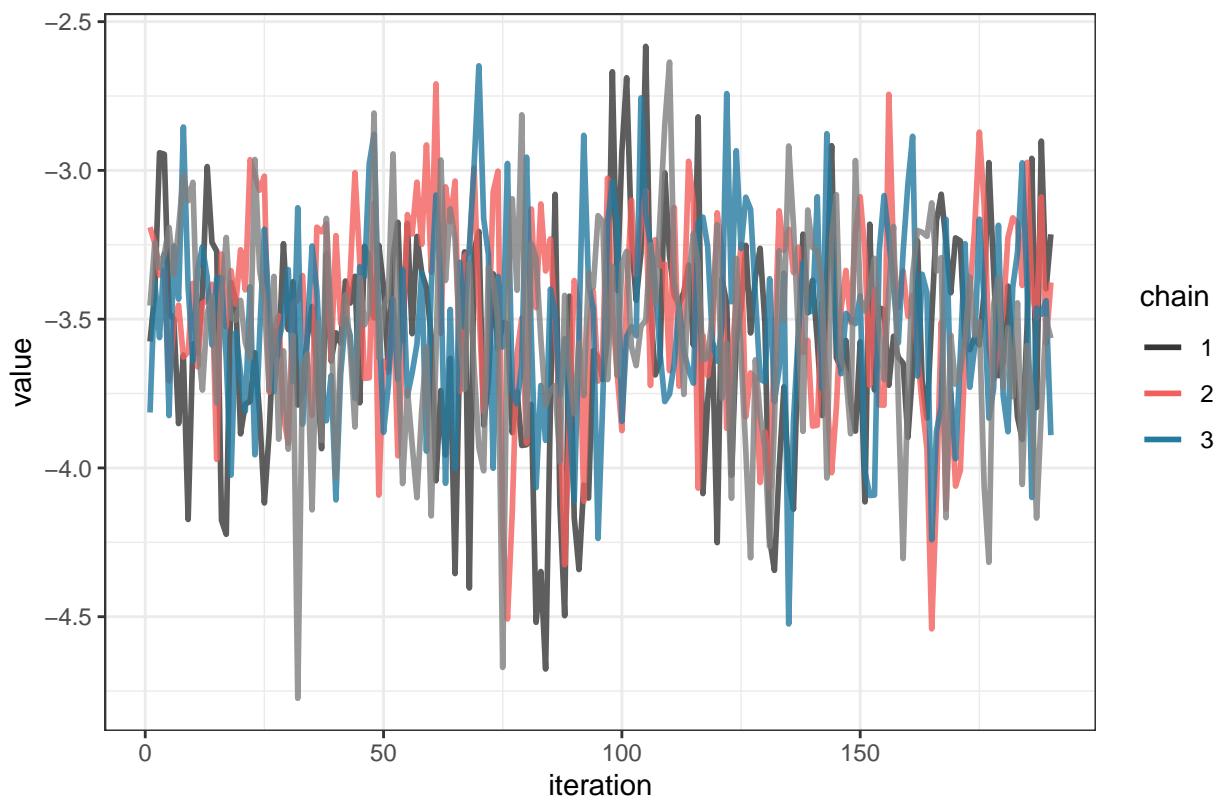
Traceplot of bs_gammas_4



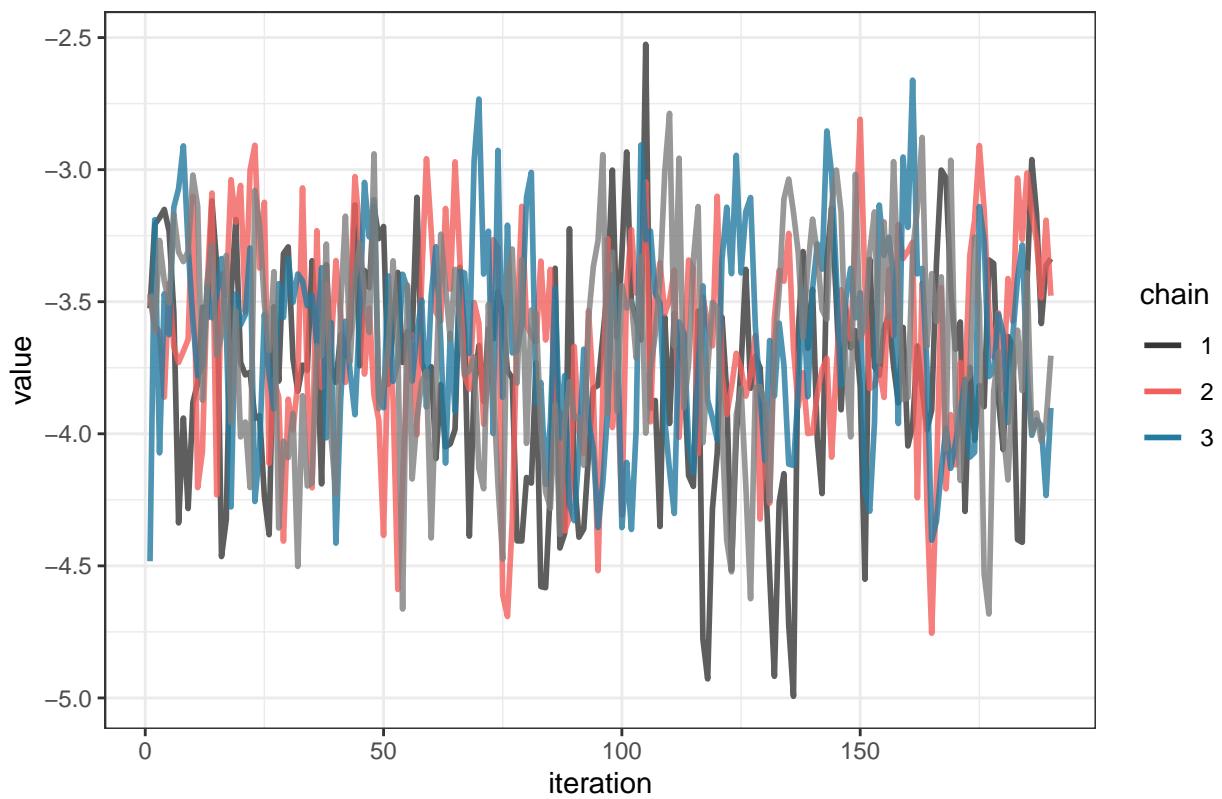
Traceplot of bs_gammas_5



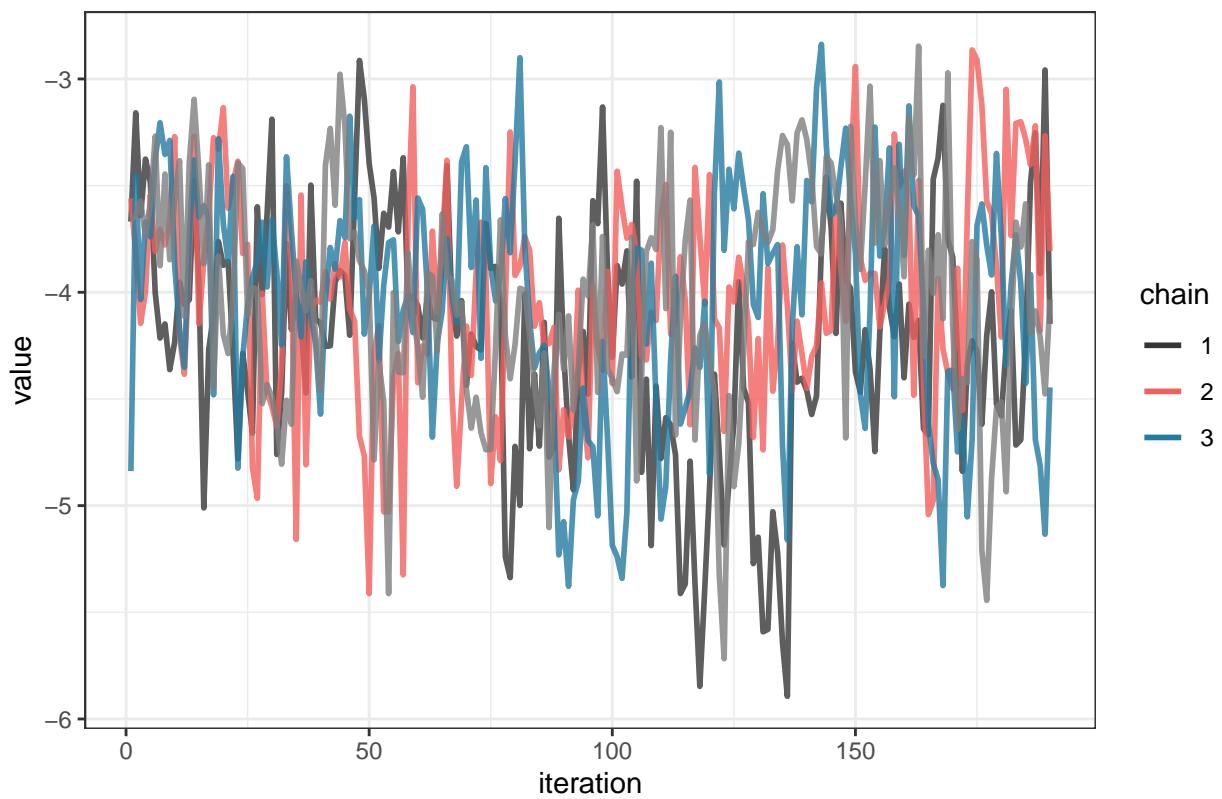
Traceplot of bs_gammas_6



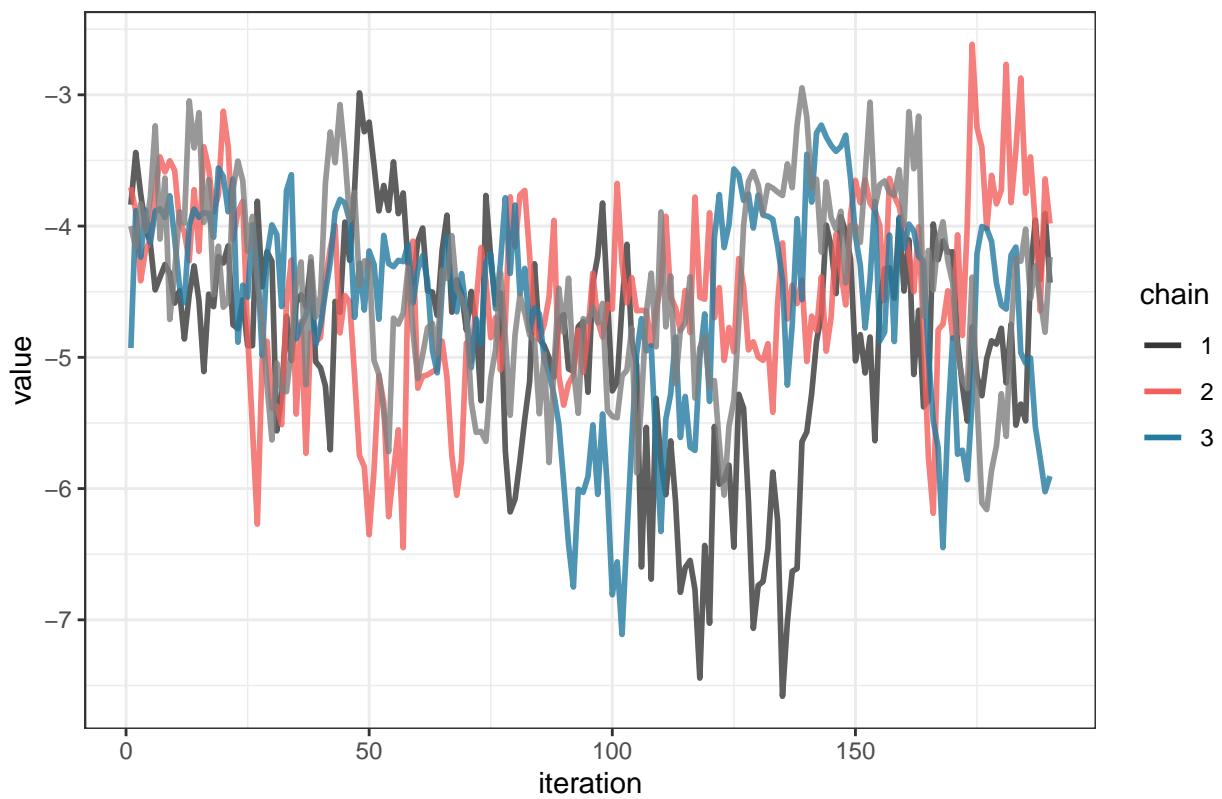
Traceplot of bs_gammas_7



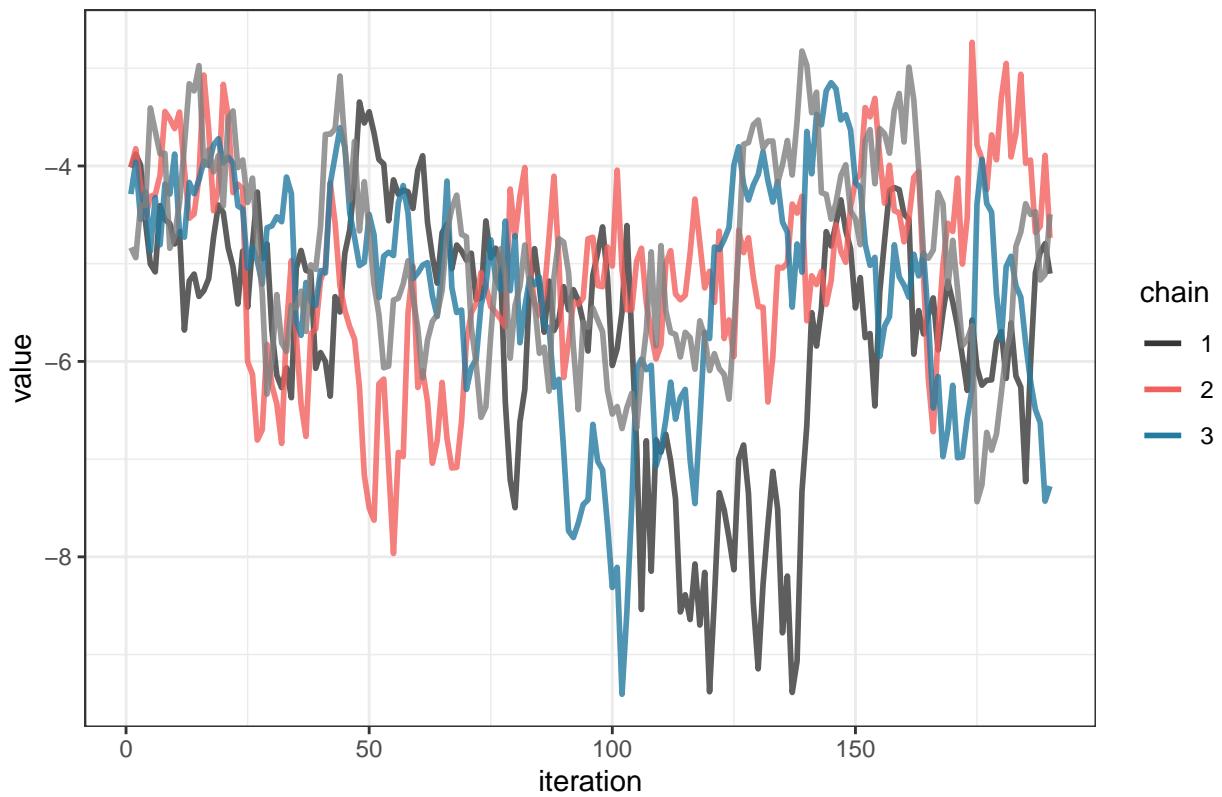
Traceplot of bs_gammas_8



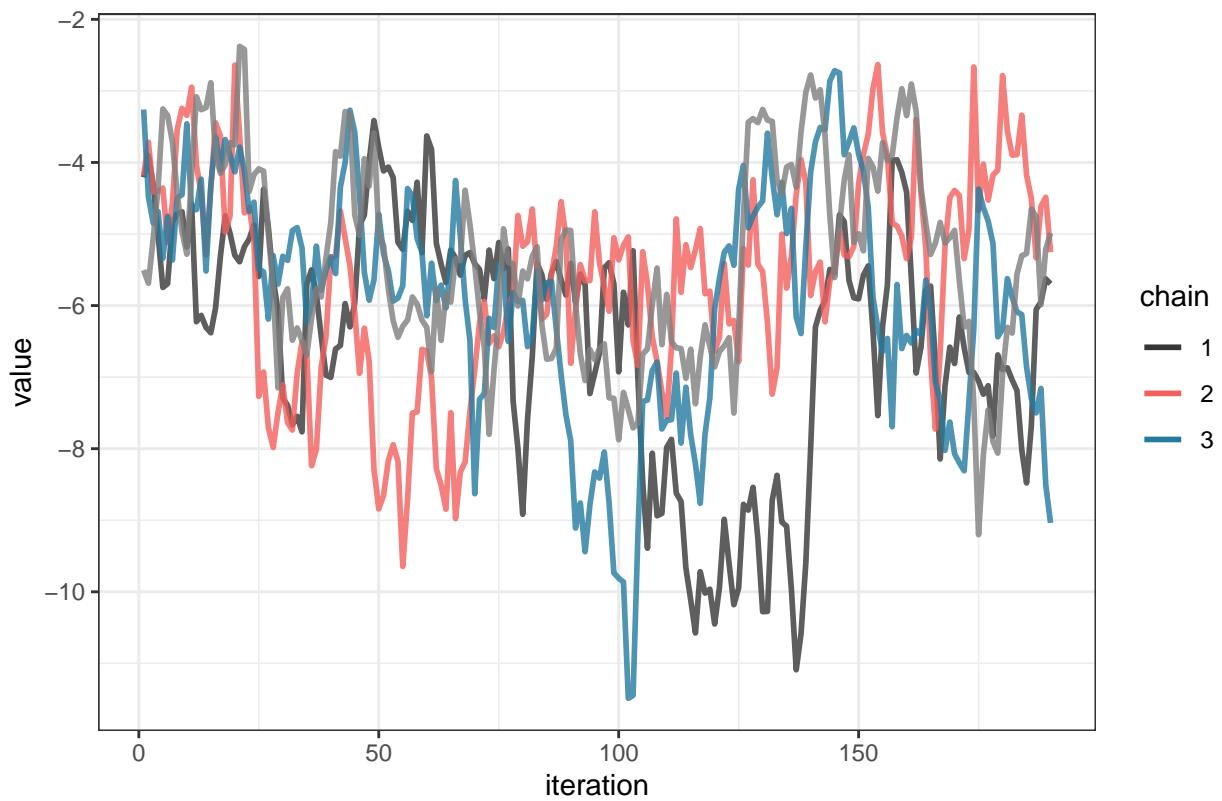
Traceplot of bs_gammas_9



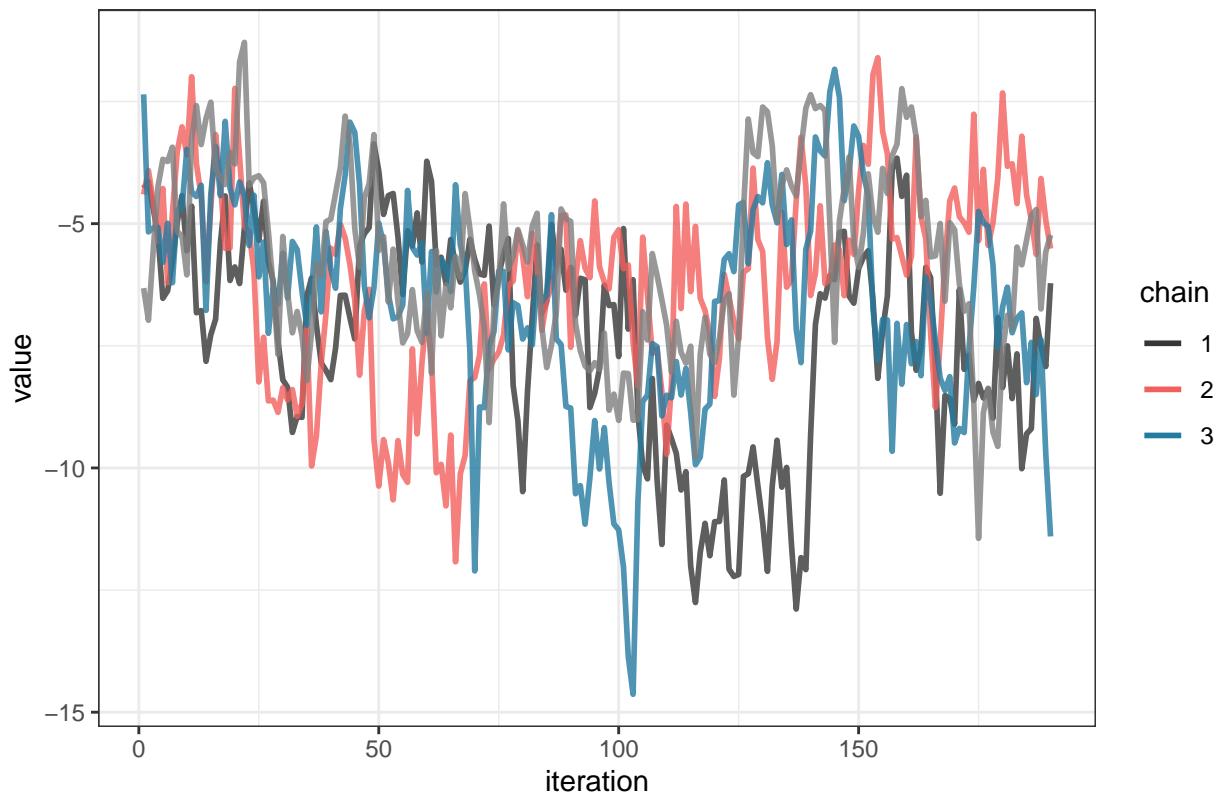
Traceplot of bs_gammas_10



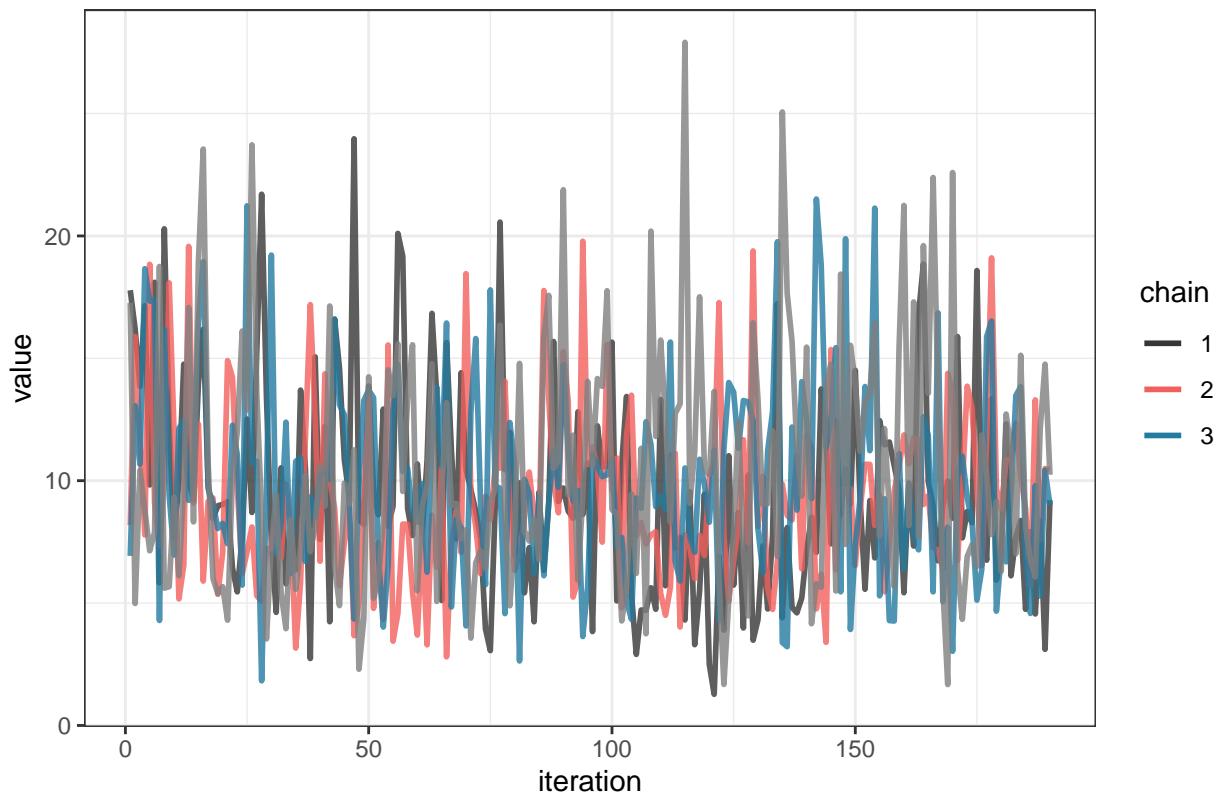
Traceplot of bs_gammas_11



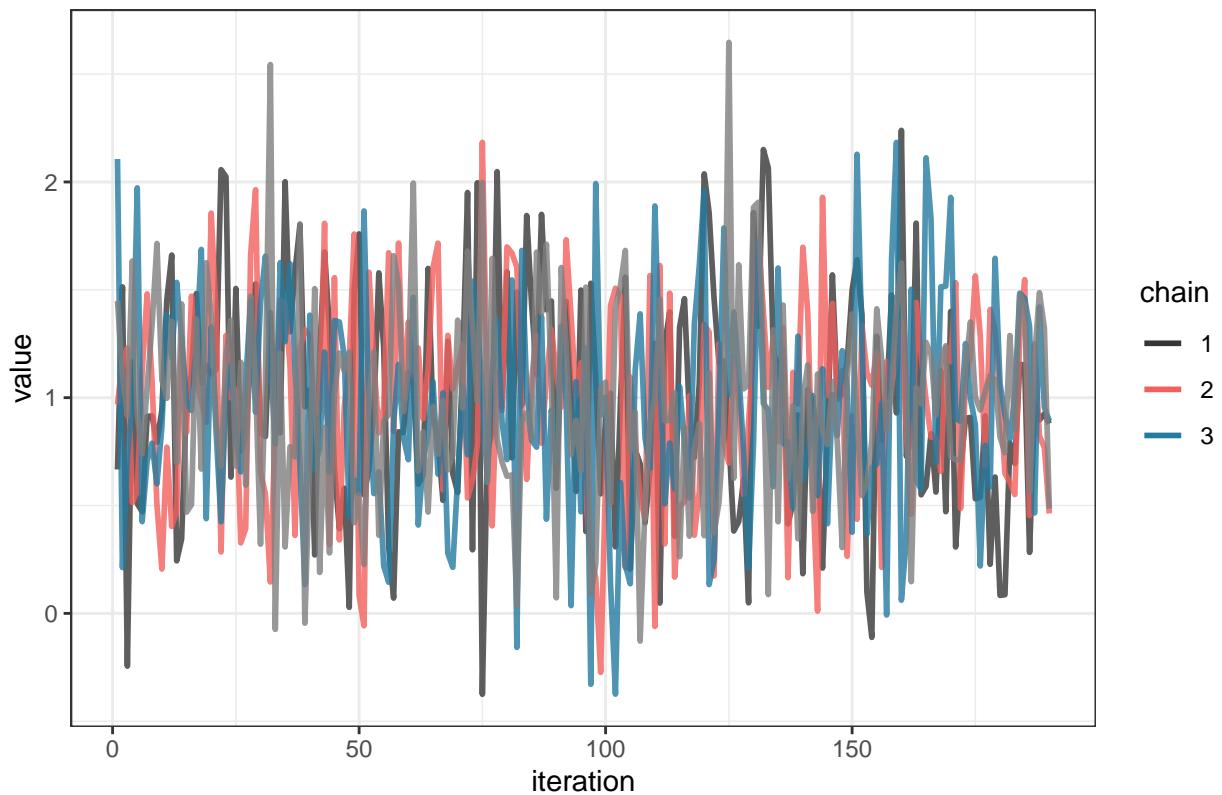
Traceplot of bs_gammas_12



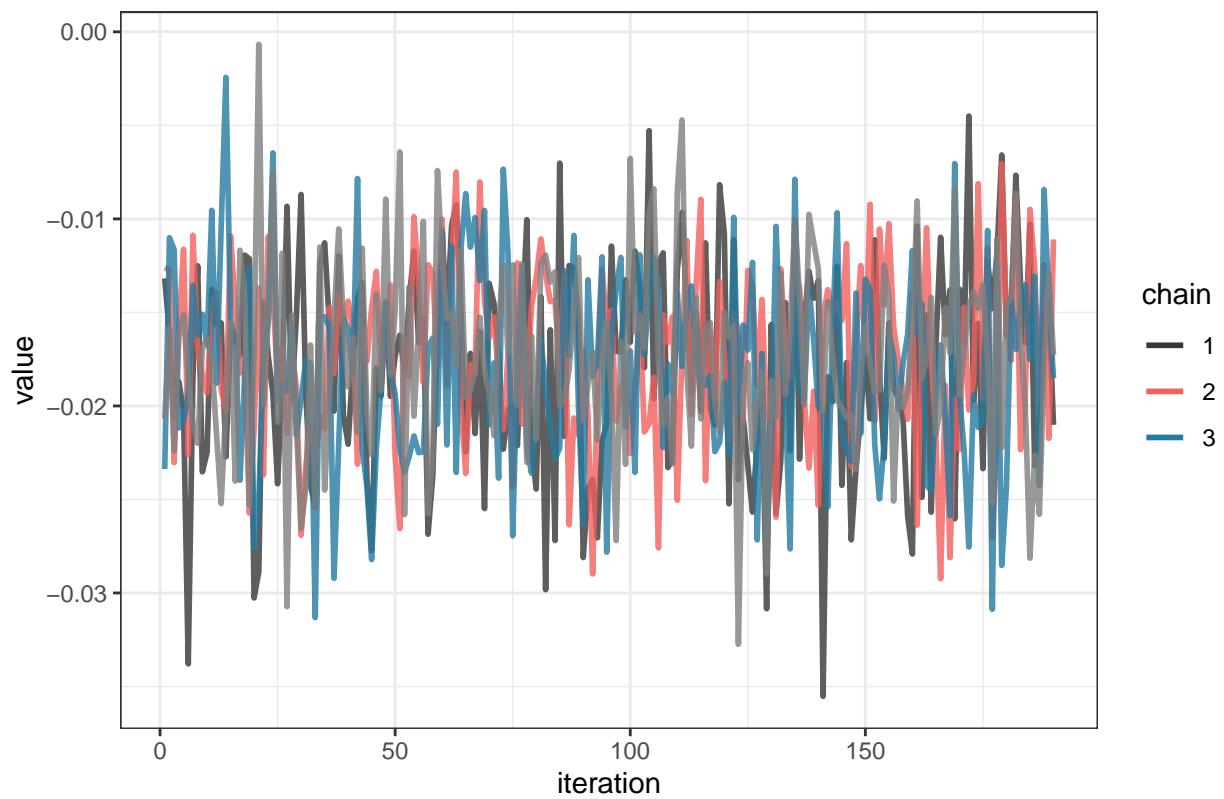
Traceplot of tau_bs_gammas



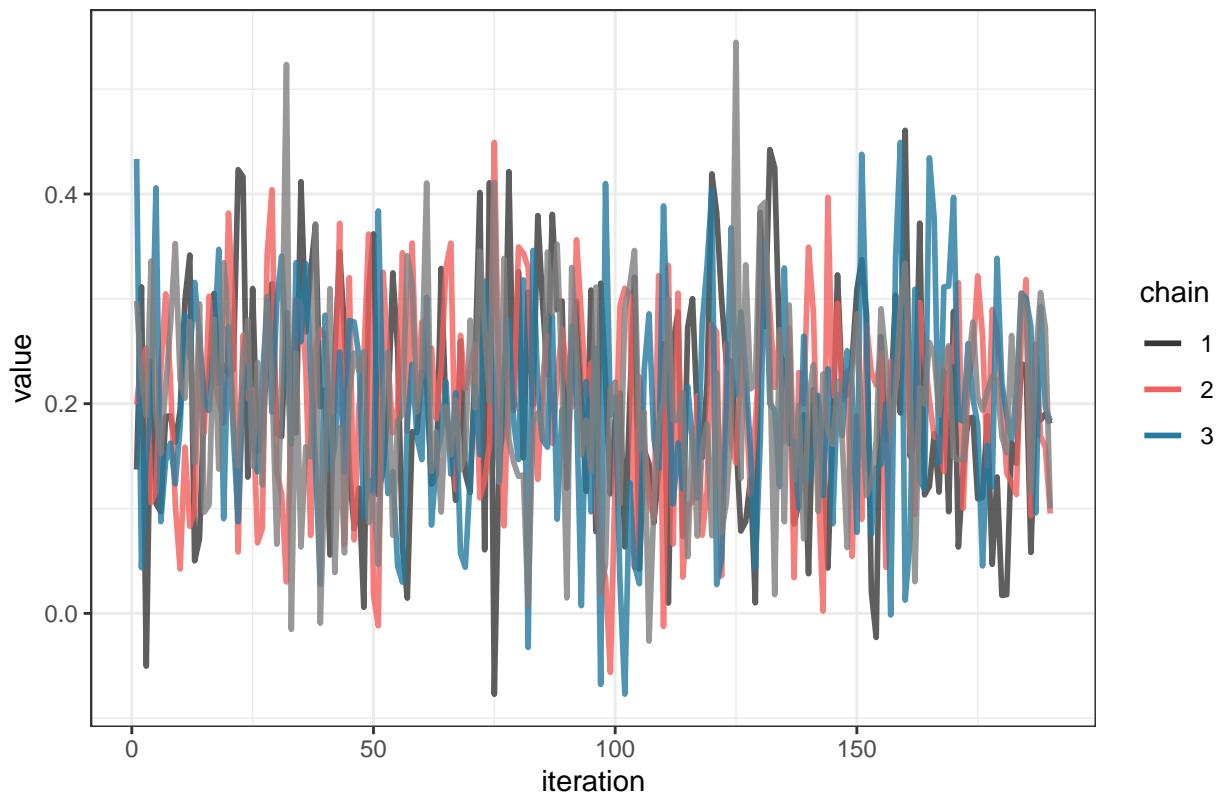
Traceplot of LOWC31



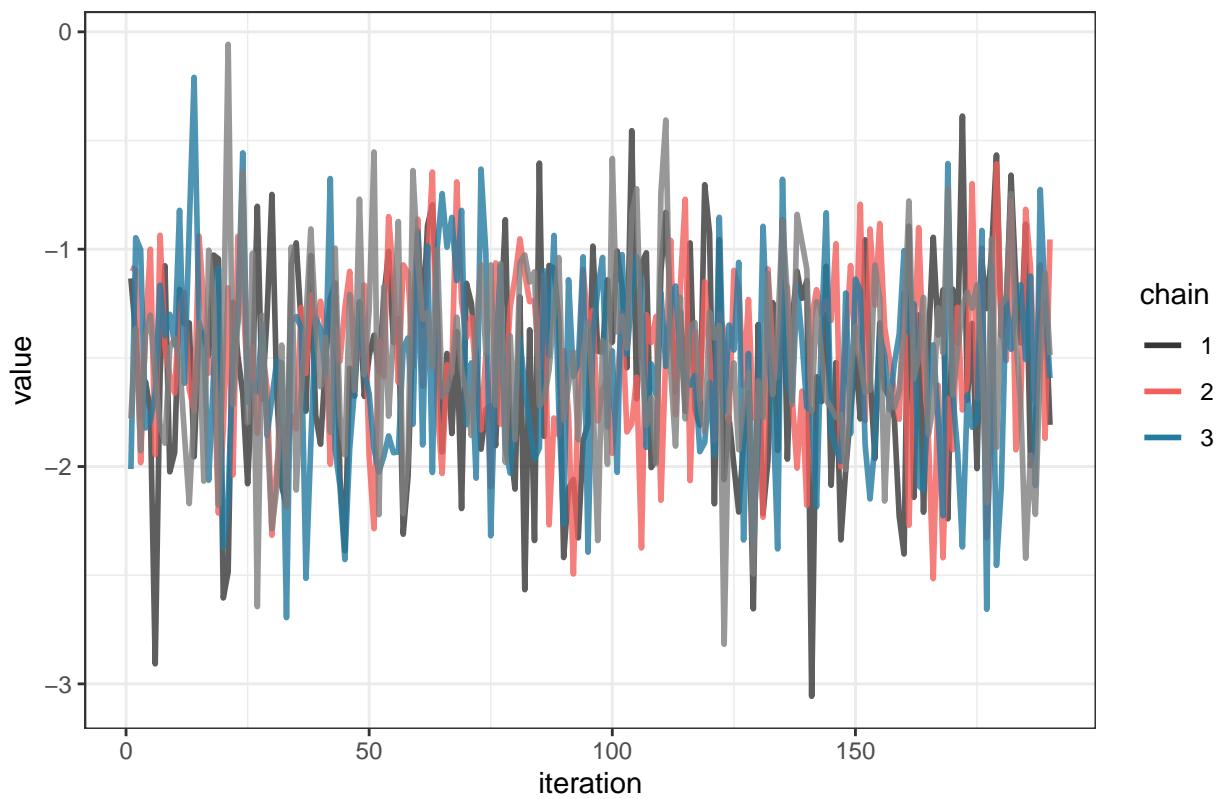
Traceplot of area(eGFR)



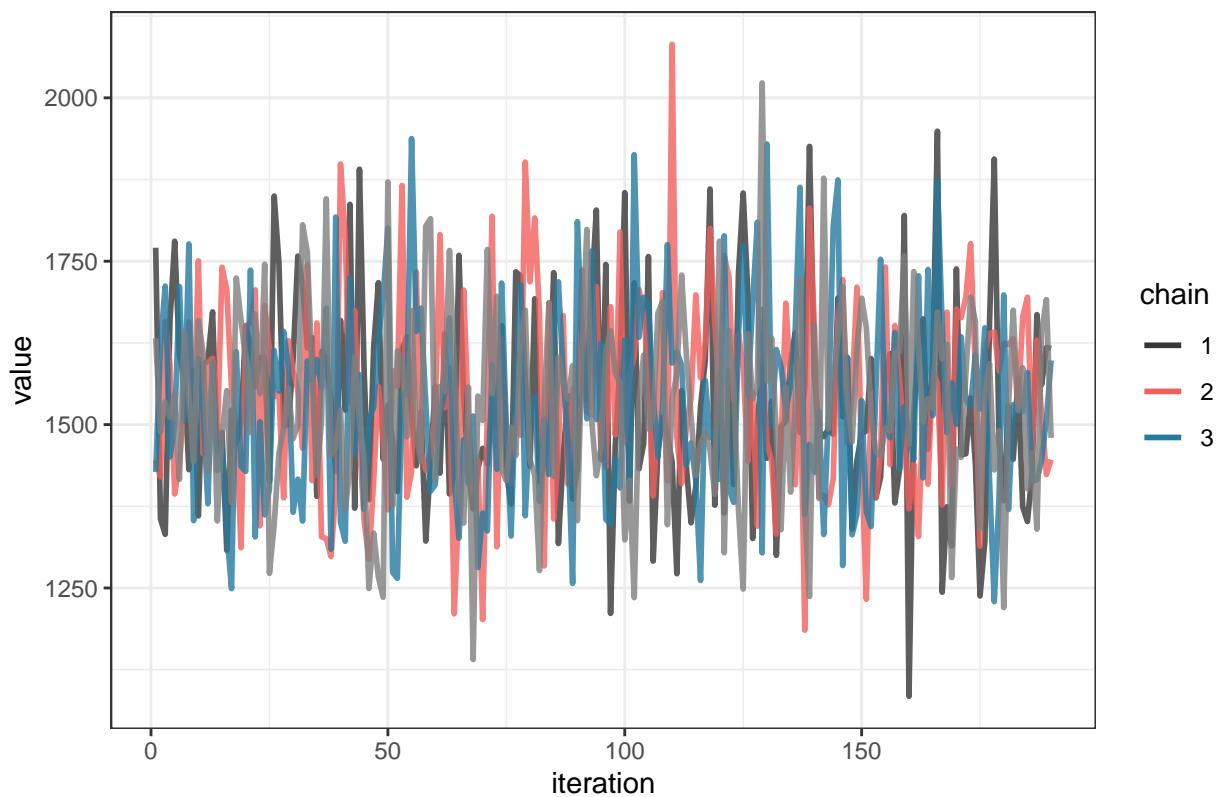
Traceplot of



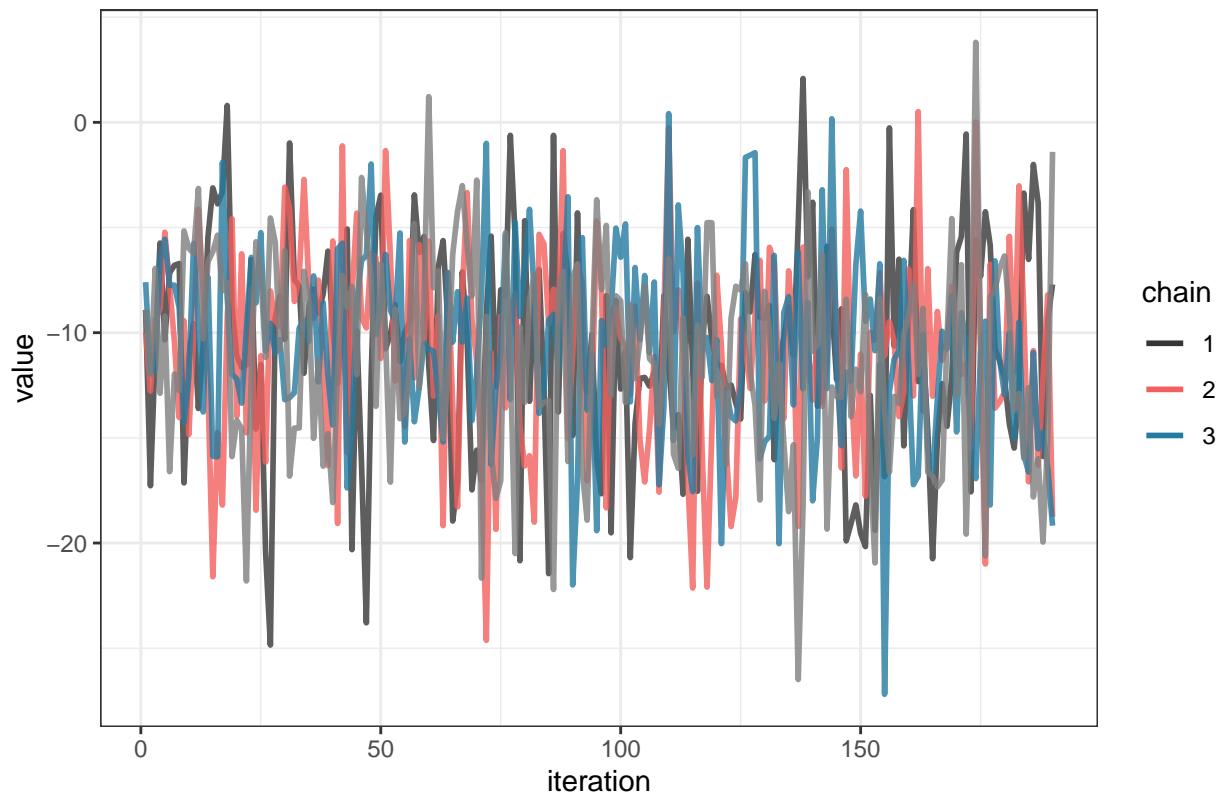
Traceplot of .1



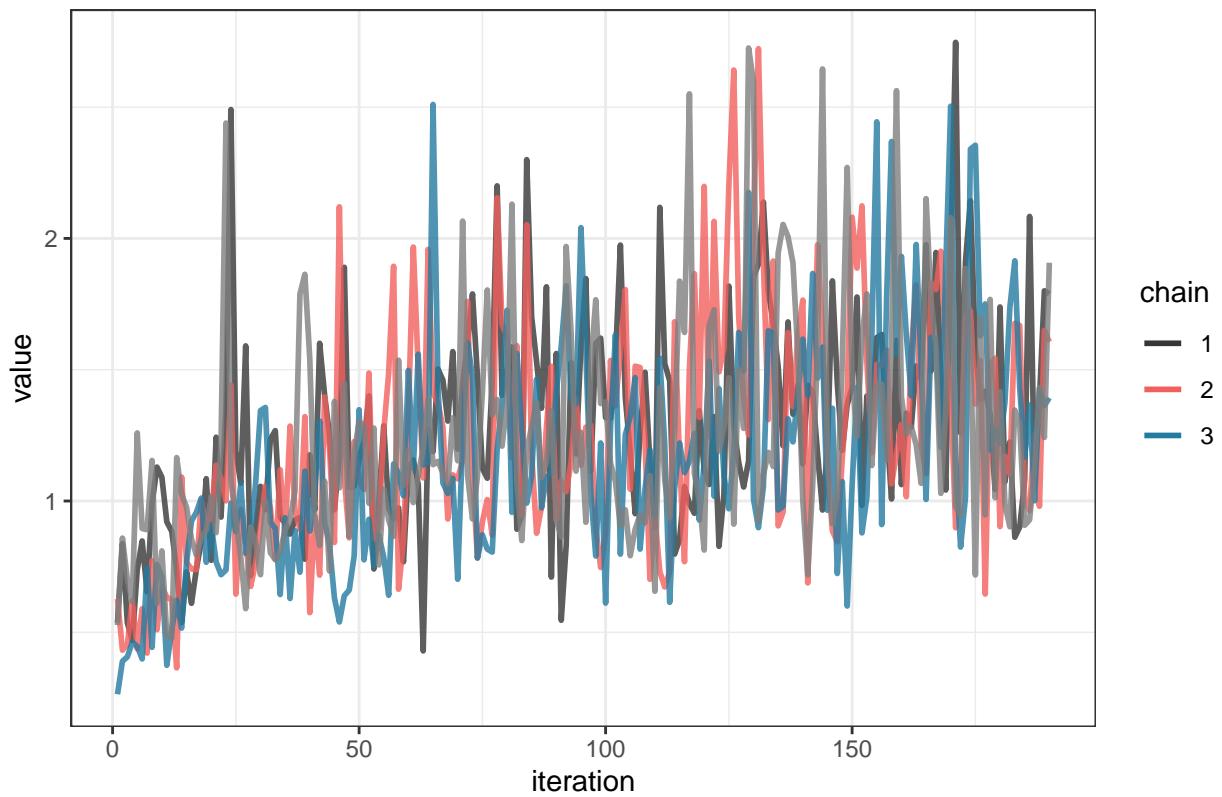
Traceplot of $D[1, 1]$



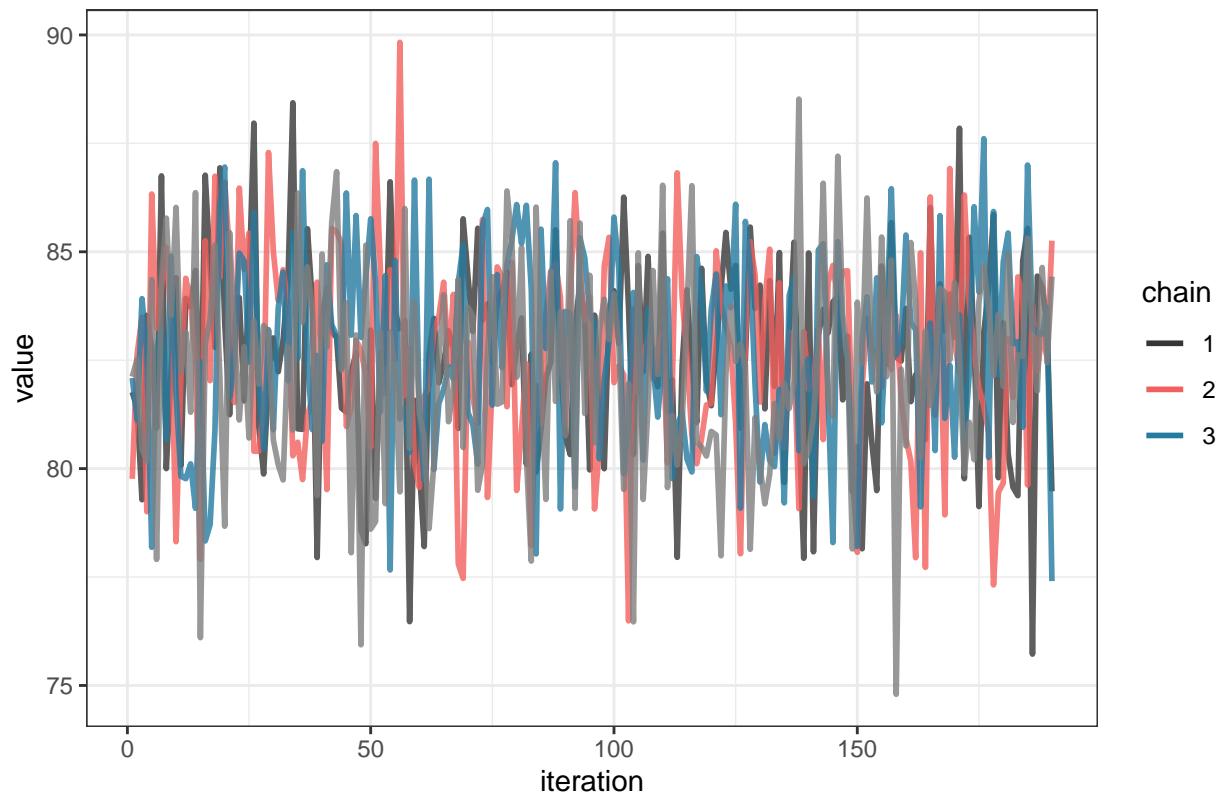
Traceplot of $D[2, 1]$



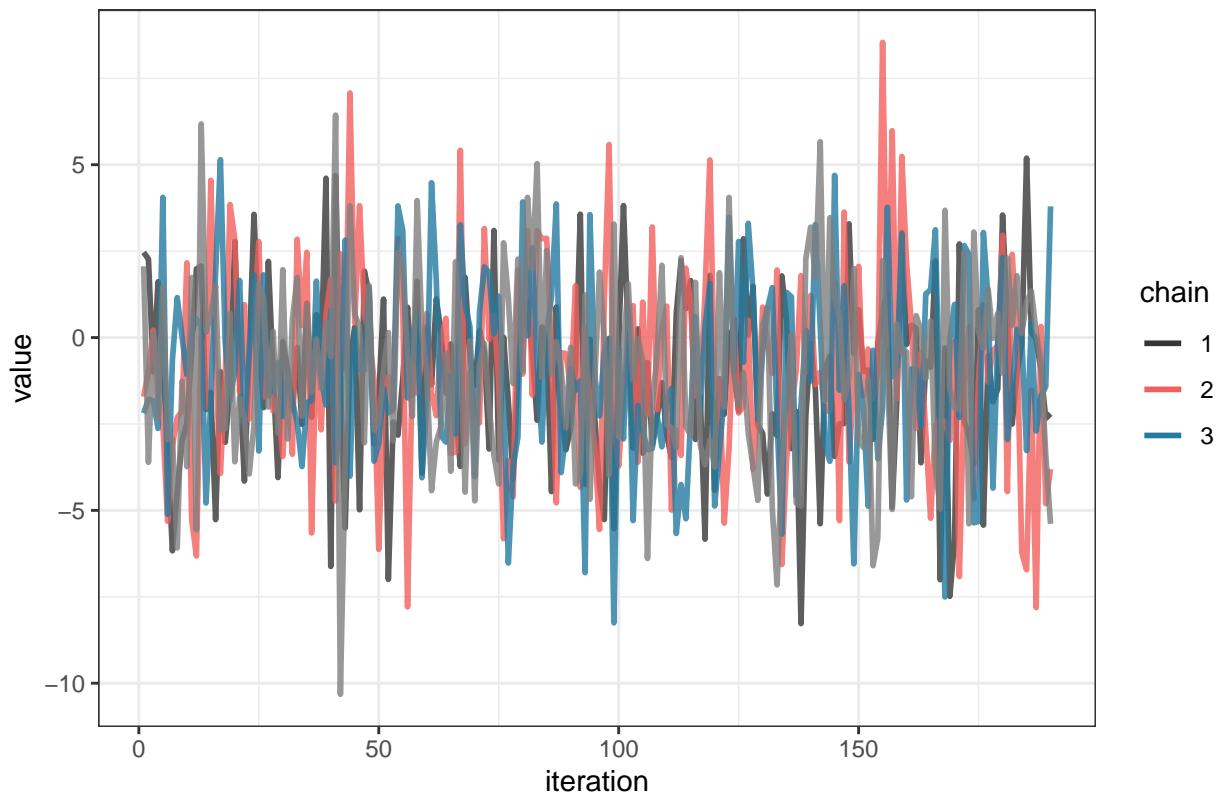
Traceplot of $D[2, 2]$



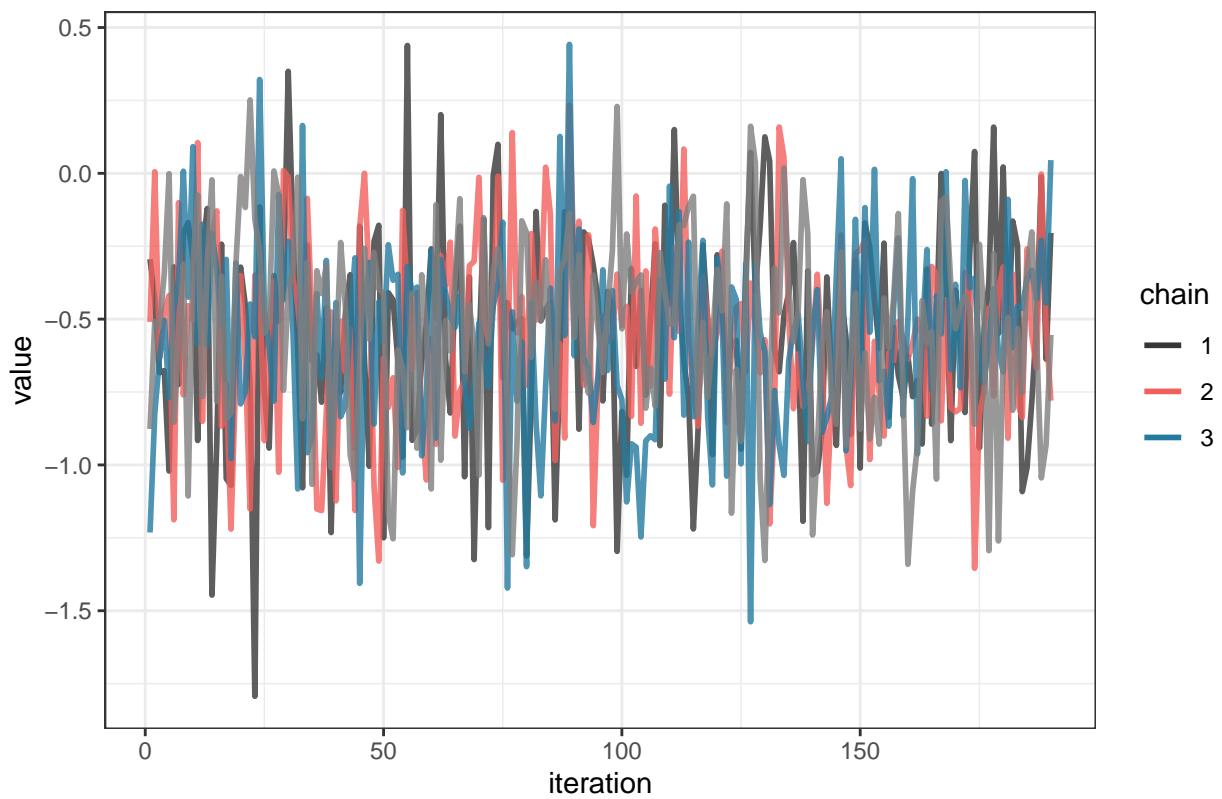
Traceplot of (Intercept)



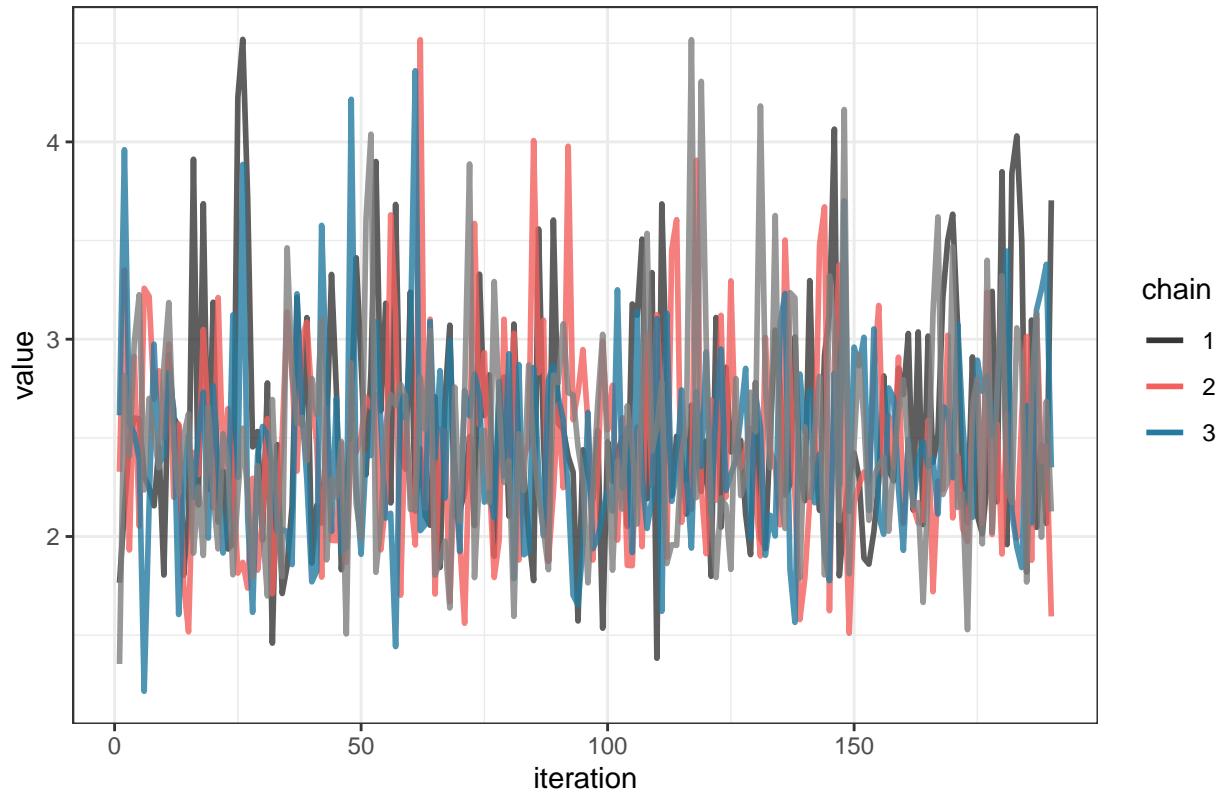
Traceplot of LOWC31.1



Traceplot of time



Traceplot of sigmas_1



```
traceCplt
```

```
## NULL
```

```
traceCplt1
```

```
## NULL
```

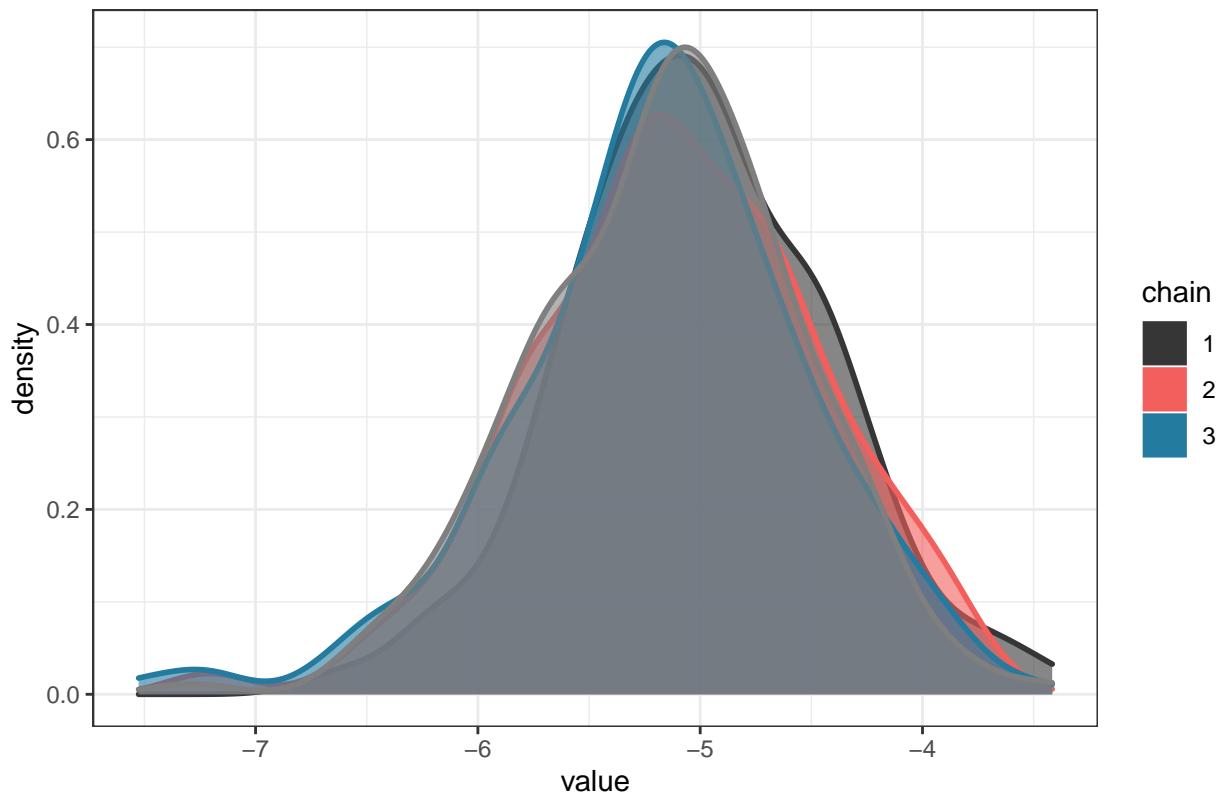
```
traceCplt2
```

```
## NULL
```

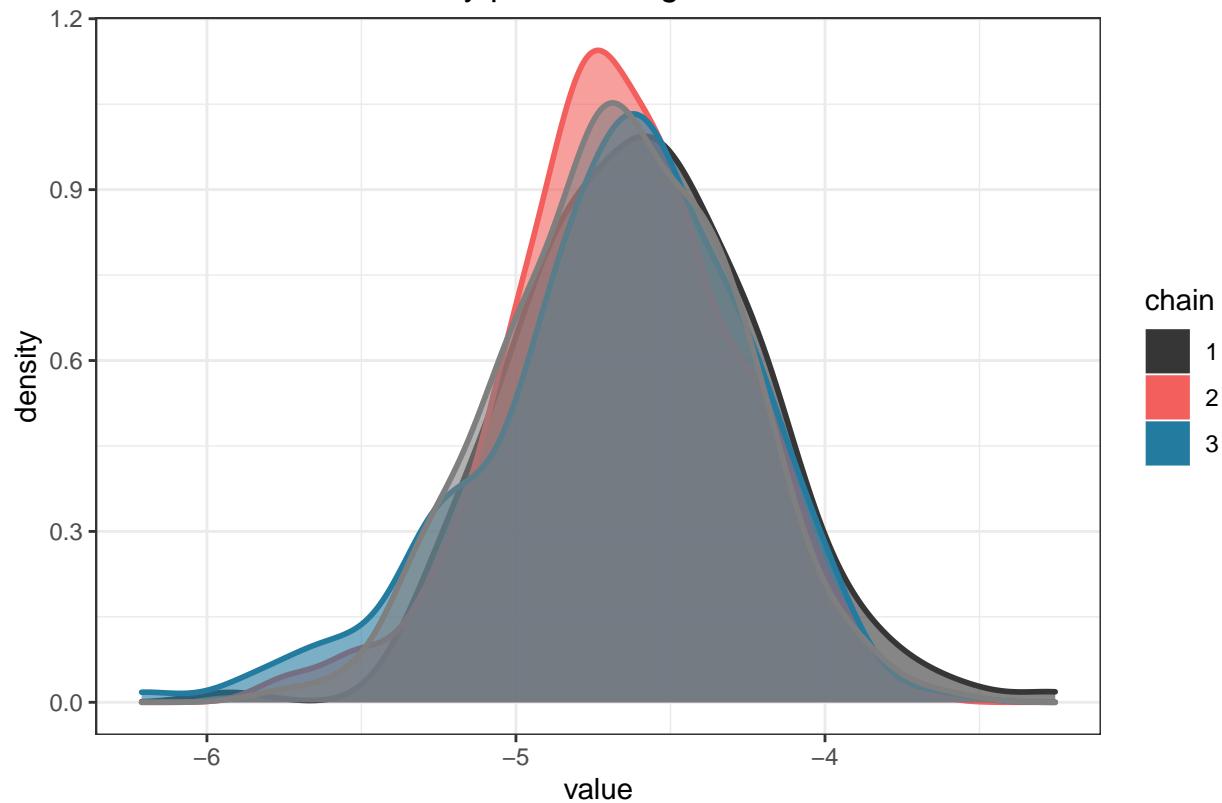
density plots (scroll with left and right arrow)

```
densplt <- ggdensityplot(jointFit)
```

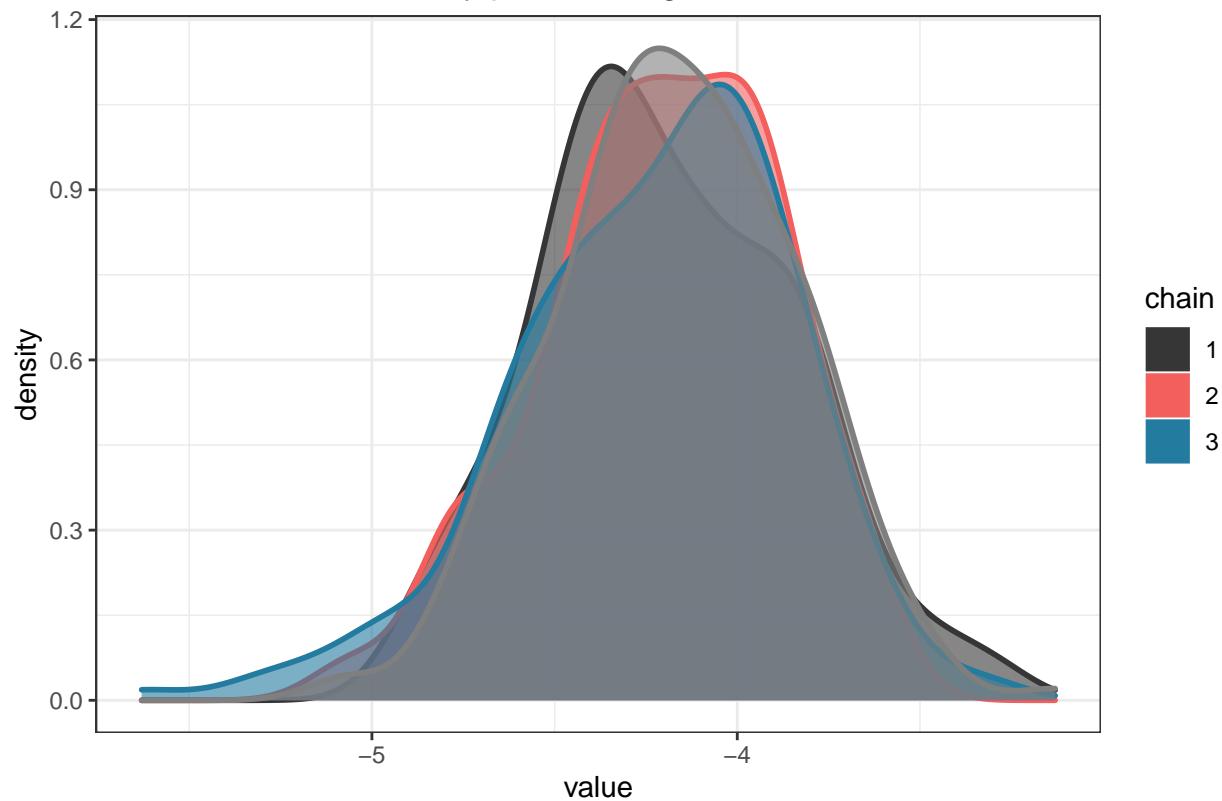
Density plot of bs_gammas_1



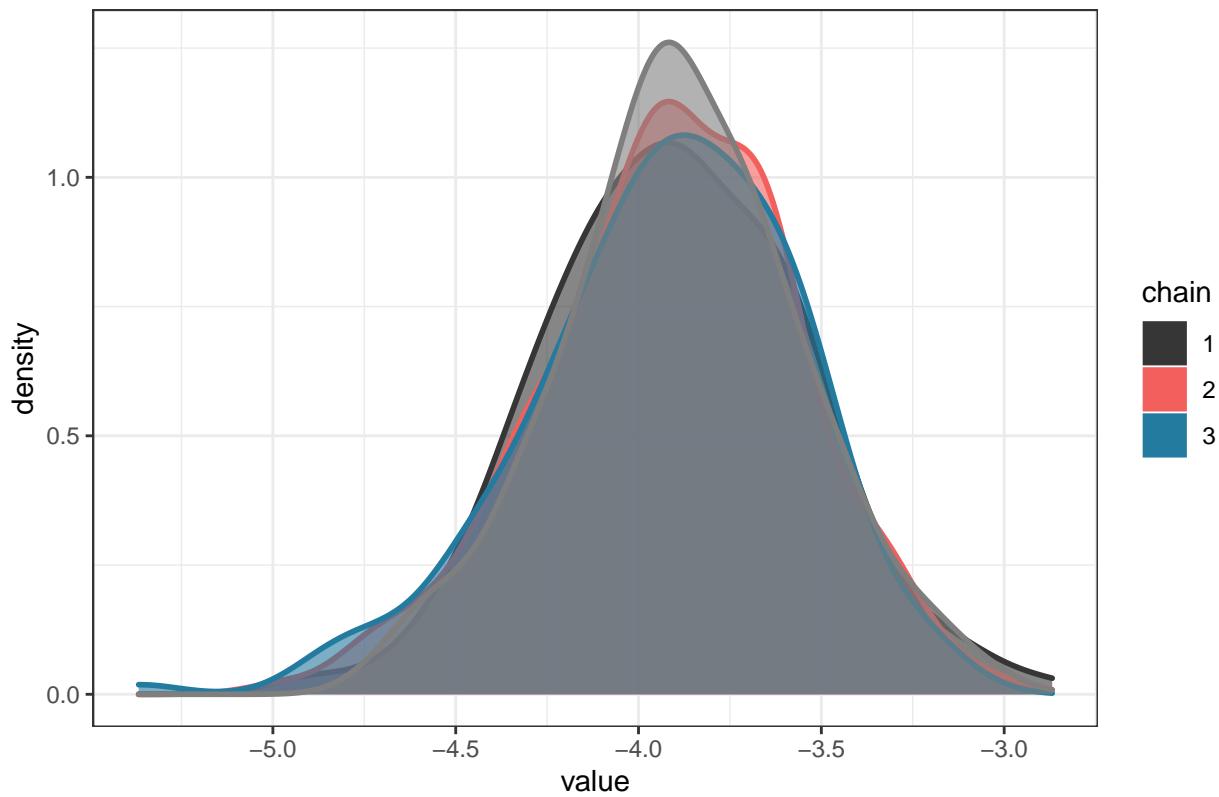
Density plot of bs_gammas_2



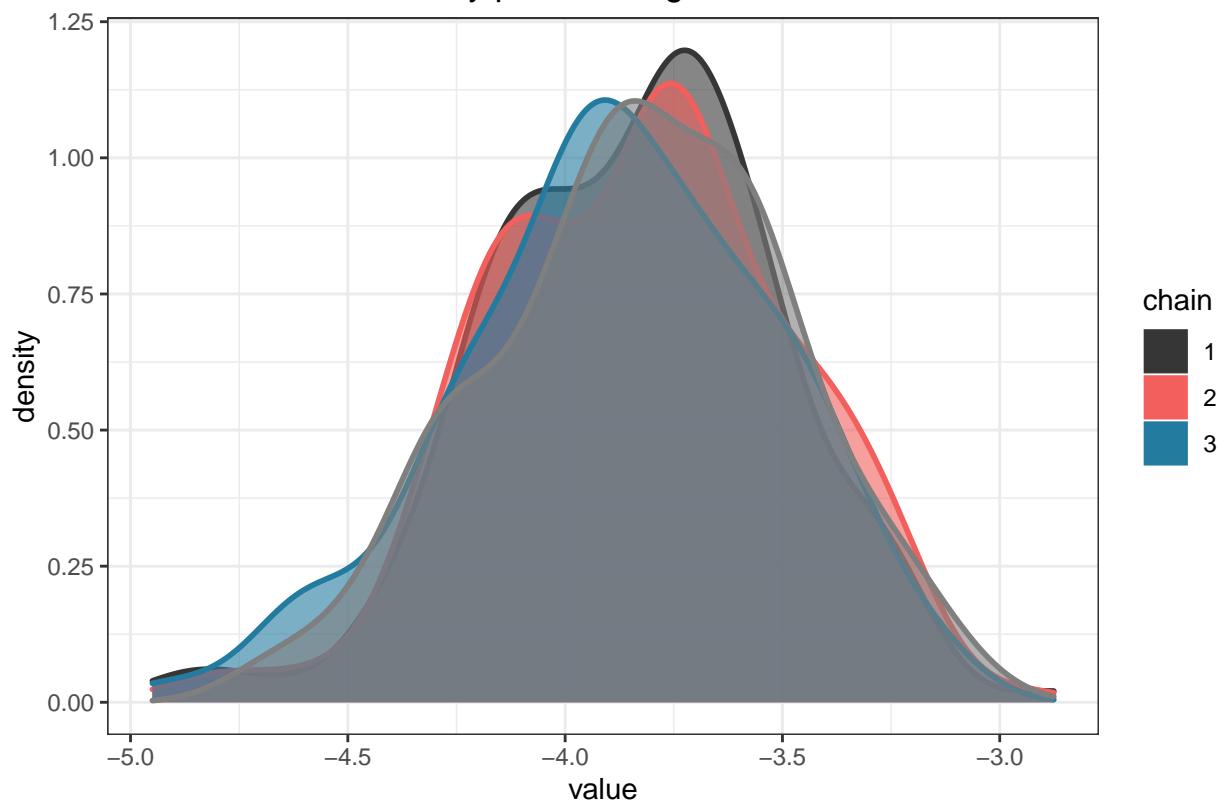
Density plot of bs_gammas_3



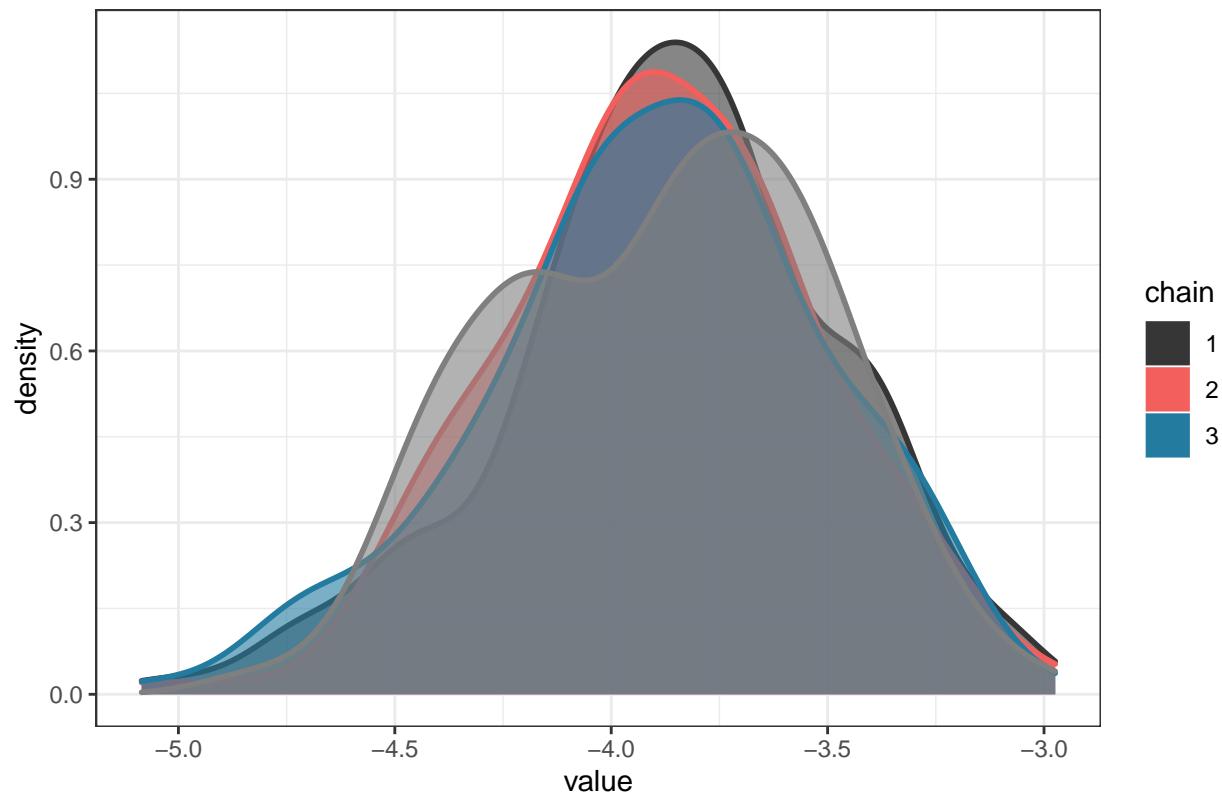
Density plot of bs_gammas_4



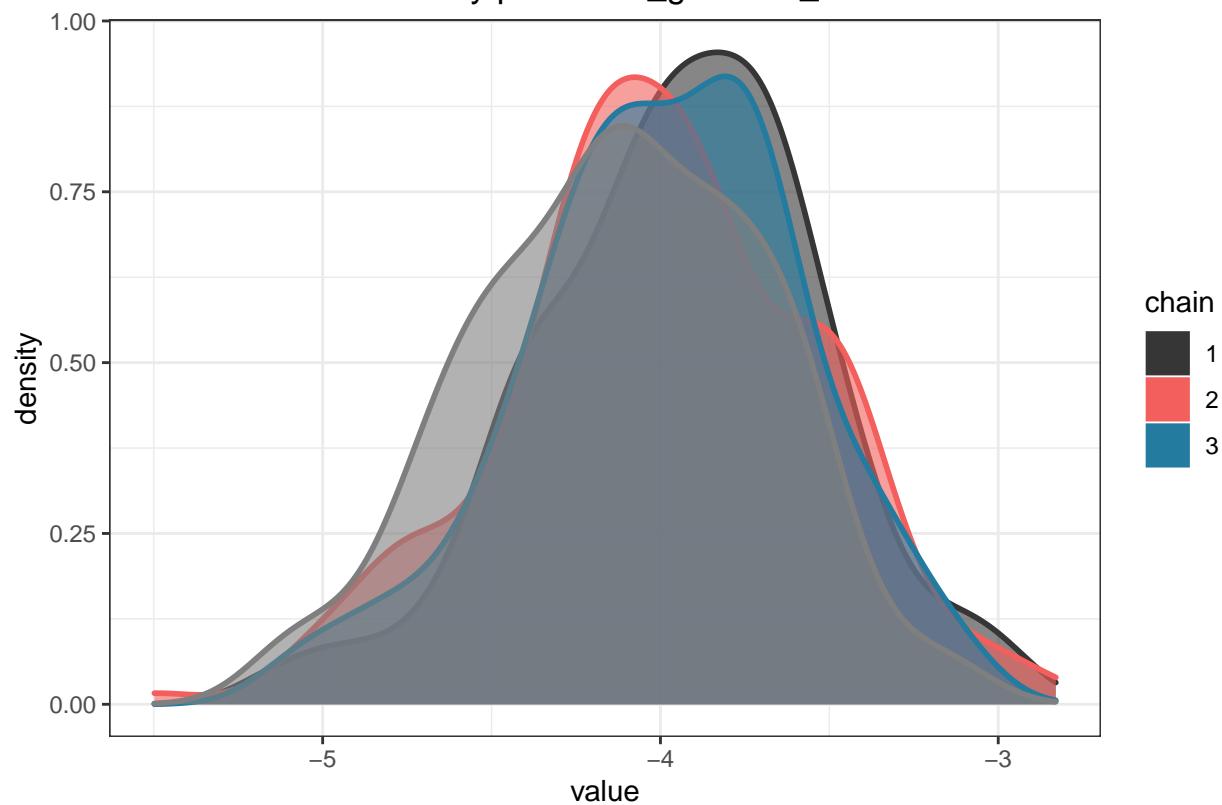
Density plot of bs_gammas_5



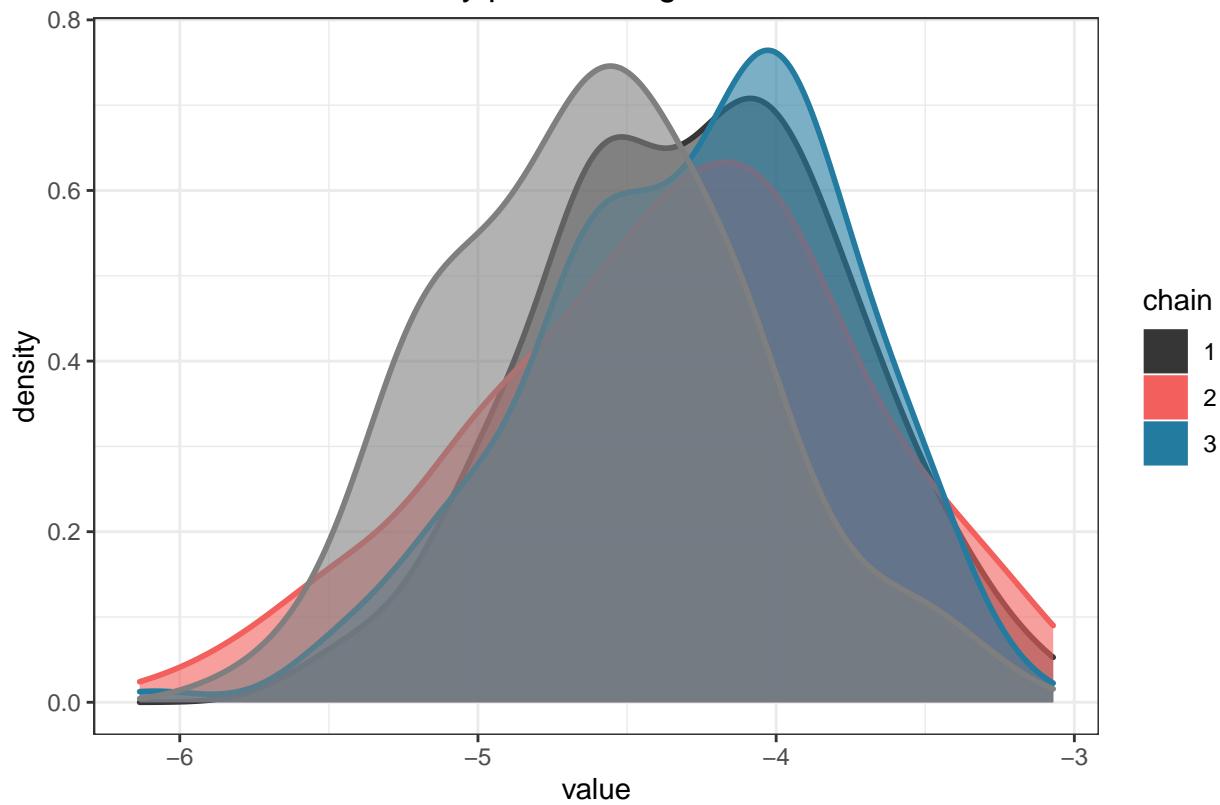
Density plot of bs_gammas_6



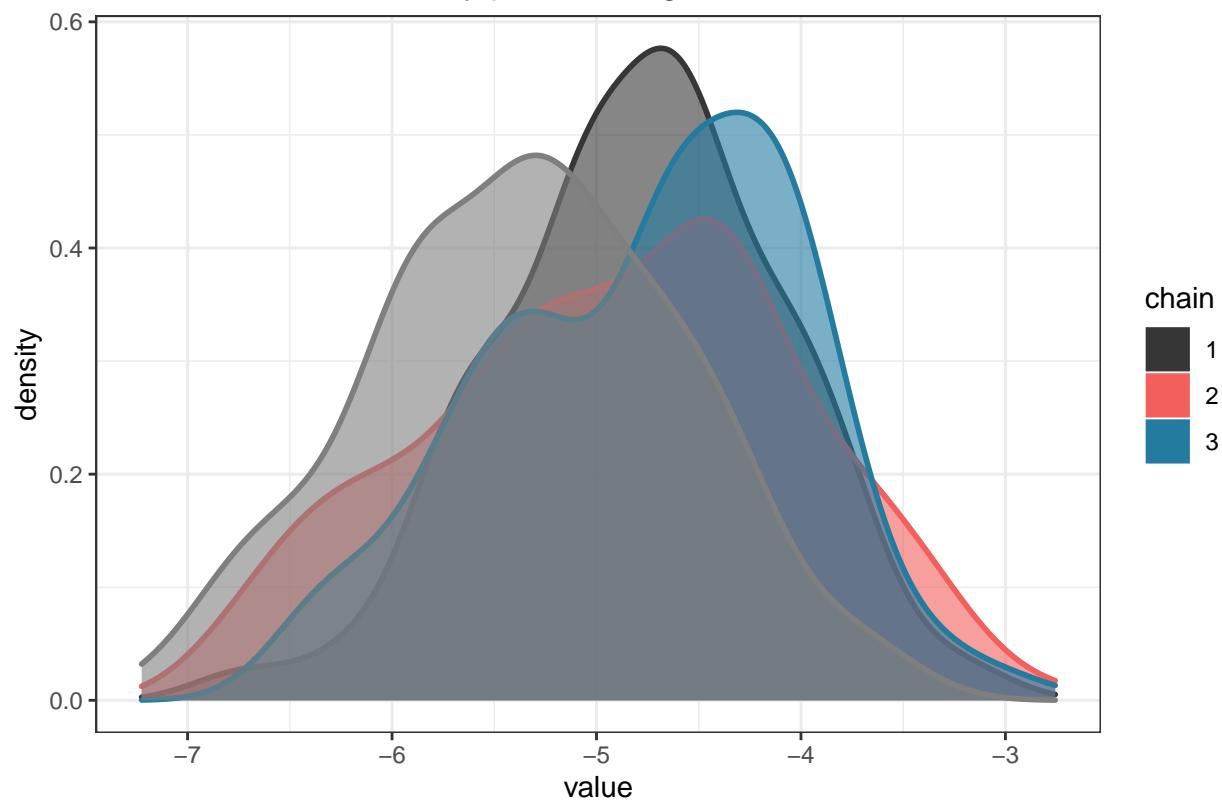
Density plot of bs_gammas_7



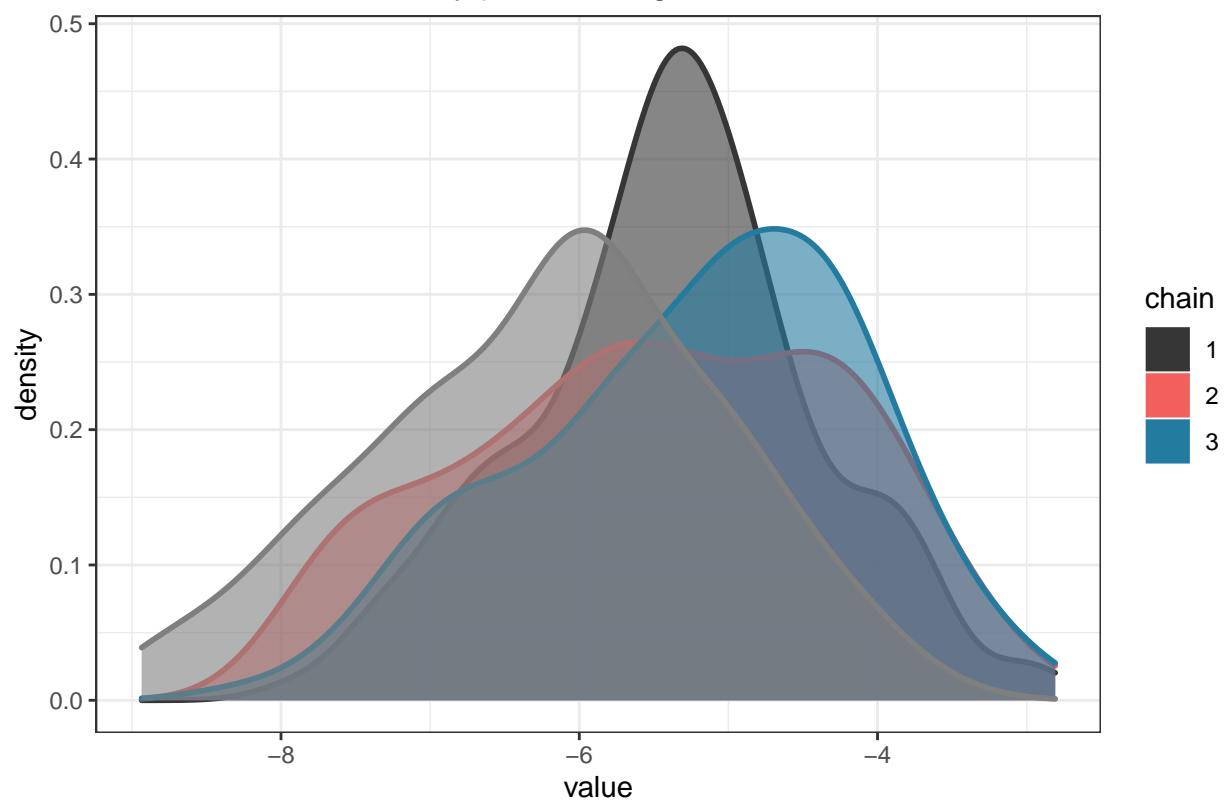
Density plot of bs_gammas_8



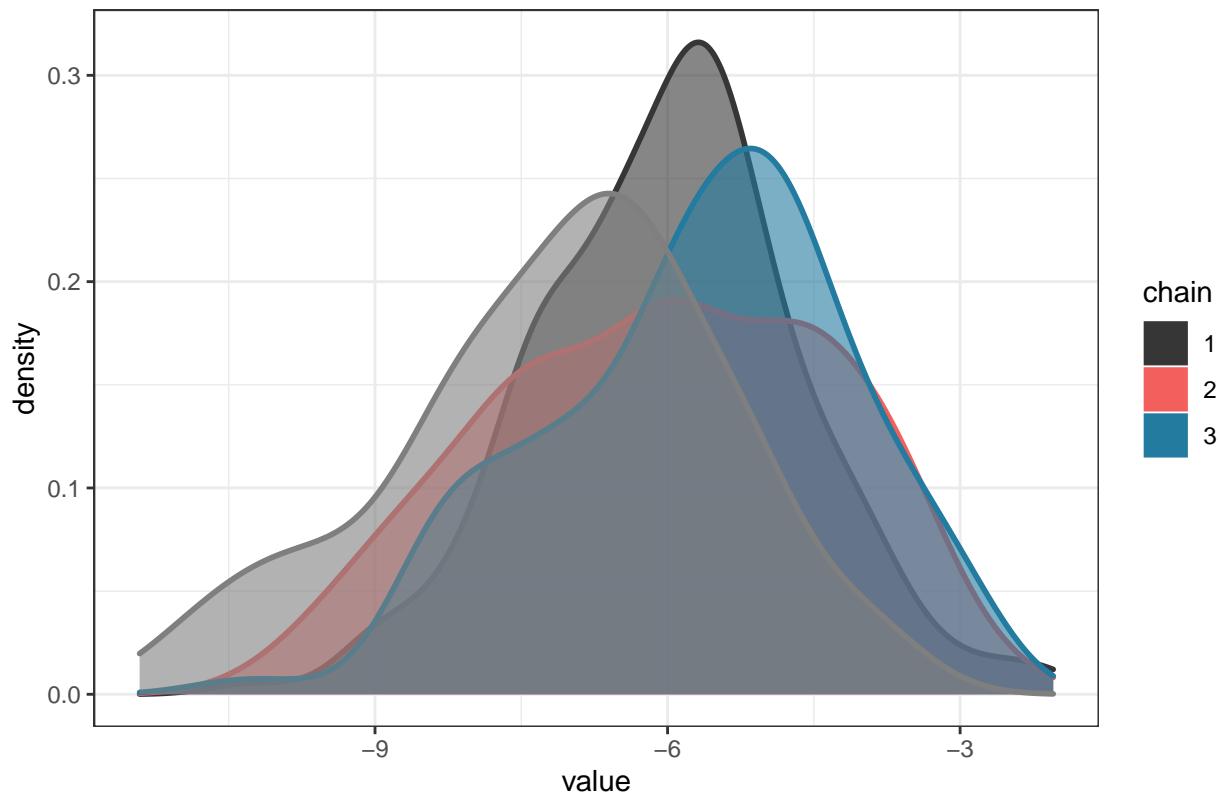
Density plot of bs_gammas_9



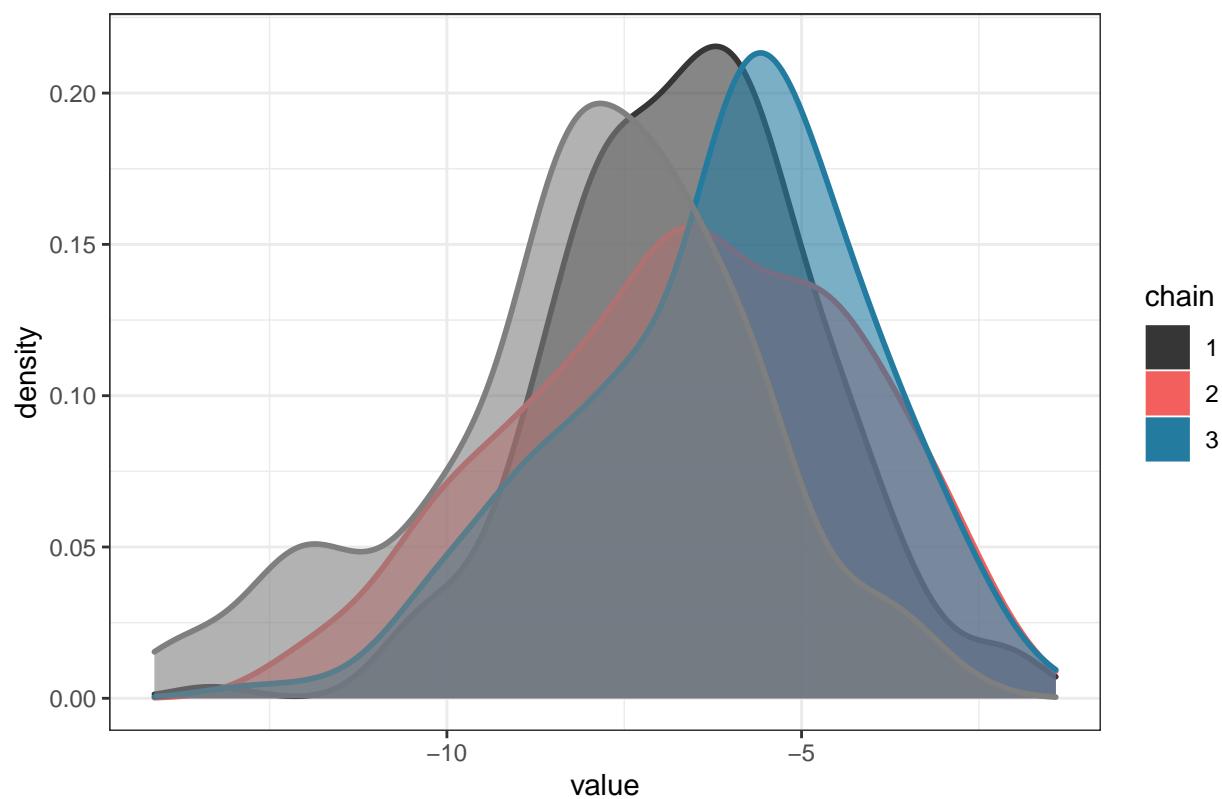
Density plot of bs_gammas_10



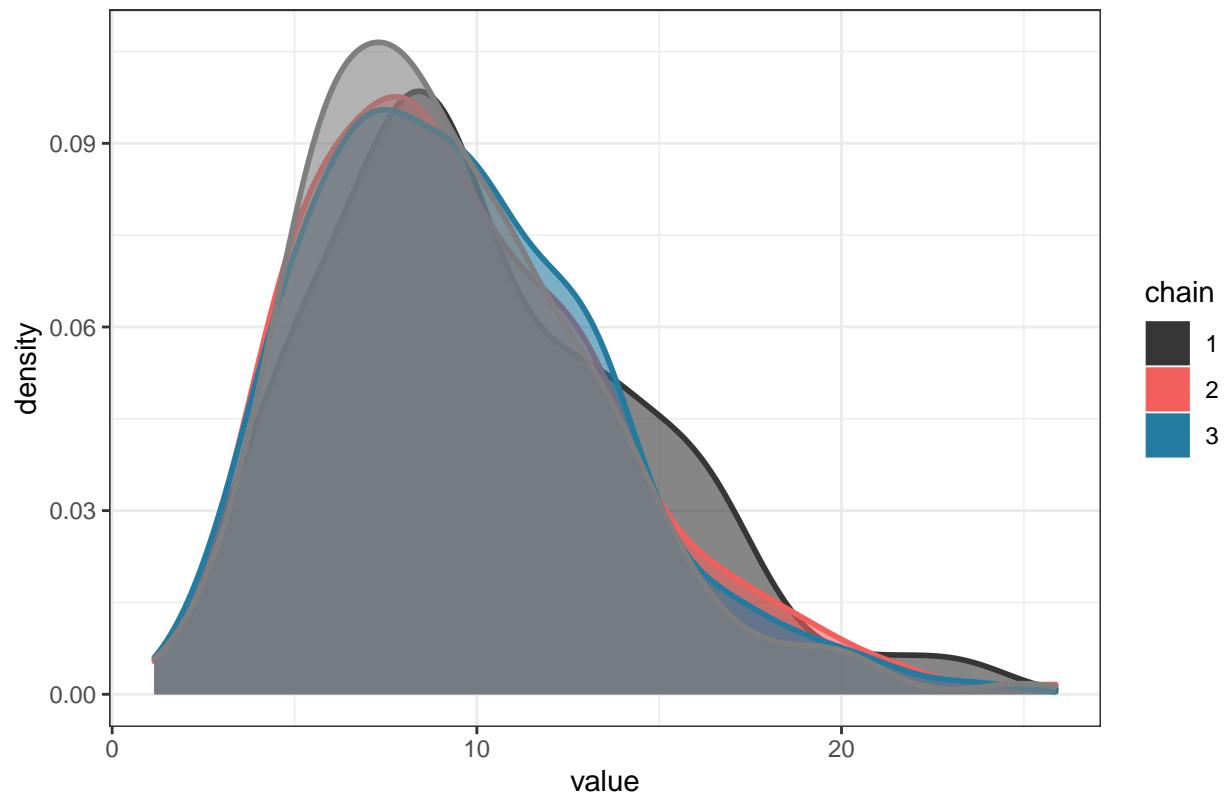
Density plot of bs_gammas_11



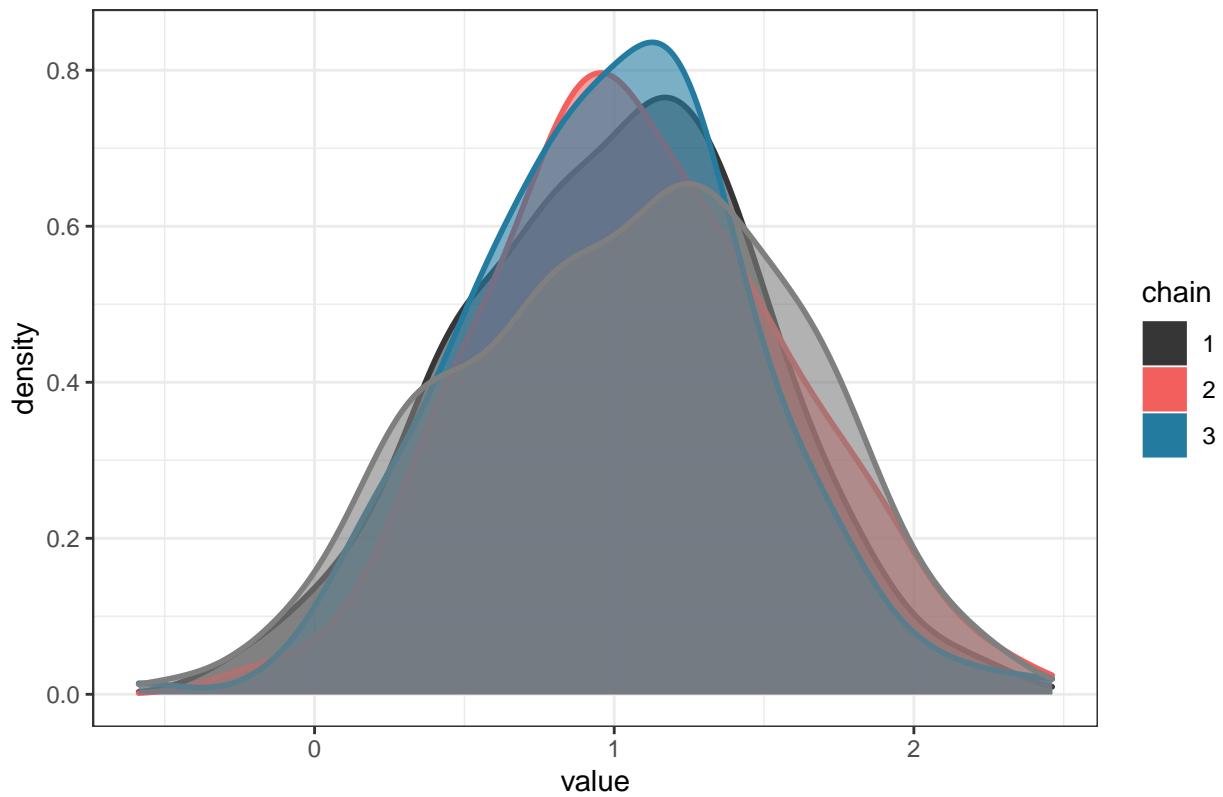
Density plot of bs_gammas_12



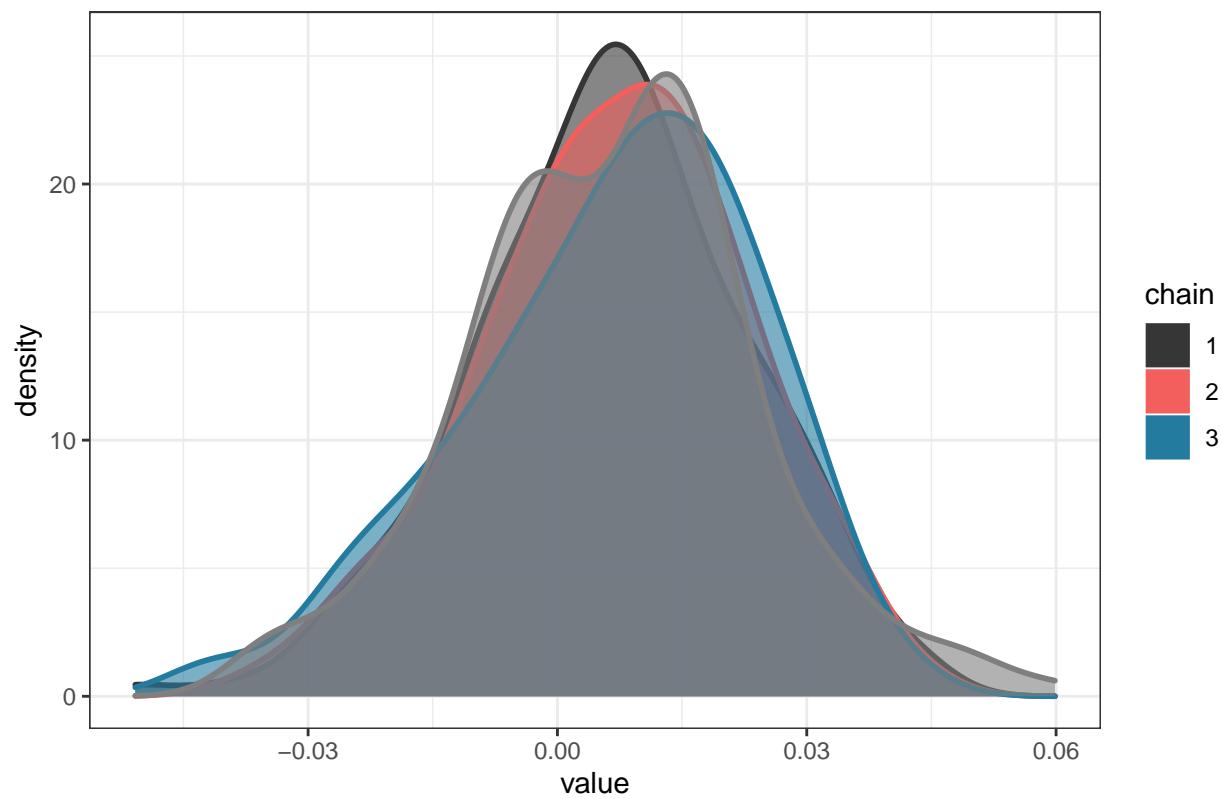
Density plot of tau_bs_gammas



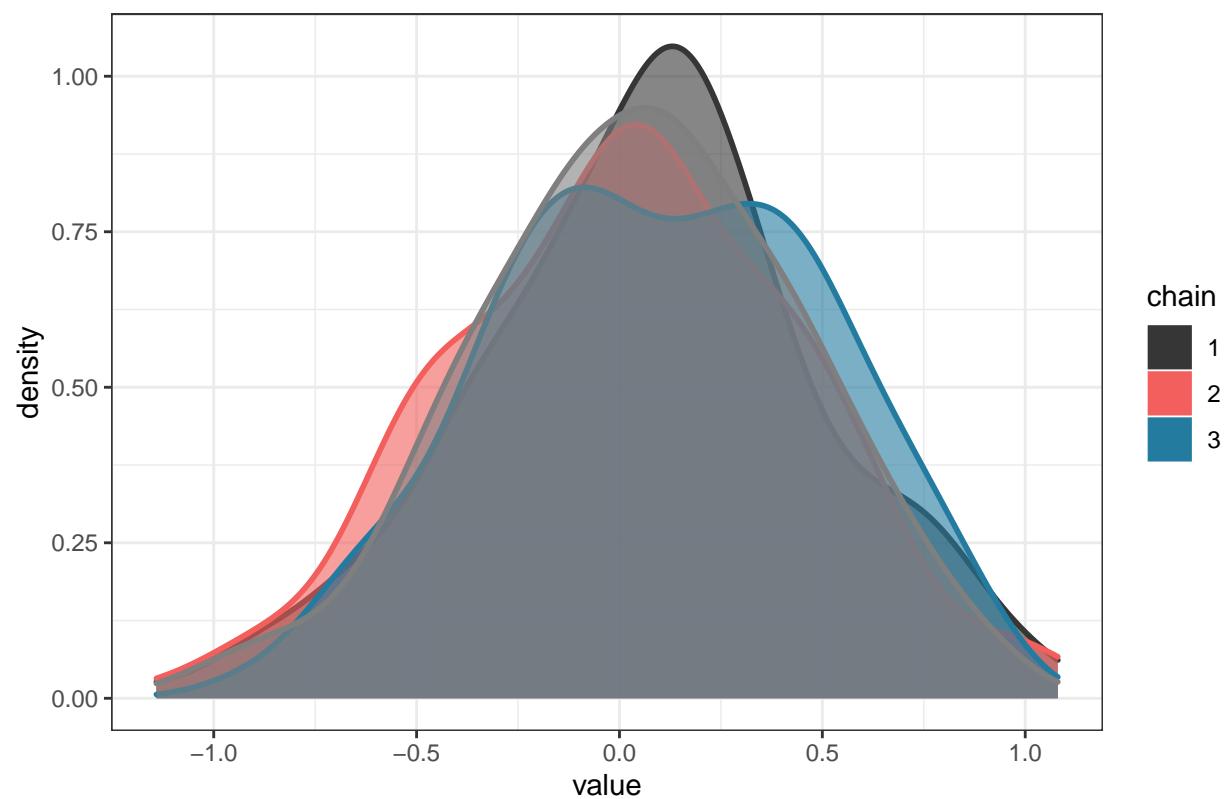
Density plot of LOWC31



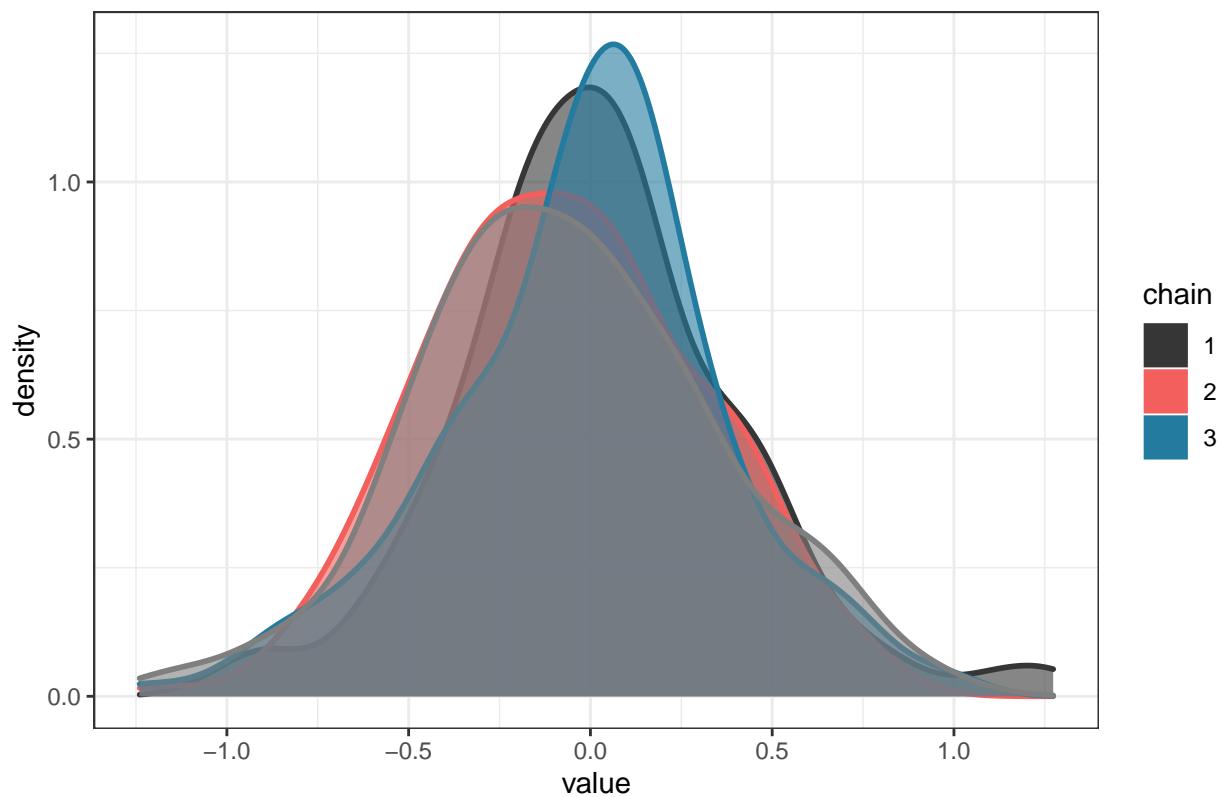
Density plot of ageatbiopsy



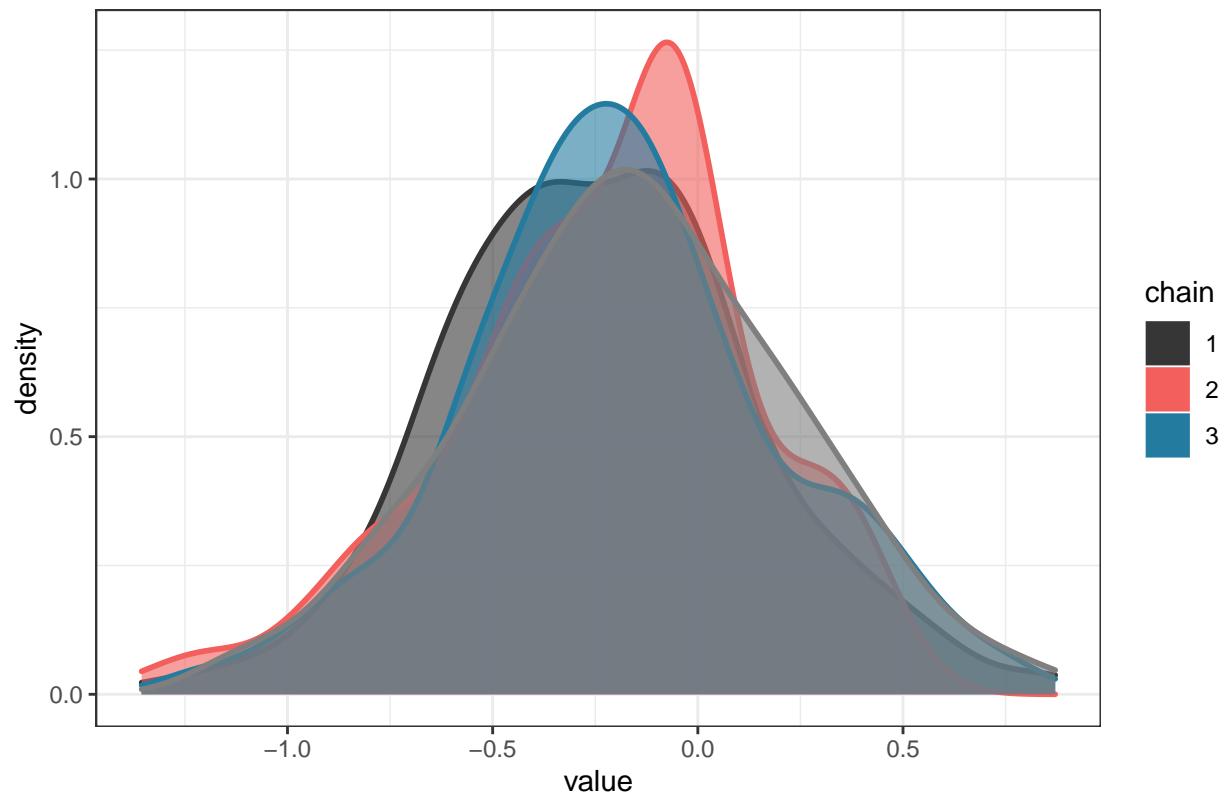
Density plot of sex



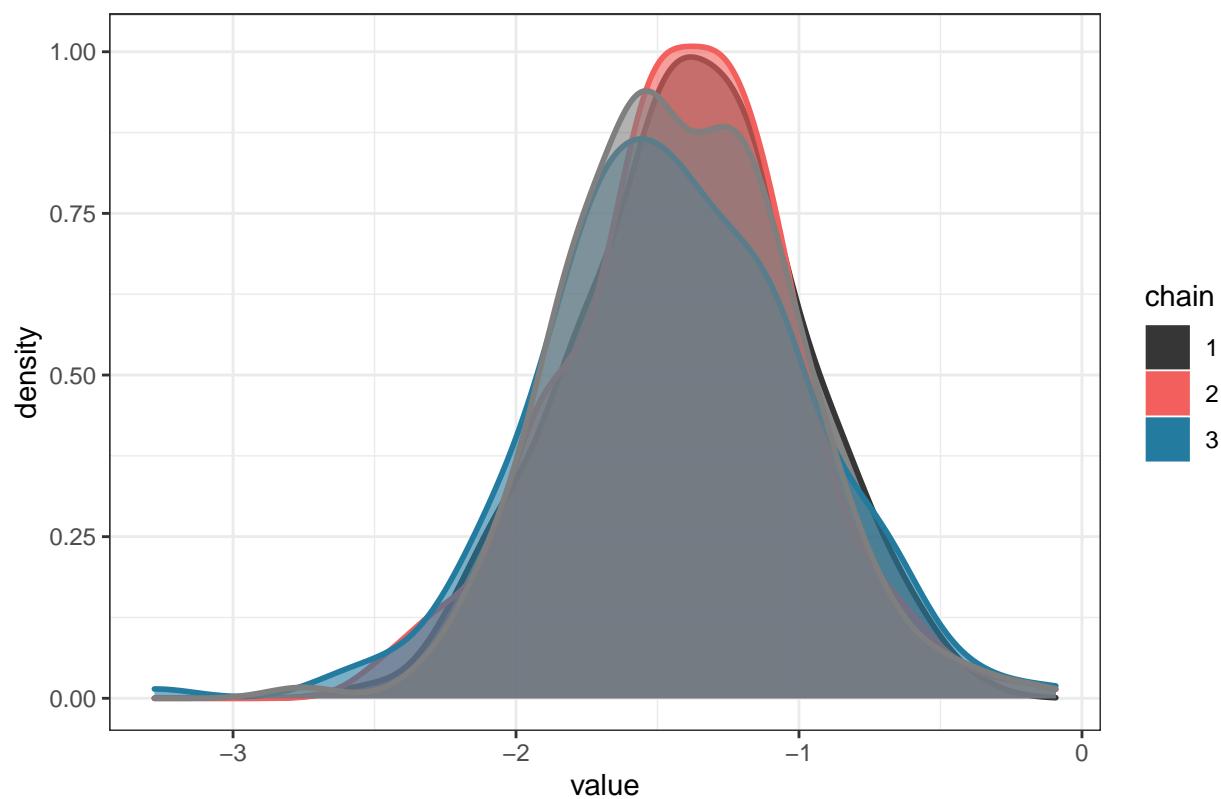
Density plot of black



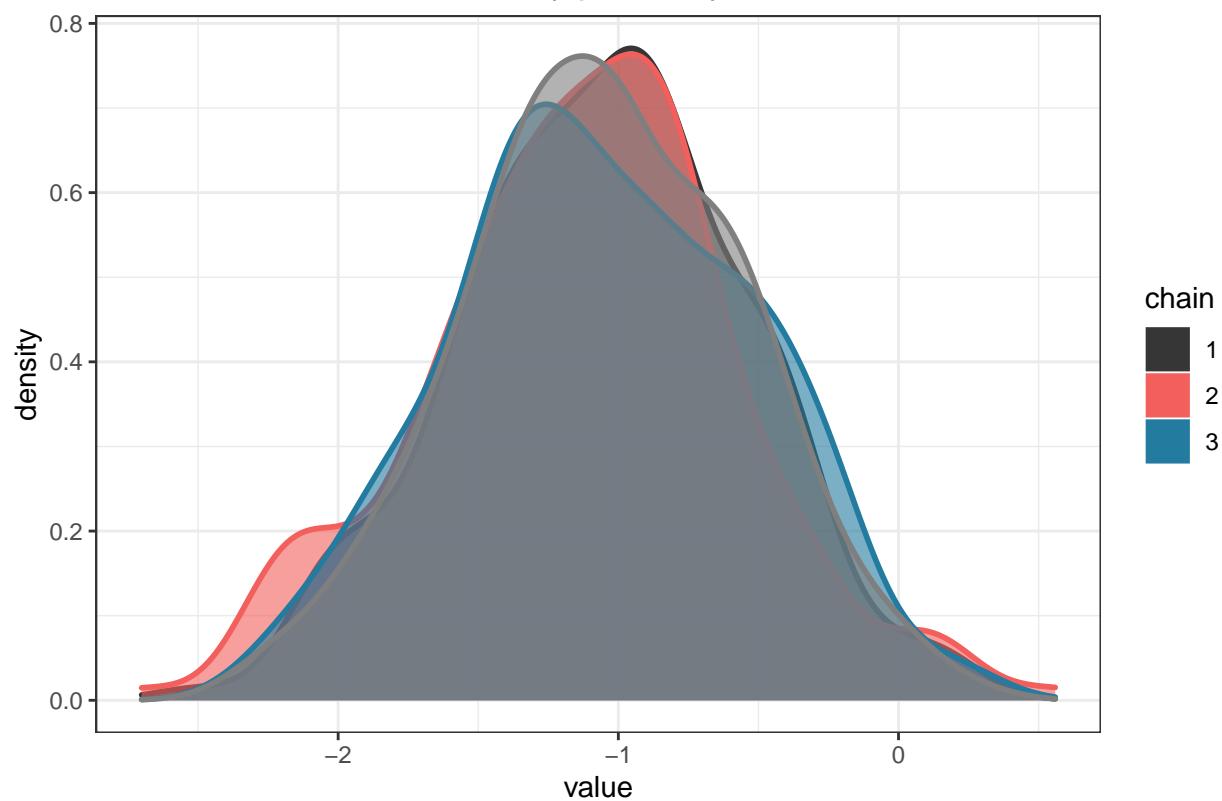
Density plot of hypertension



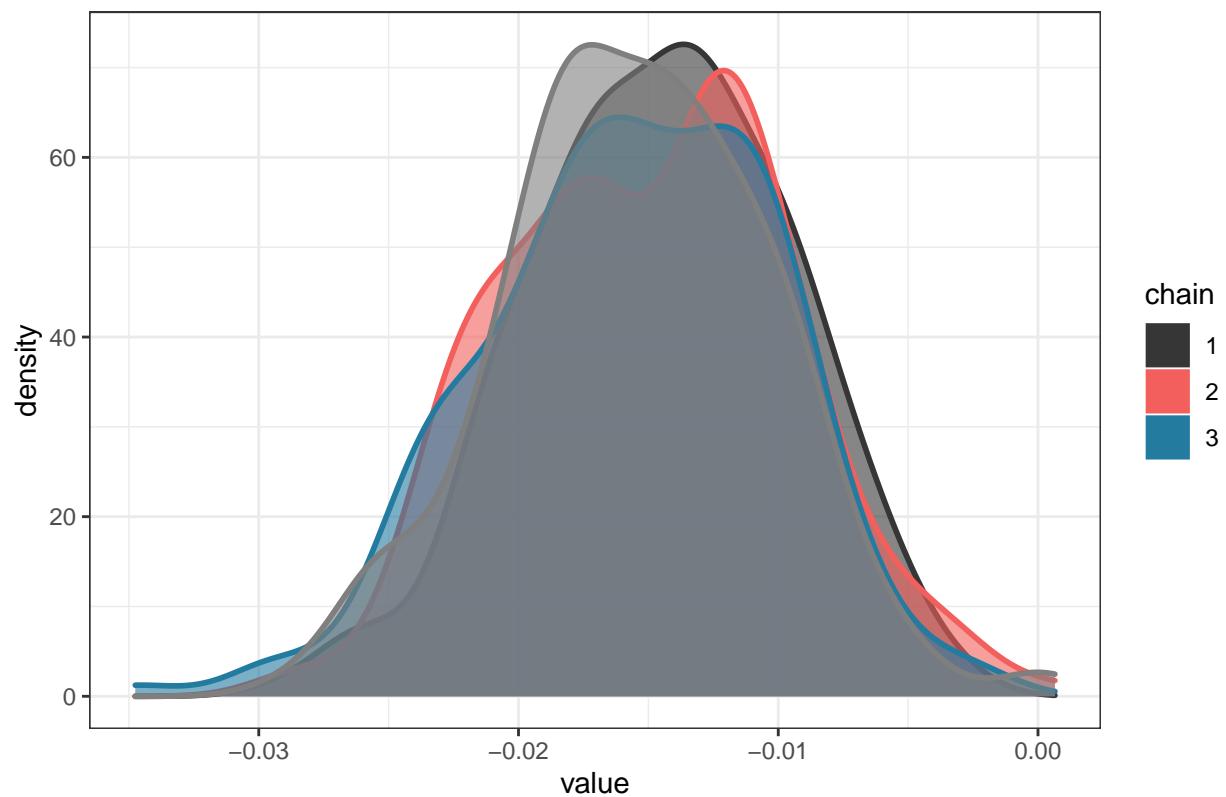
Density plot of mmf



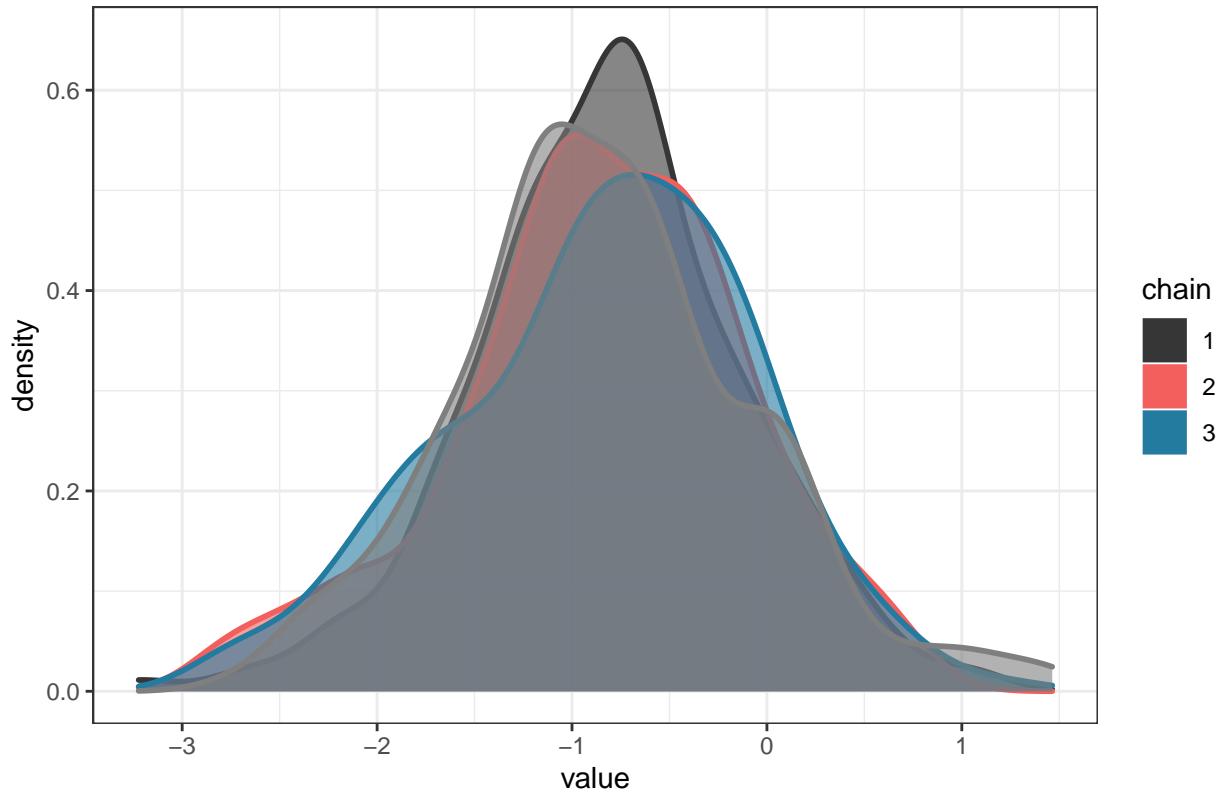
Density plot of cyc



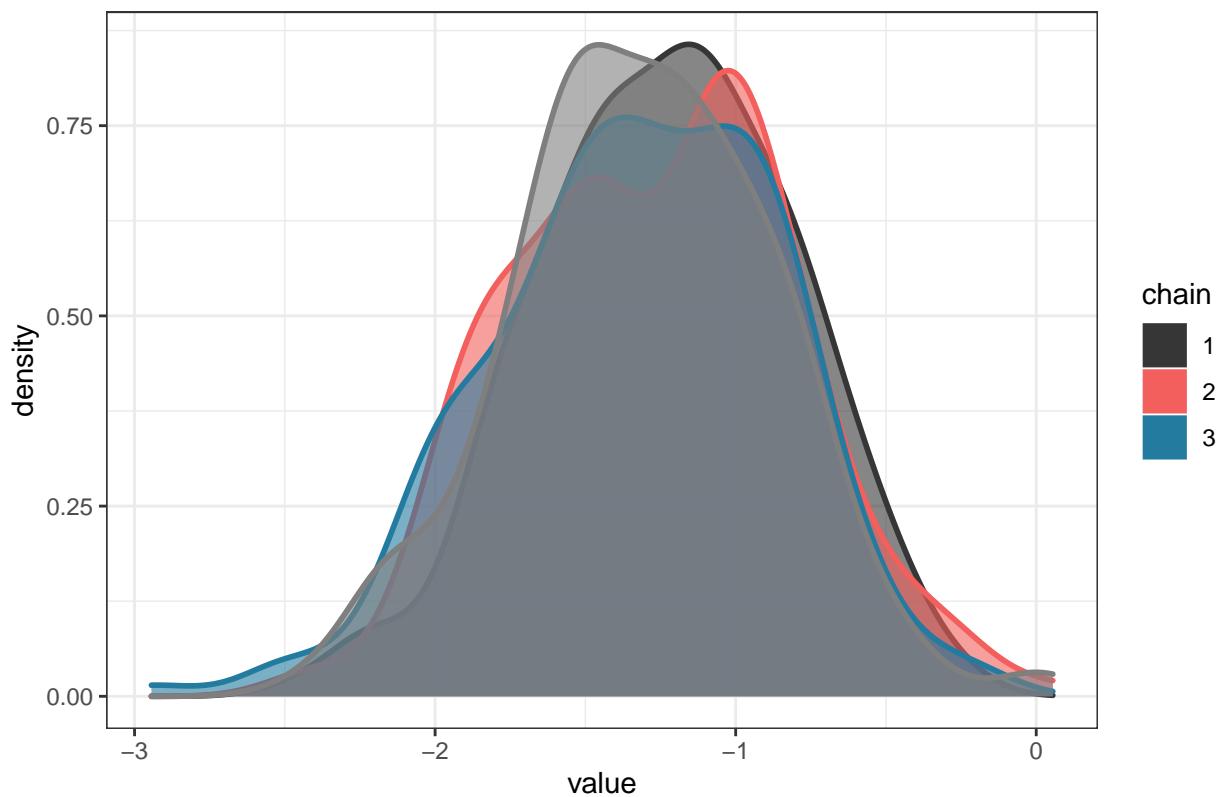
Density plot of value(eGFR)



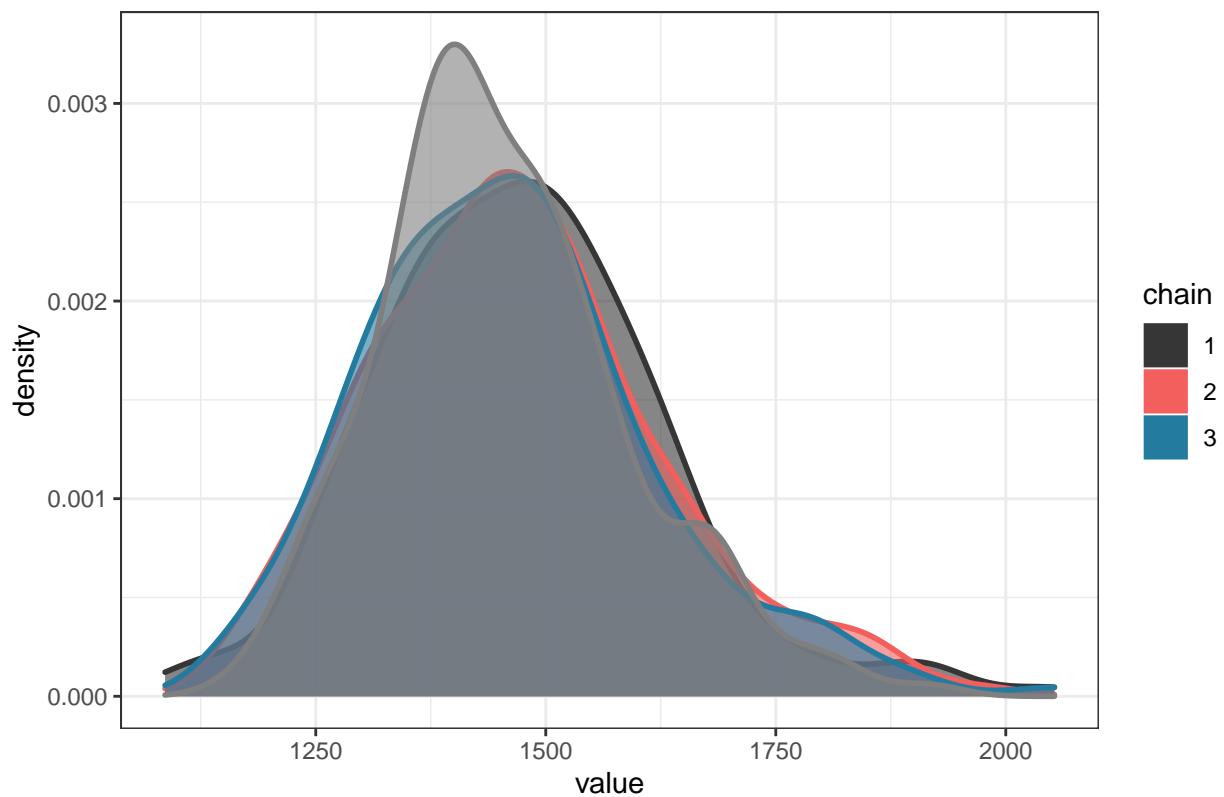
Density plot of



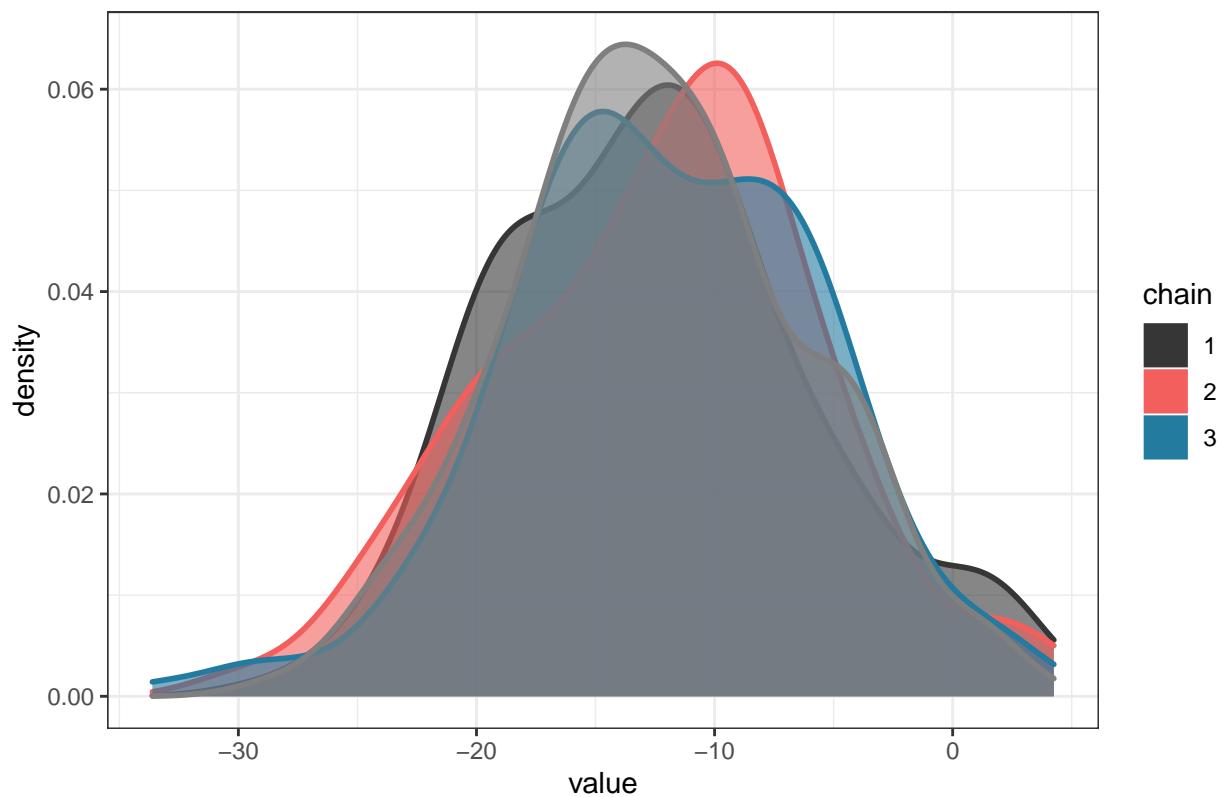
Density plot of .1



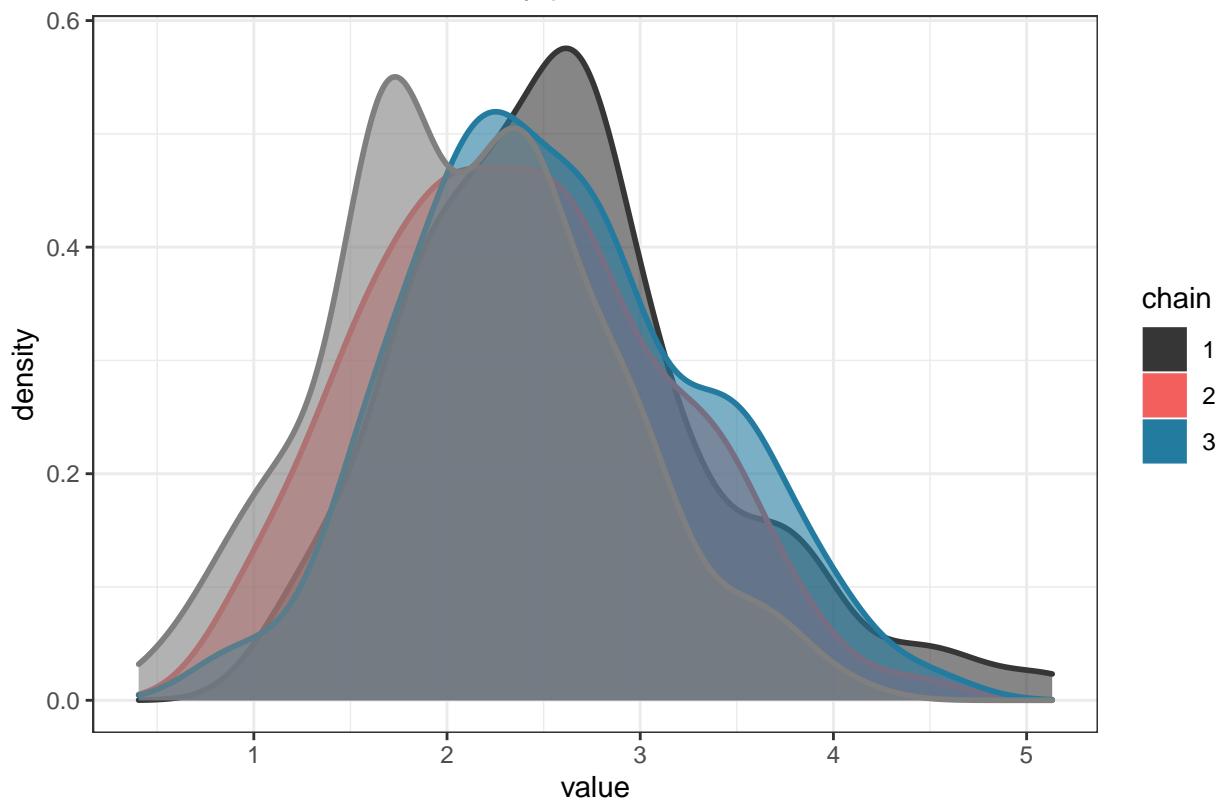
Density plot of $D[1, 1]$



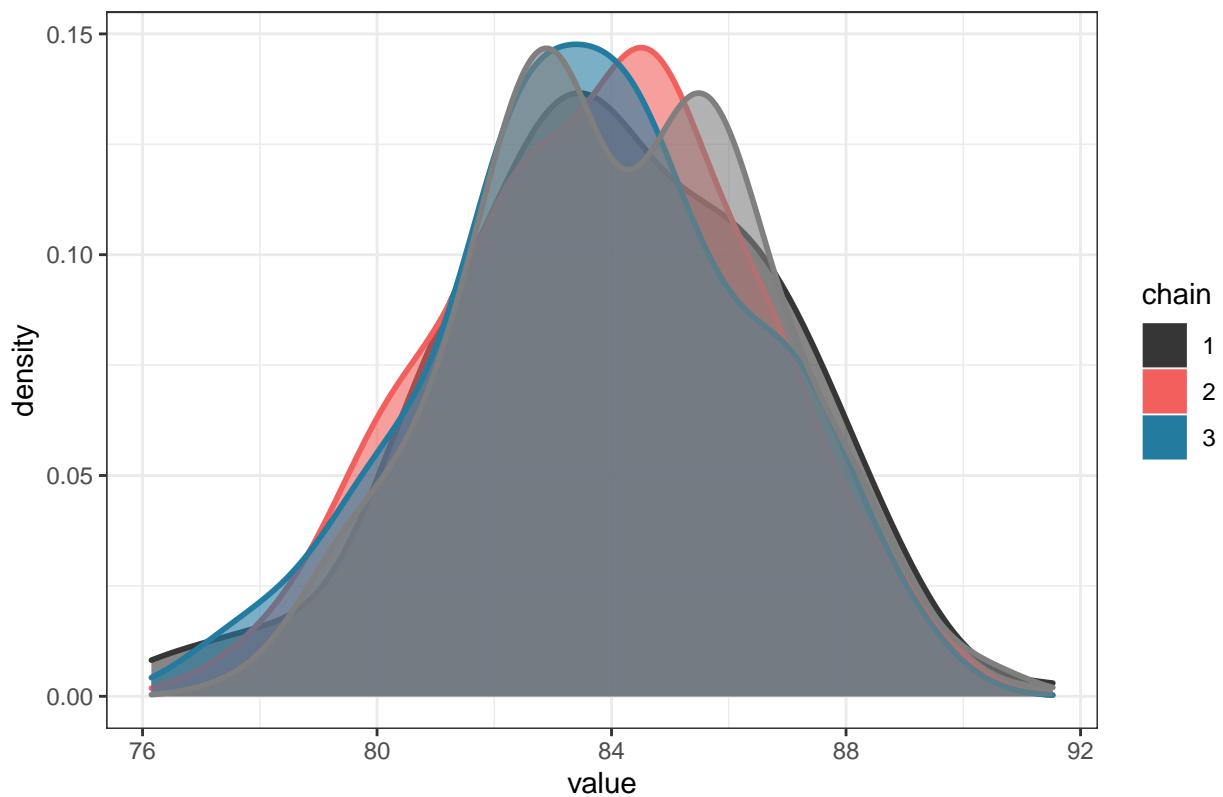
Density plot of $D[2, 1]$



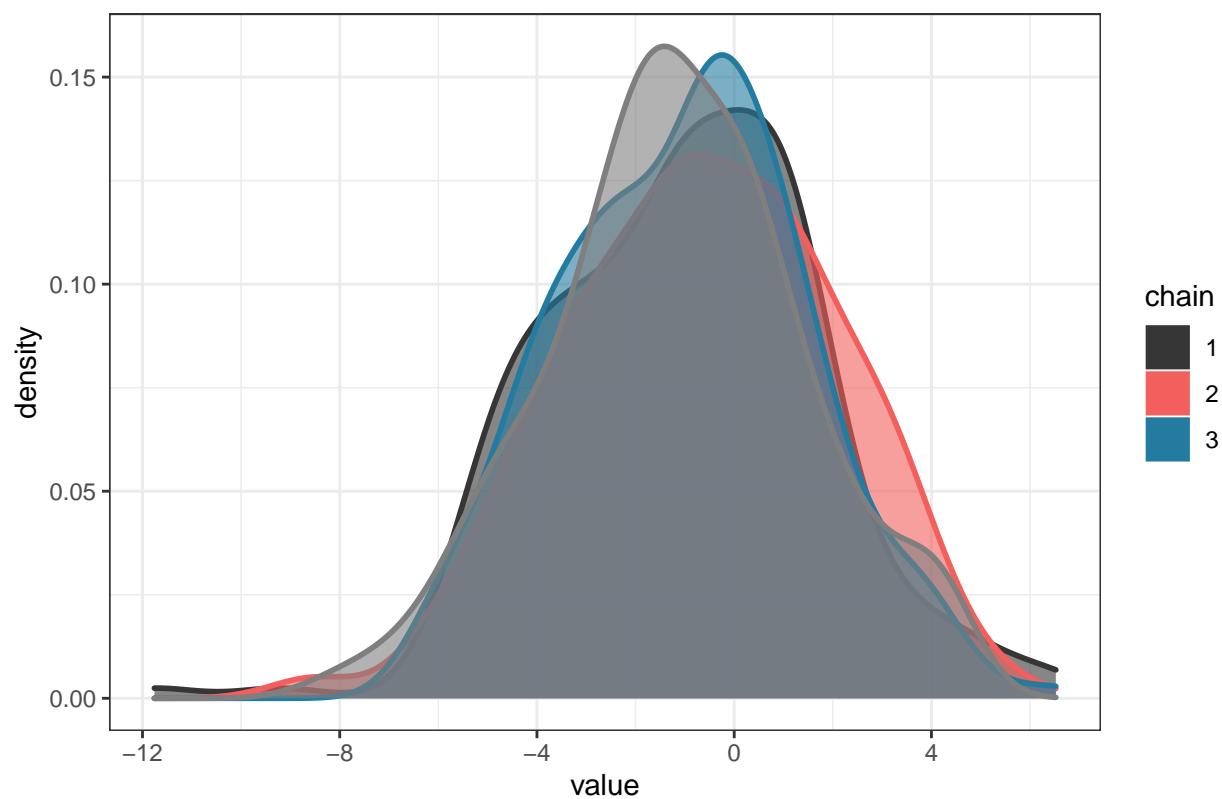
Density plot of $D[2, 2]$



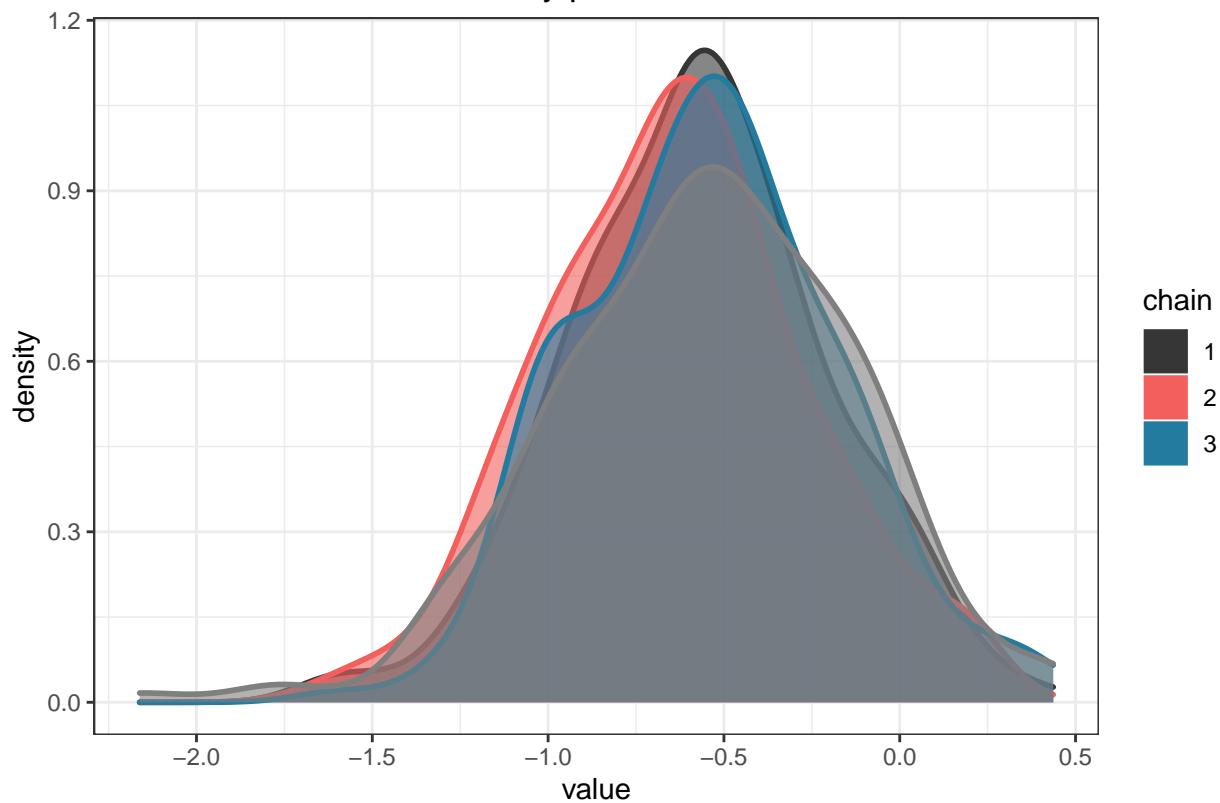
Density plot of (Intercept)



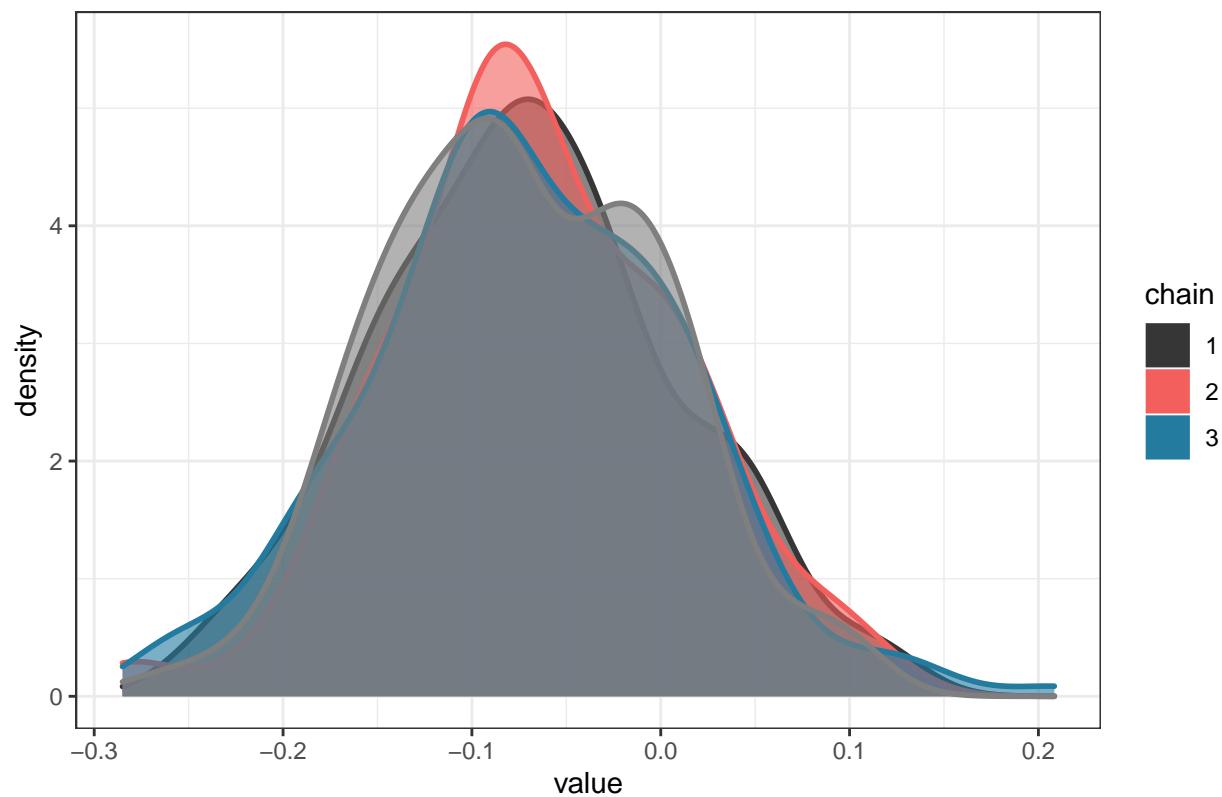
Density plot of LOWC31.1



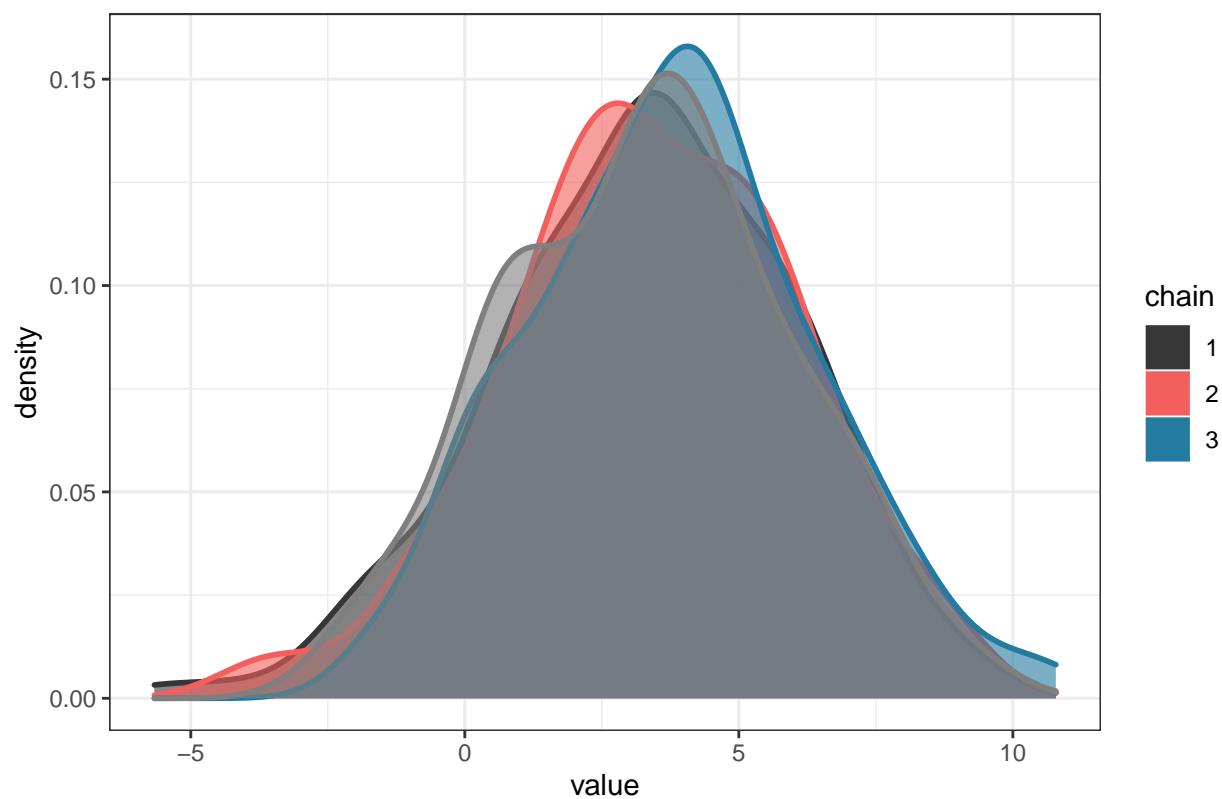
Density plot of time



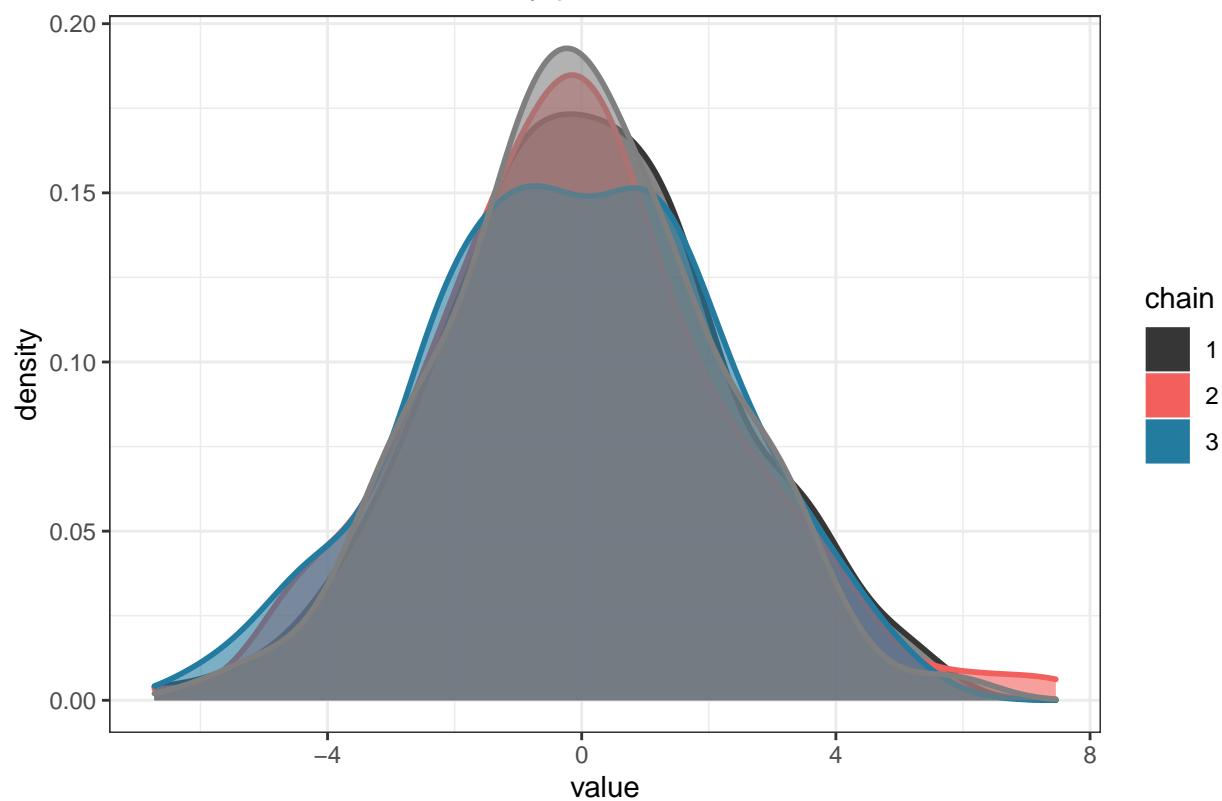
Density plot of ageatbiopsy.1



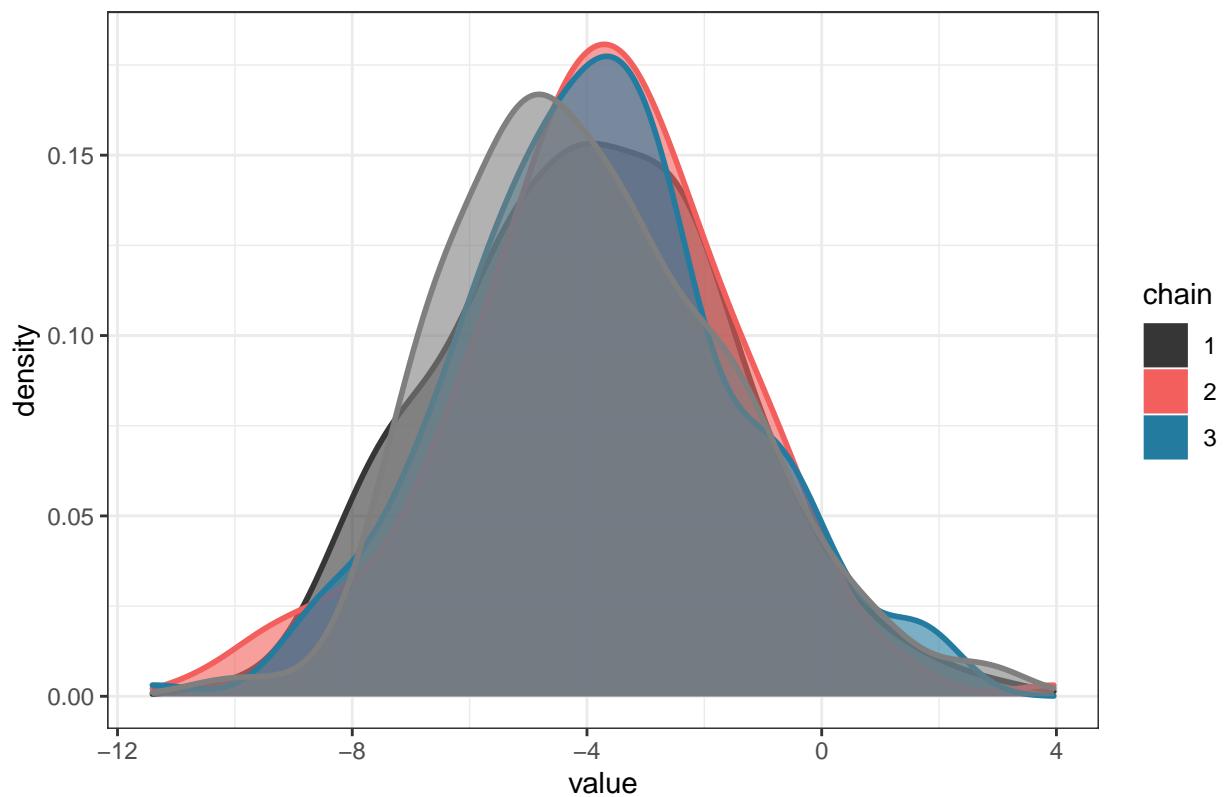
Density plot of sex.1



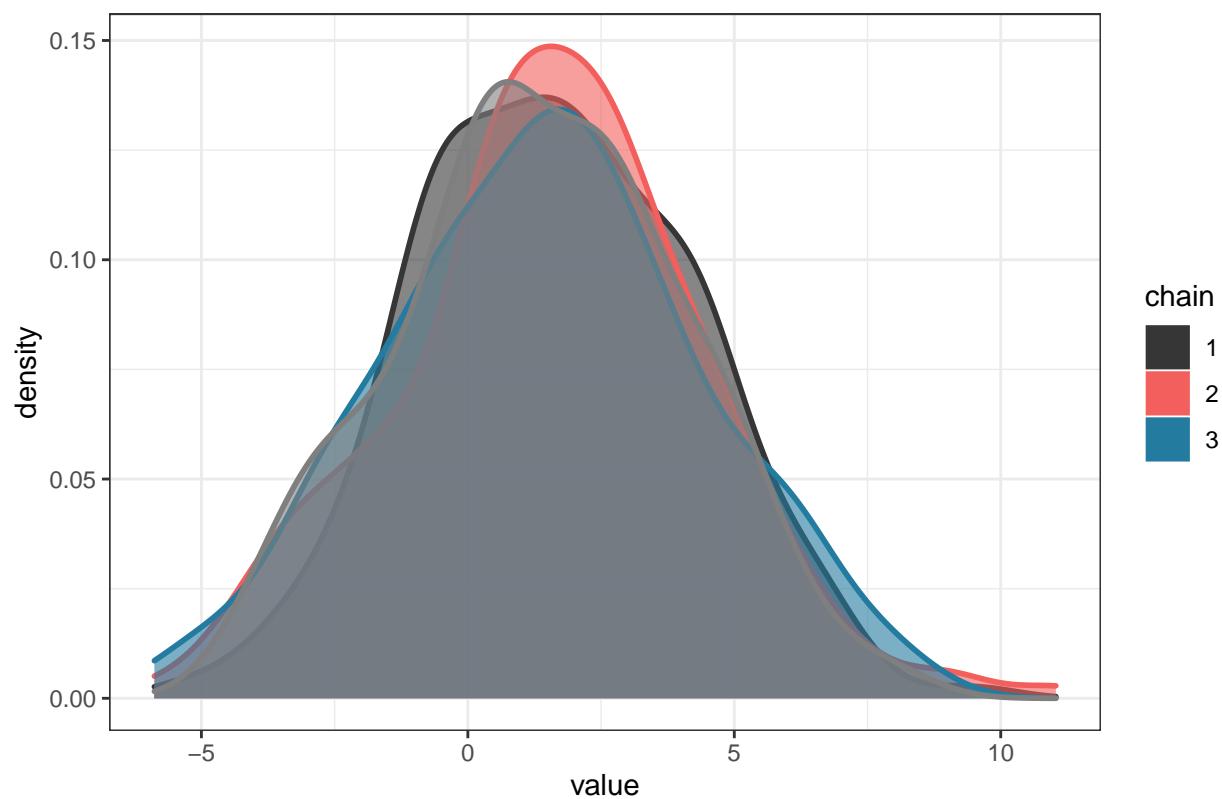
Density plot of black.1



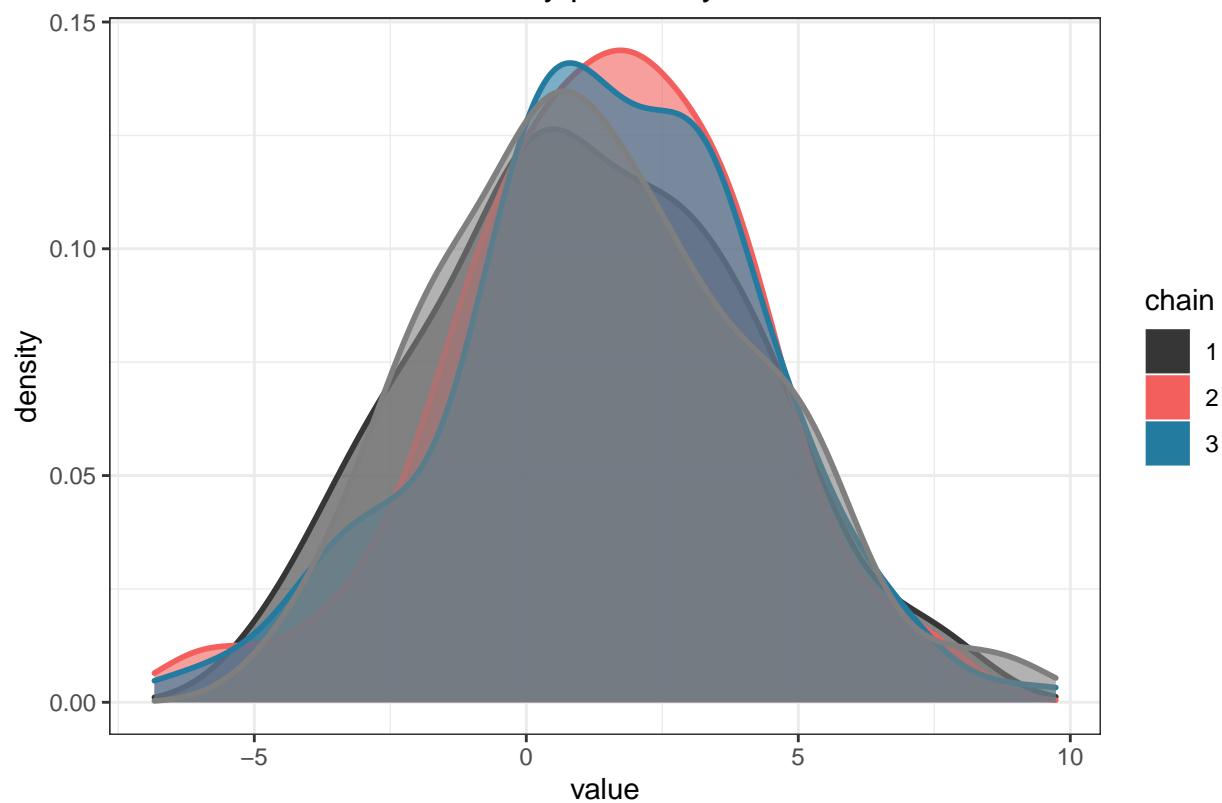
Density plot of hypertension.1



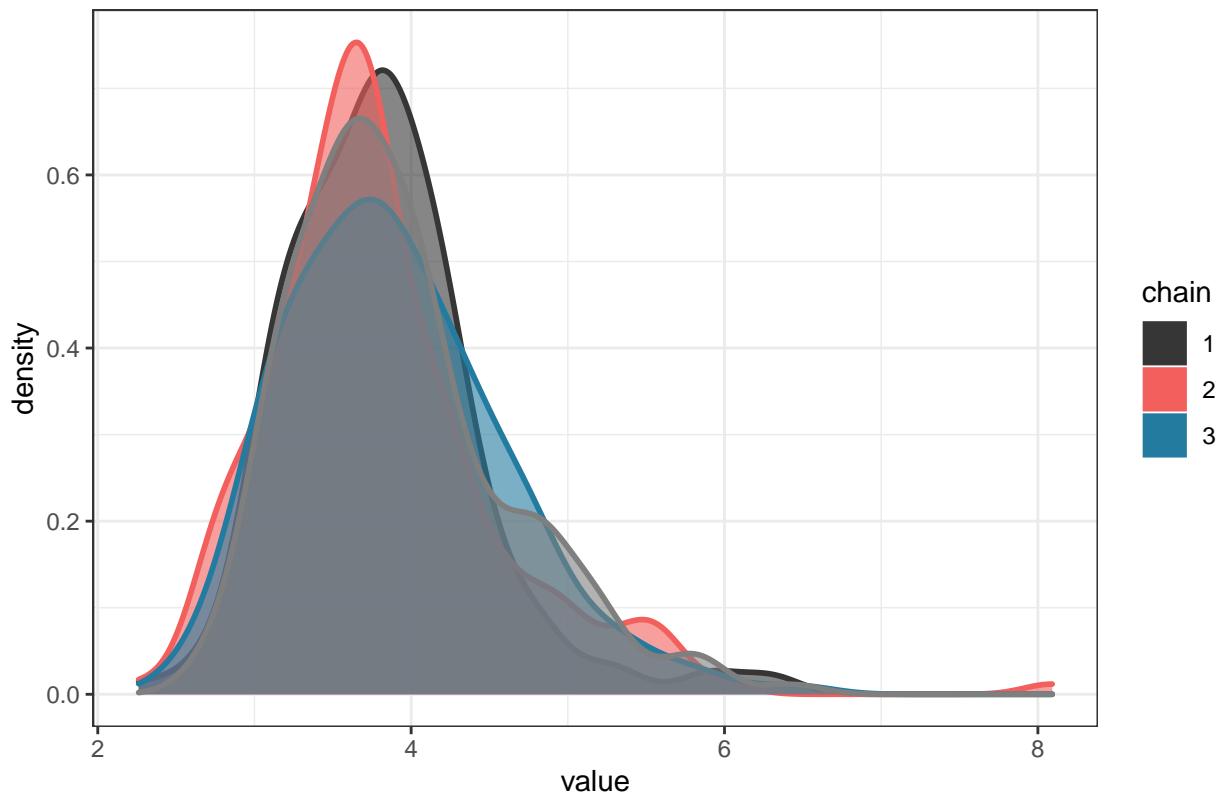
Density plot of mmf.1



Density plot of cyc.1

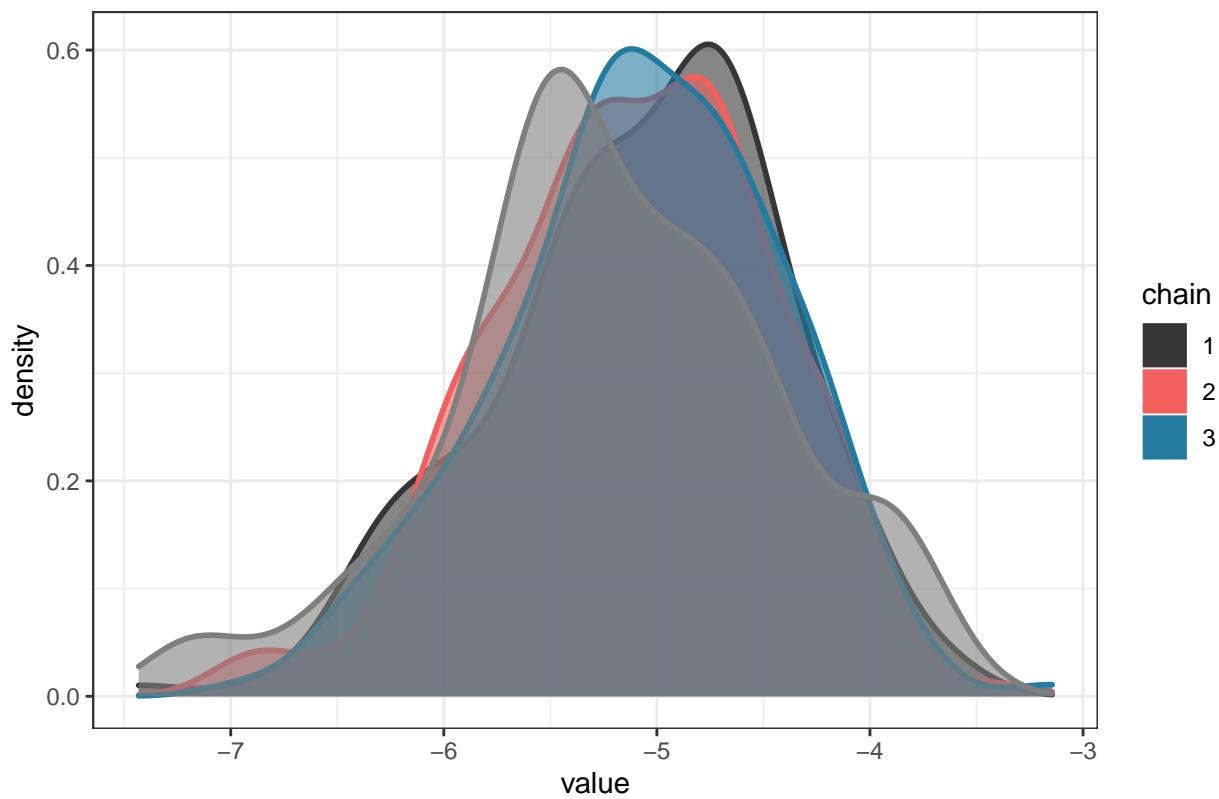


Density plot of sigmas_1

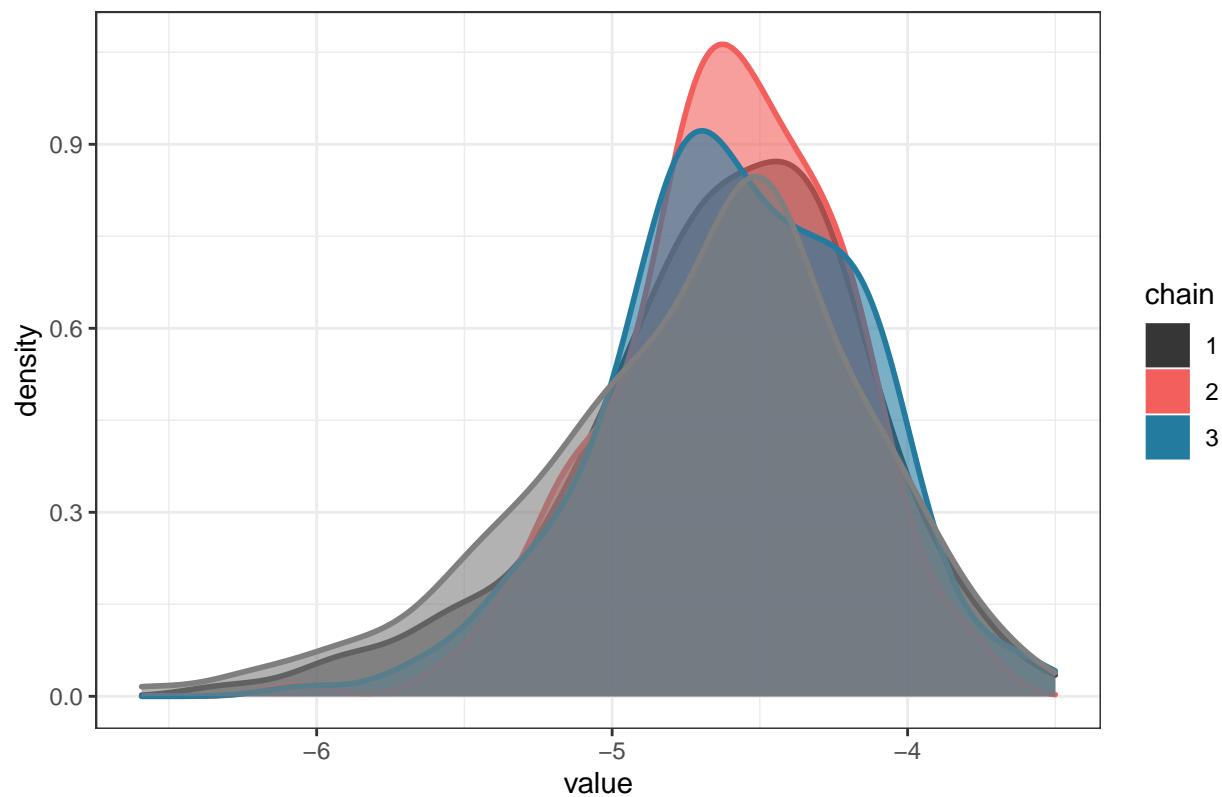


```
densplt1 <- ggdensityplot(jointFit1)
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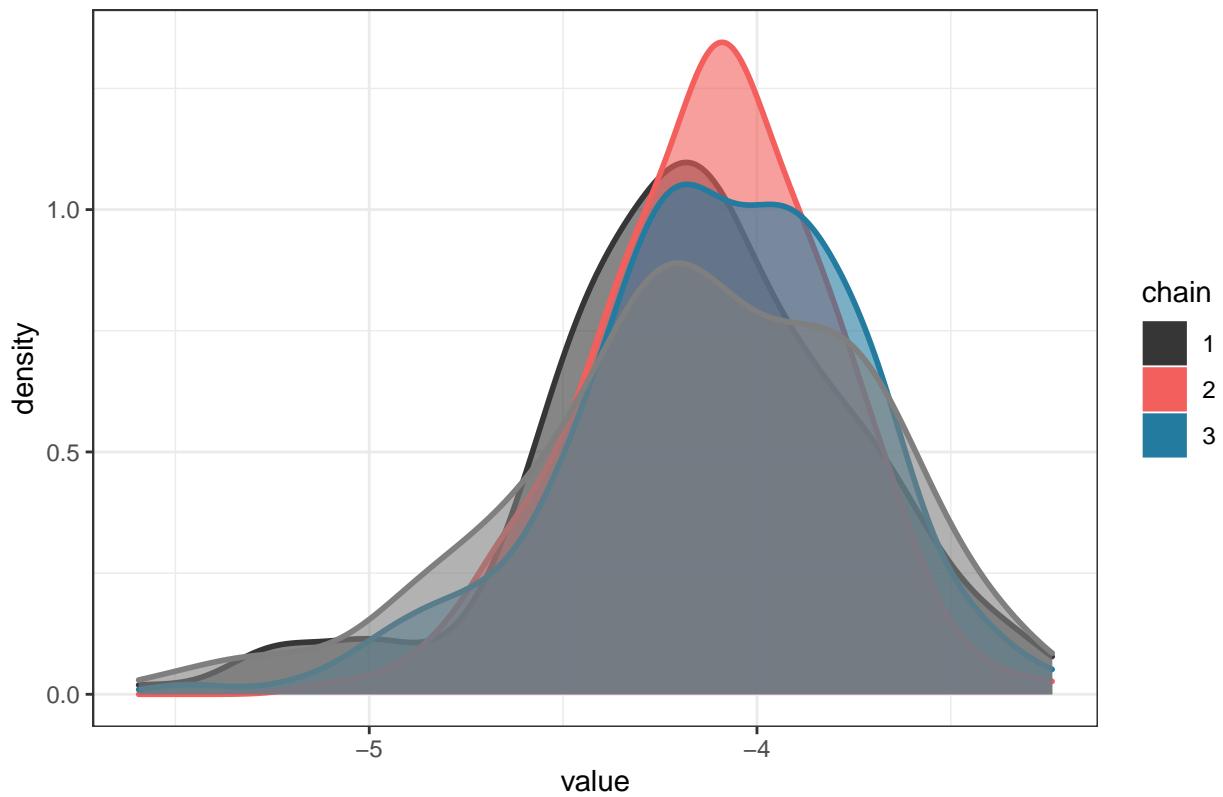
Density plot of bs_gammas_1



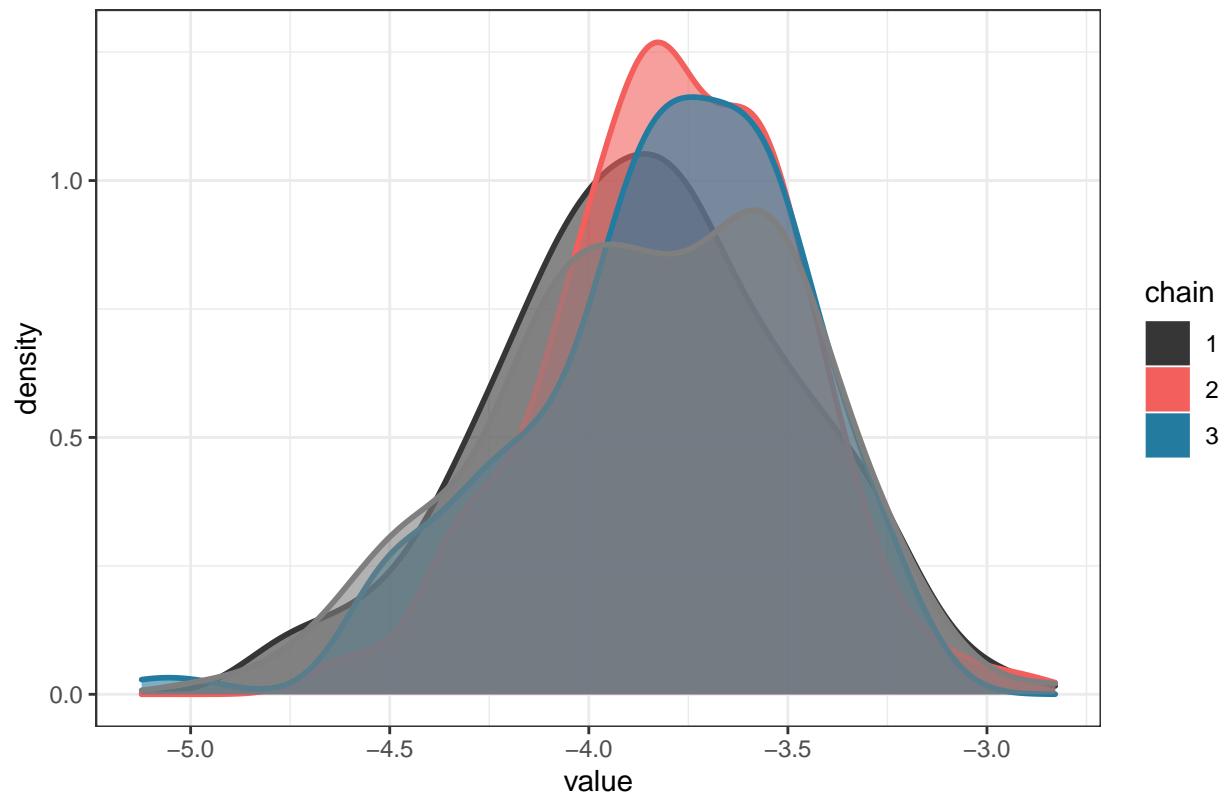
Density plot of bs_gammas_2



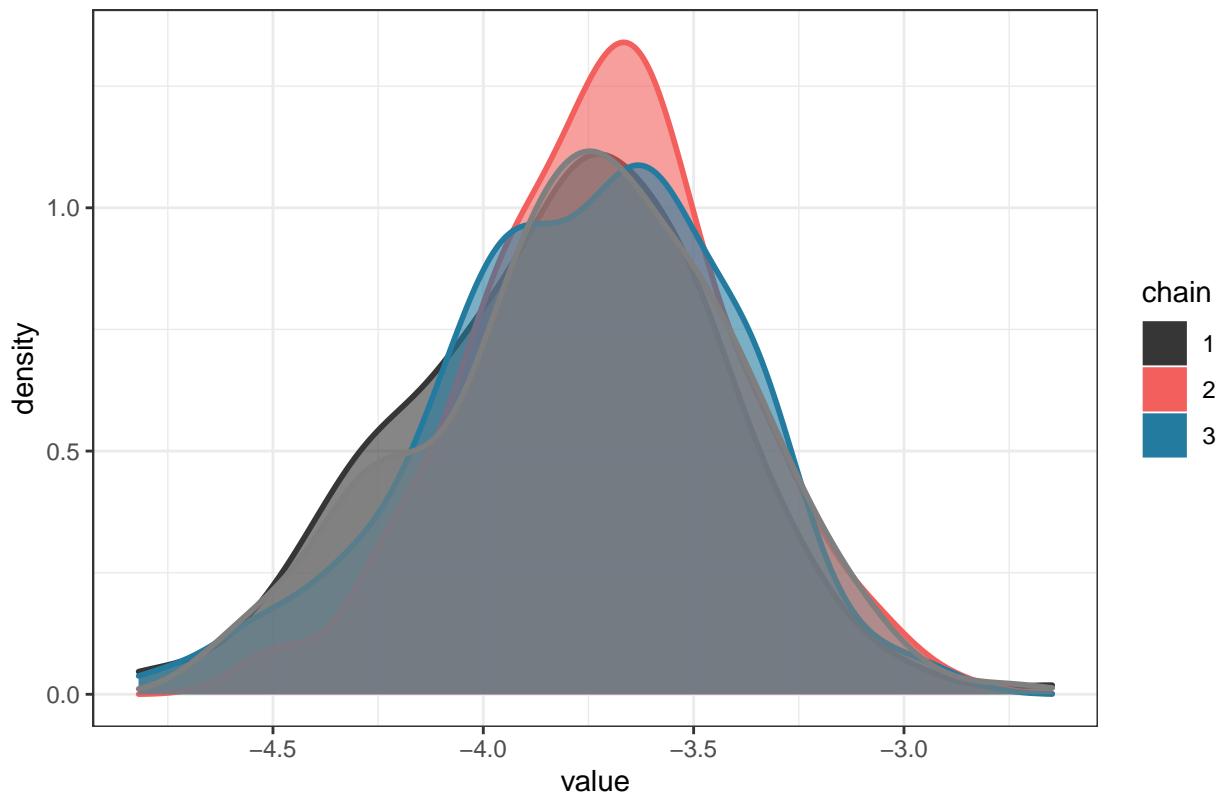
Density plot of bs_gammas_3



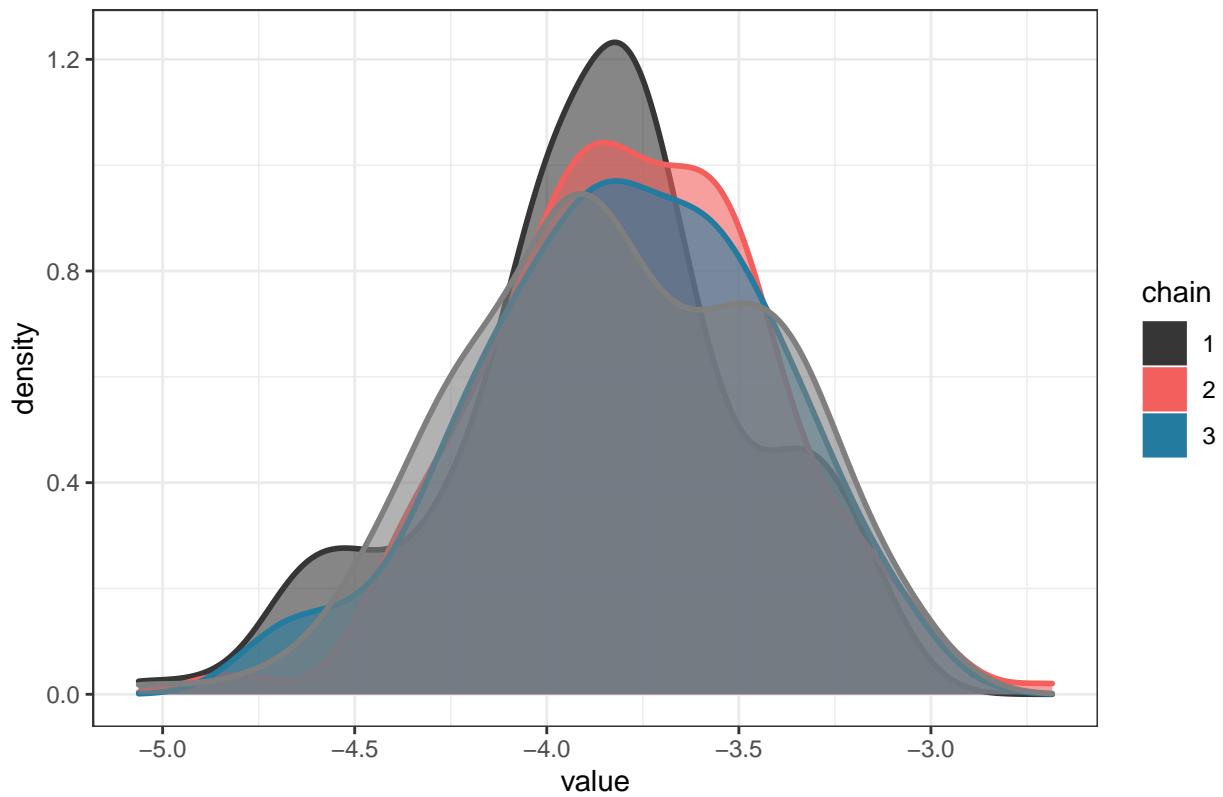
Density plot of bs_gammas_4



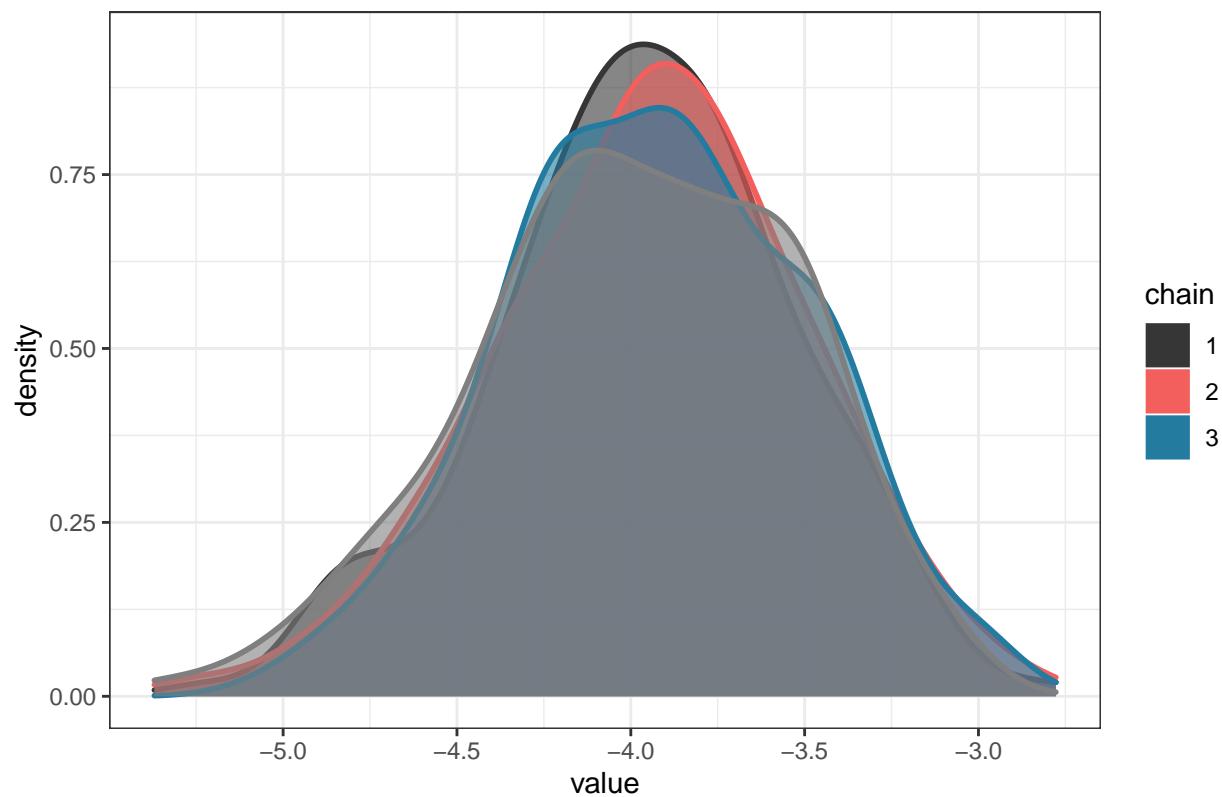
Density plot of bs_gammas_5



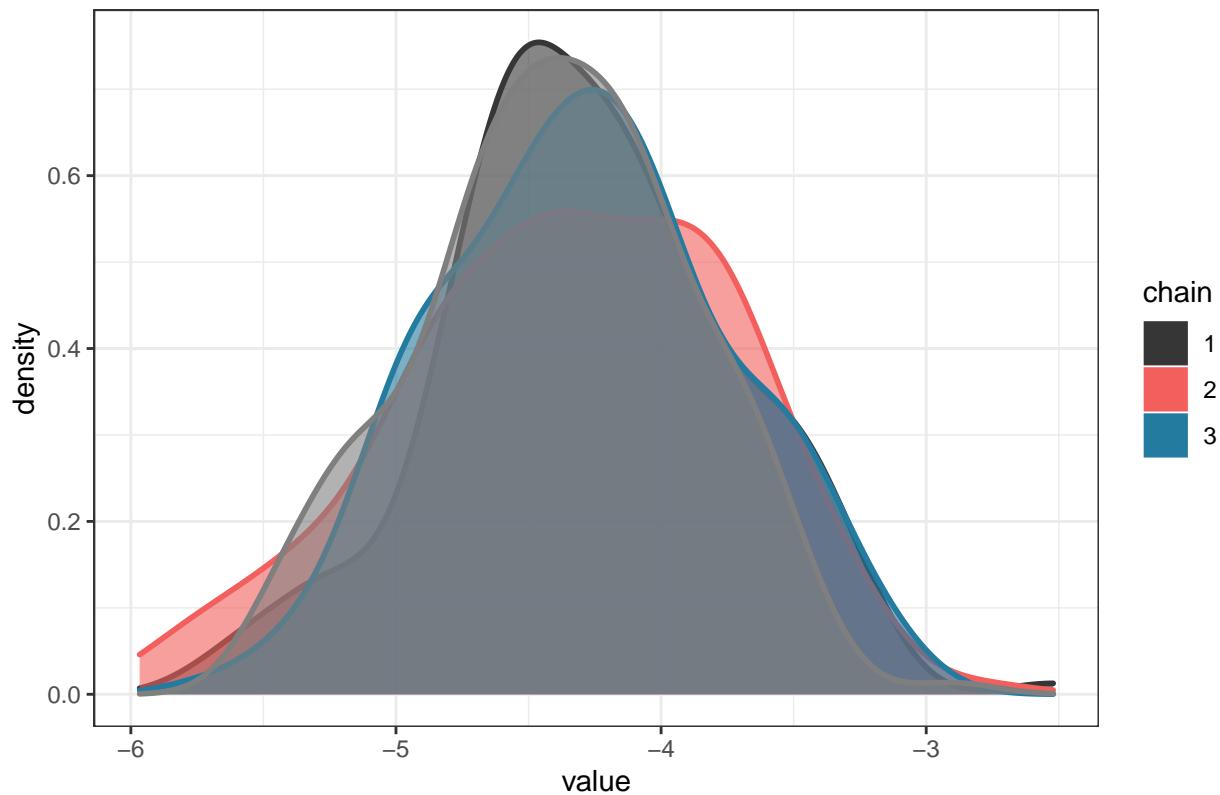
Density plot of bs_gammas_6



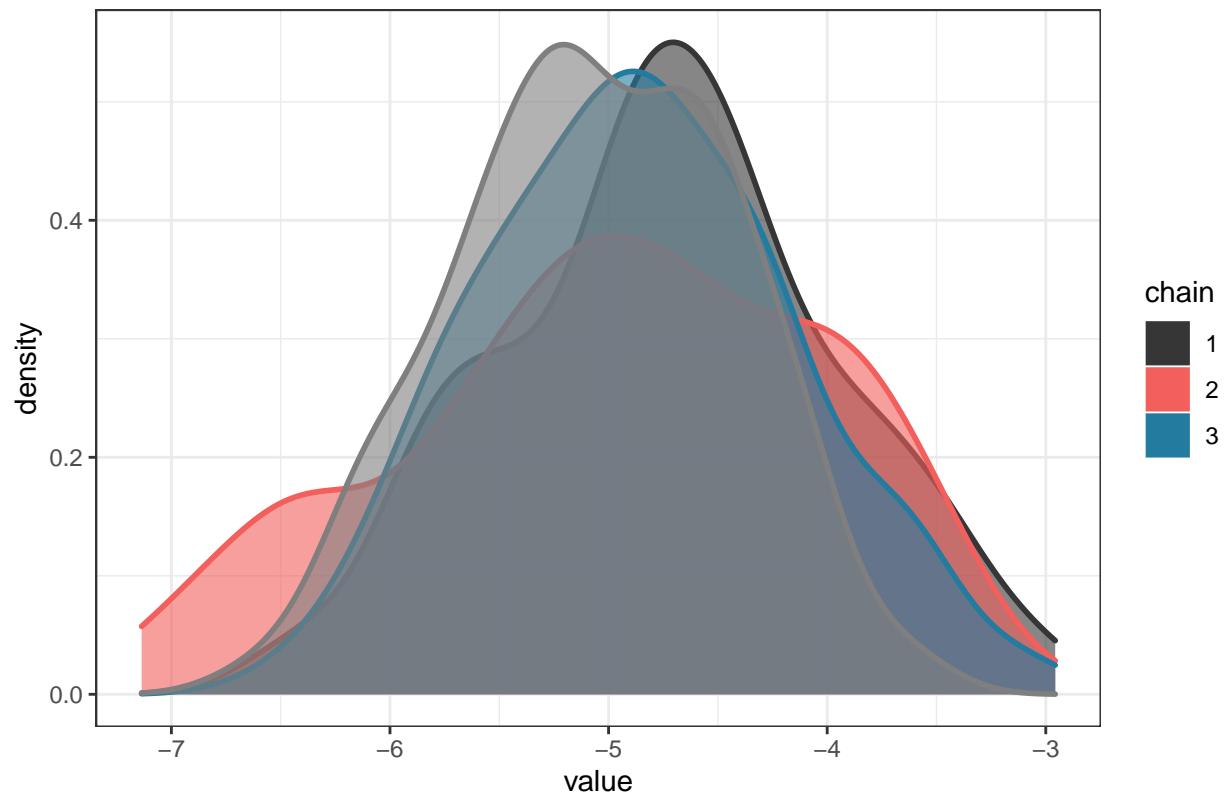
Density plot of bs_gammas_7



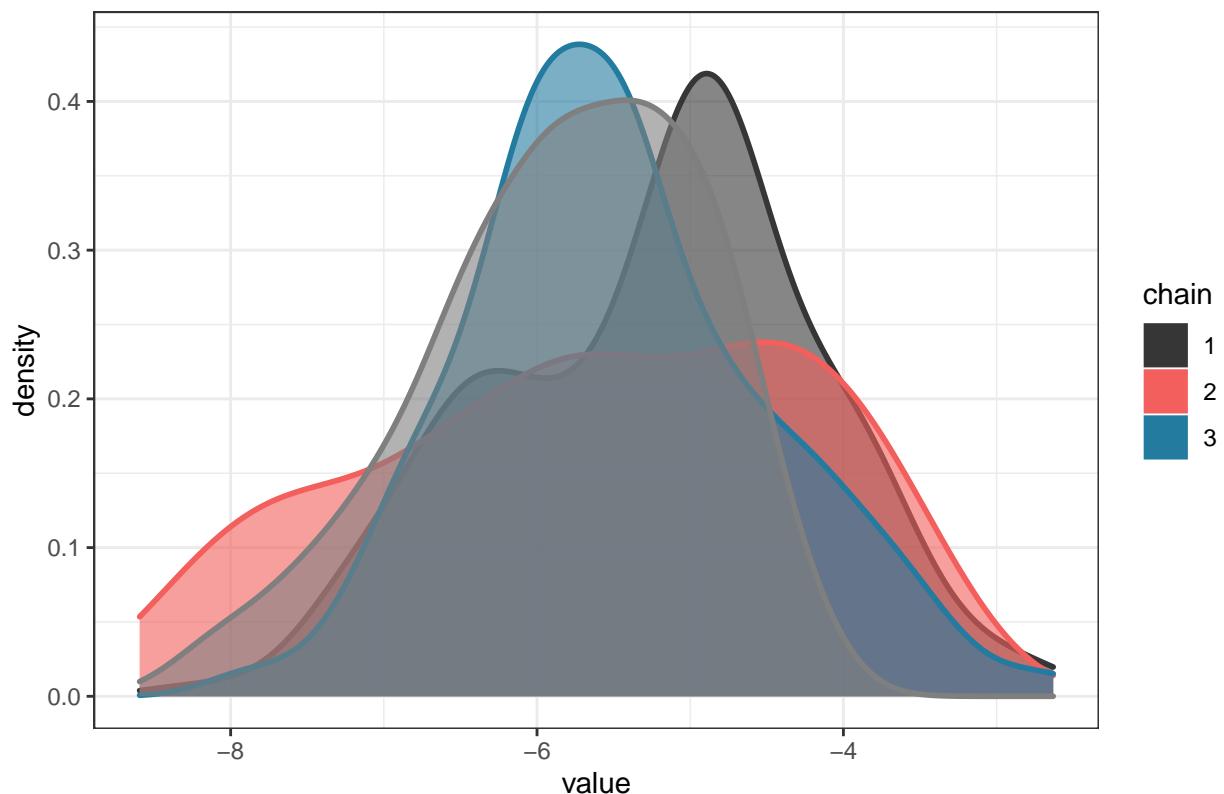
Density plot of bs_gammas_8



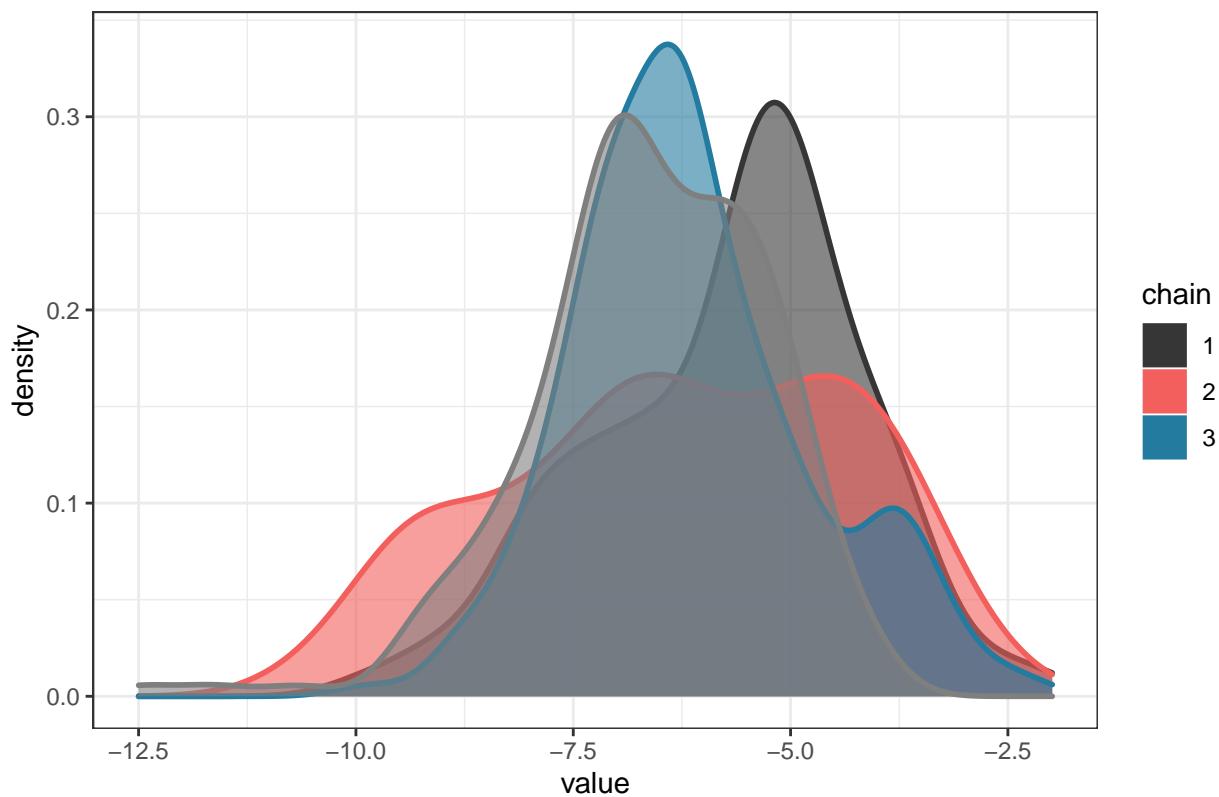
Density plot of bs_gammas_9



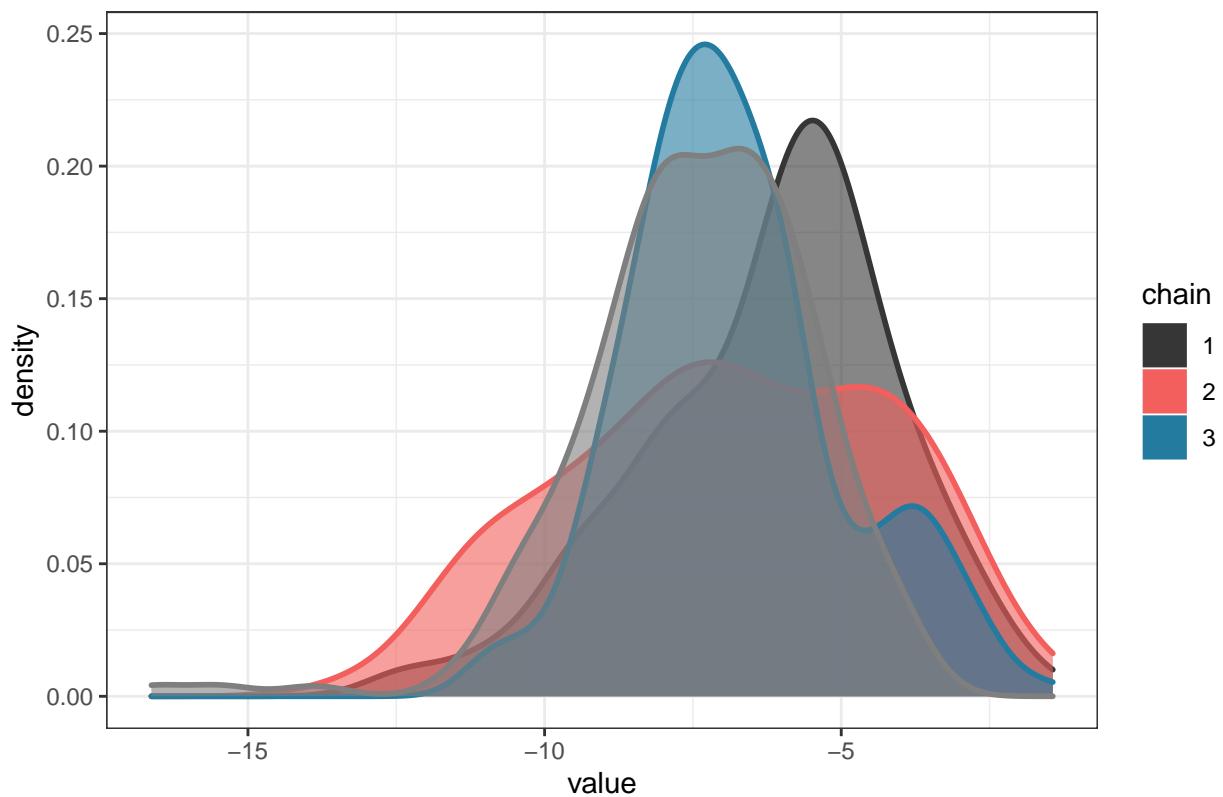
Density plot of bs_gammas_10



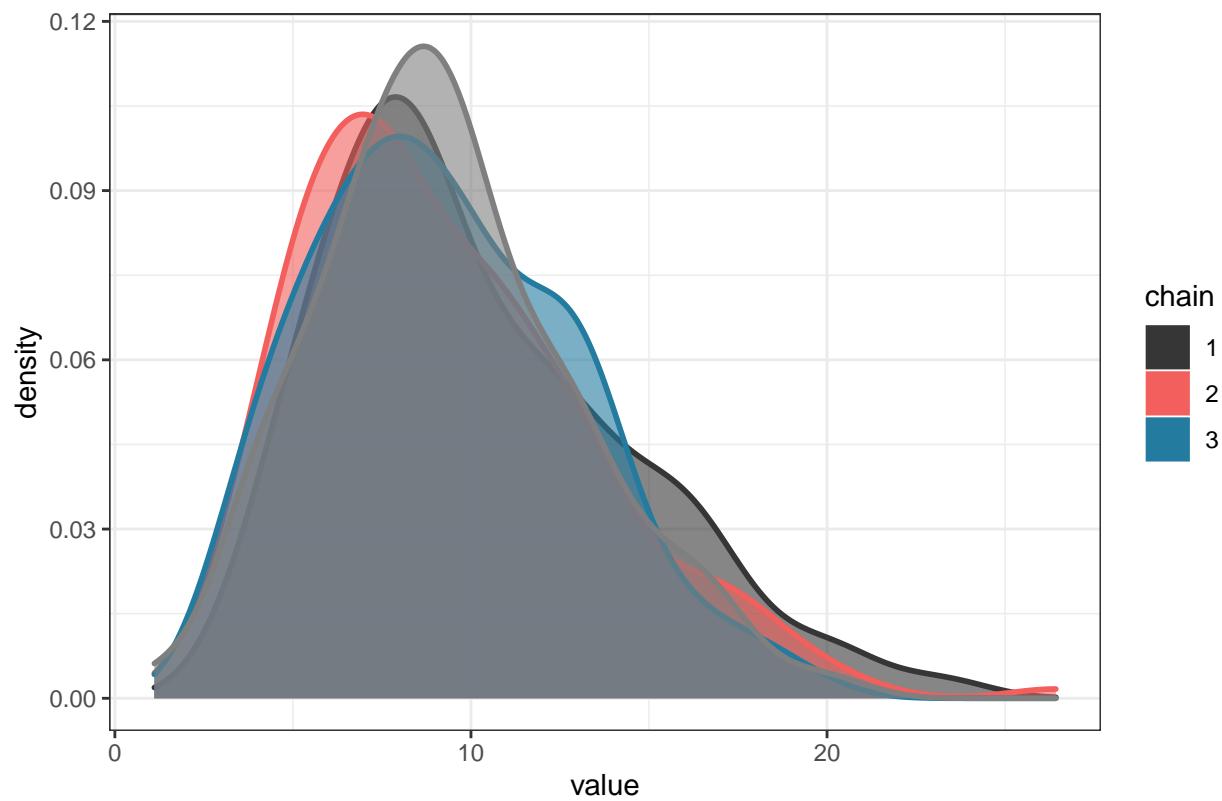
Density plot of bs_gammas_11



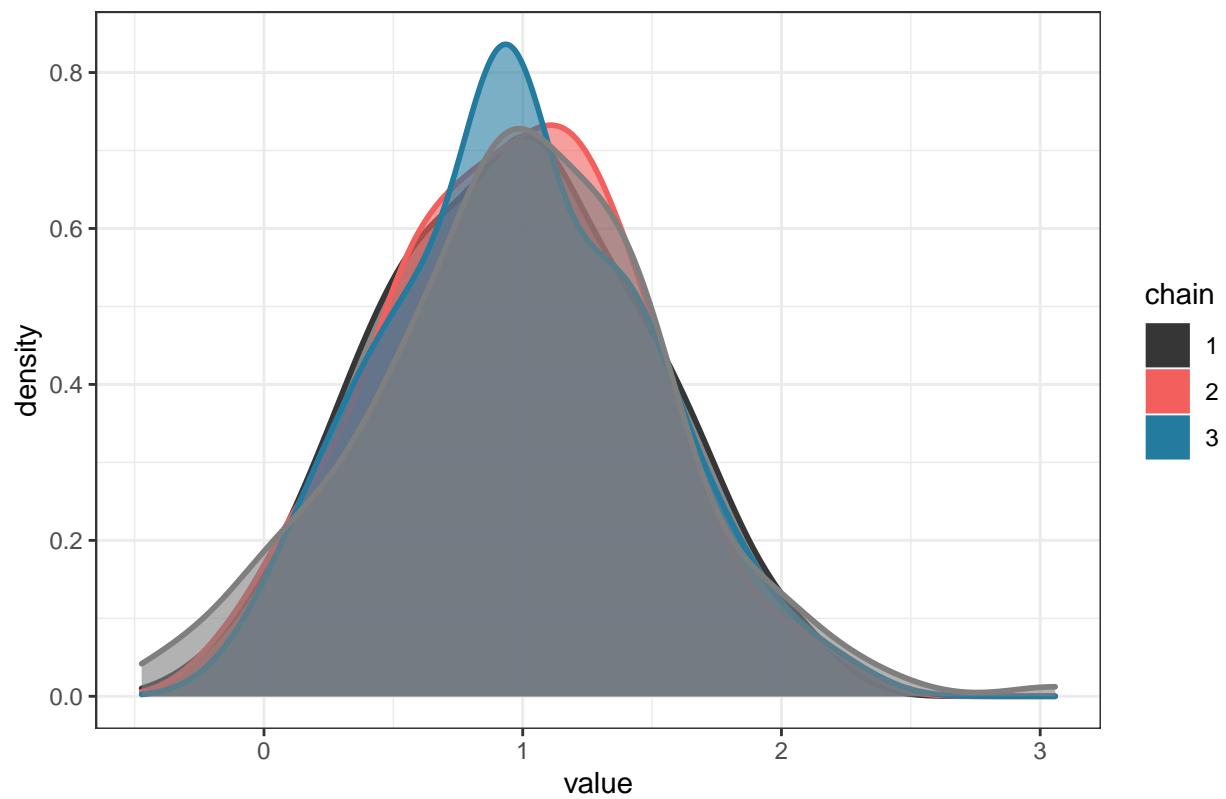
Density plot of bs_gammas_12



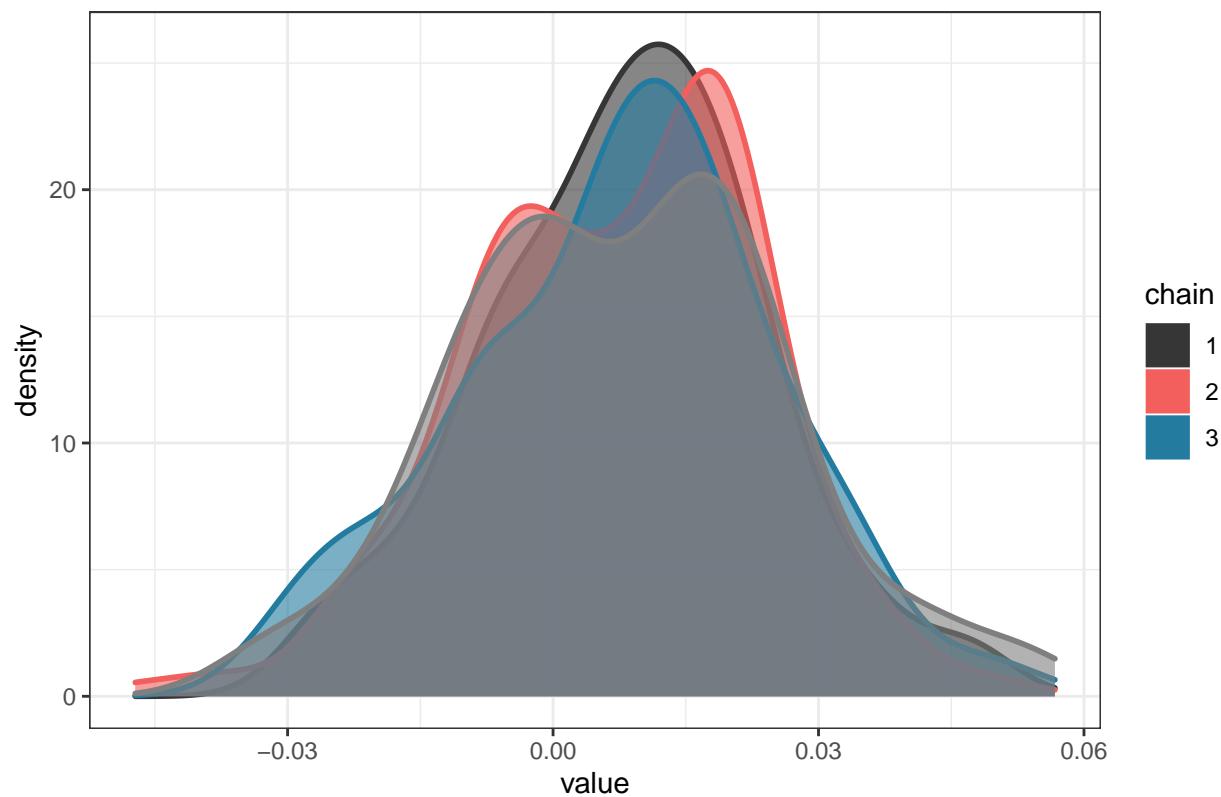
Density plot of tau_bs_gammas



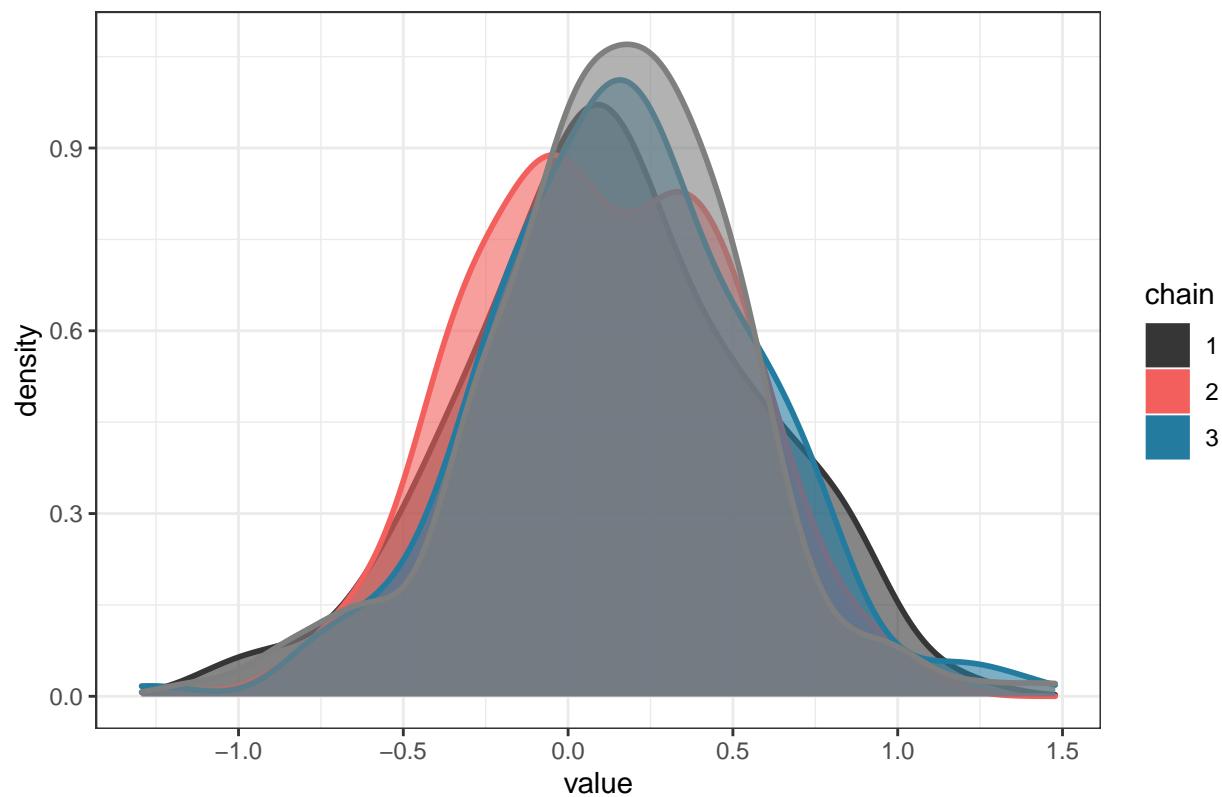
Density plot of LOWC31



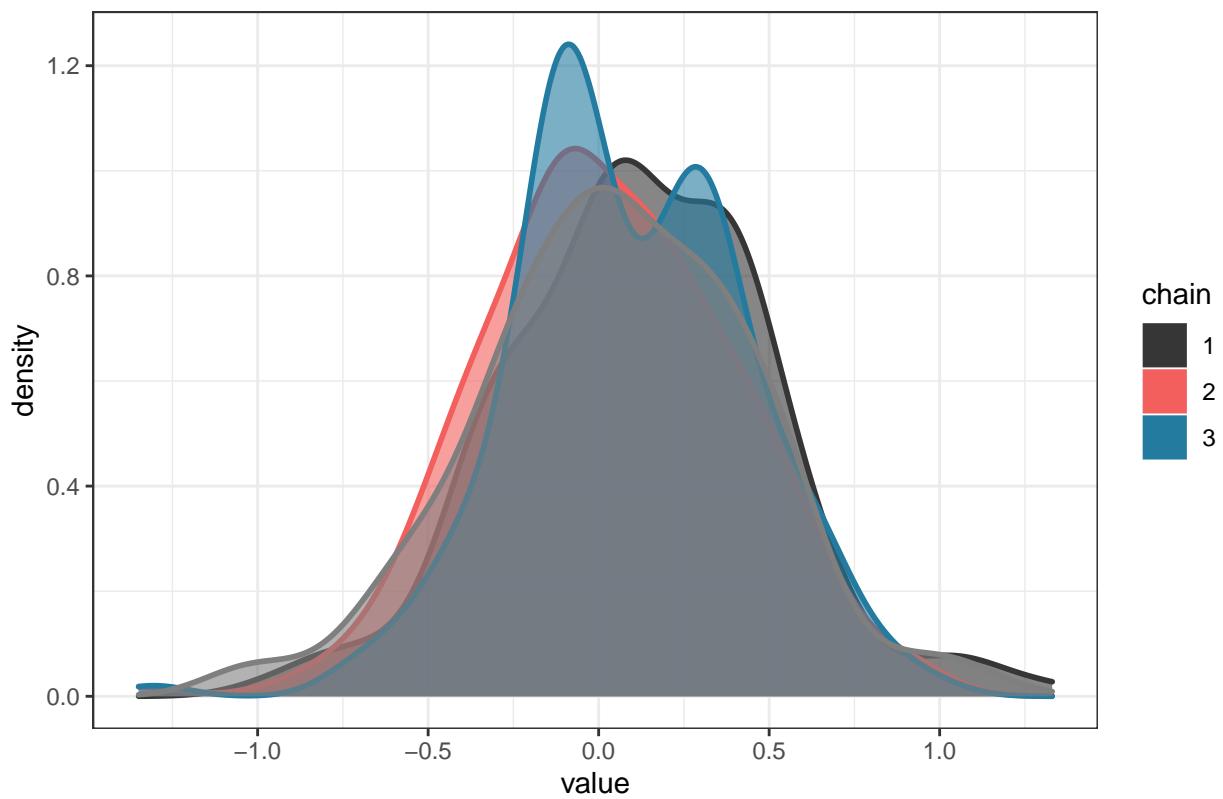
Density plot of ageatbiopsy



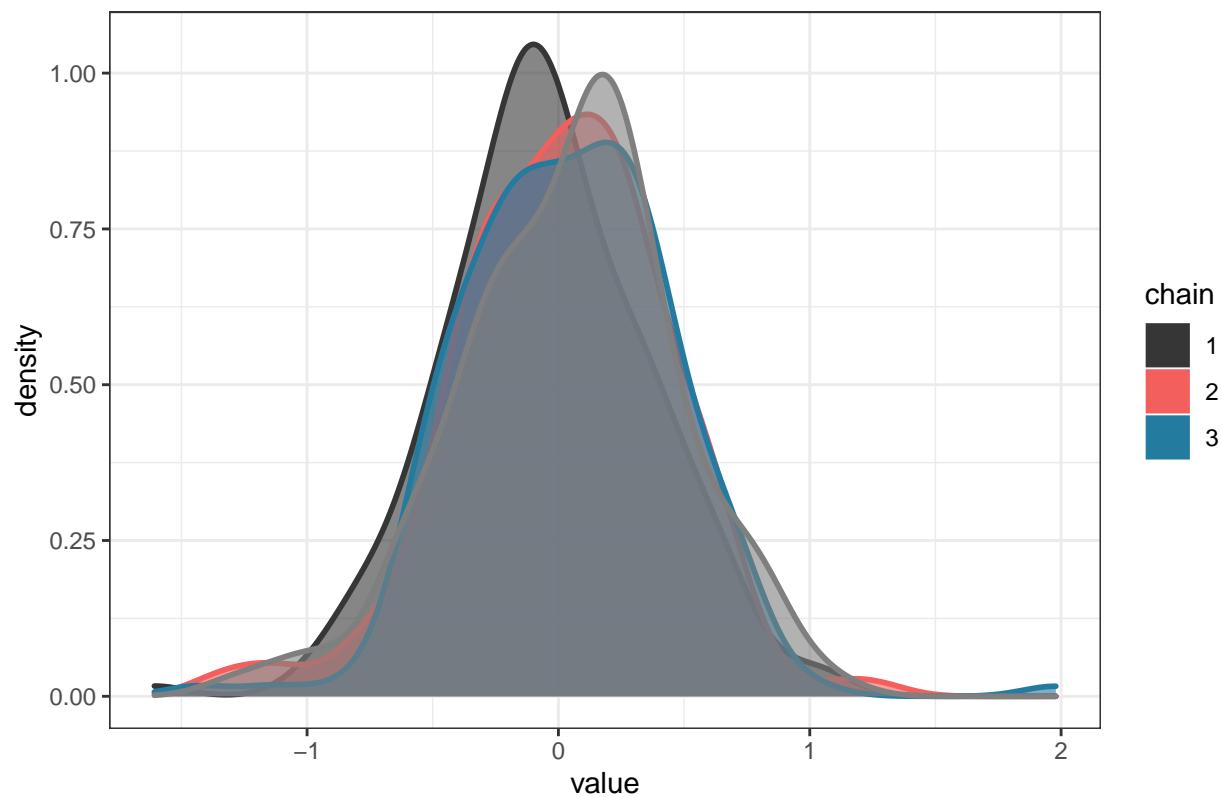
Density plot of sex



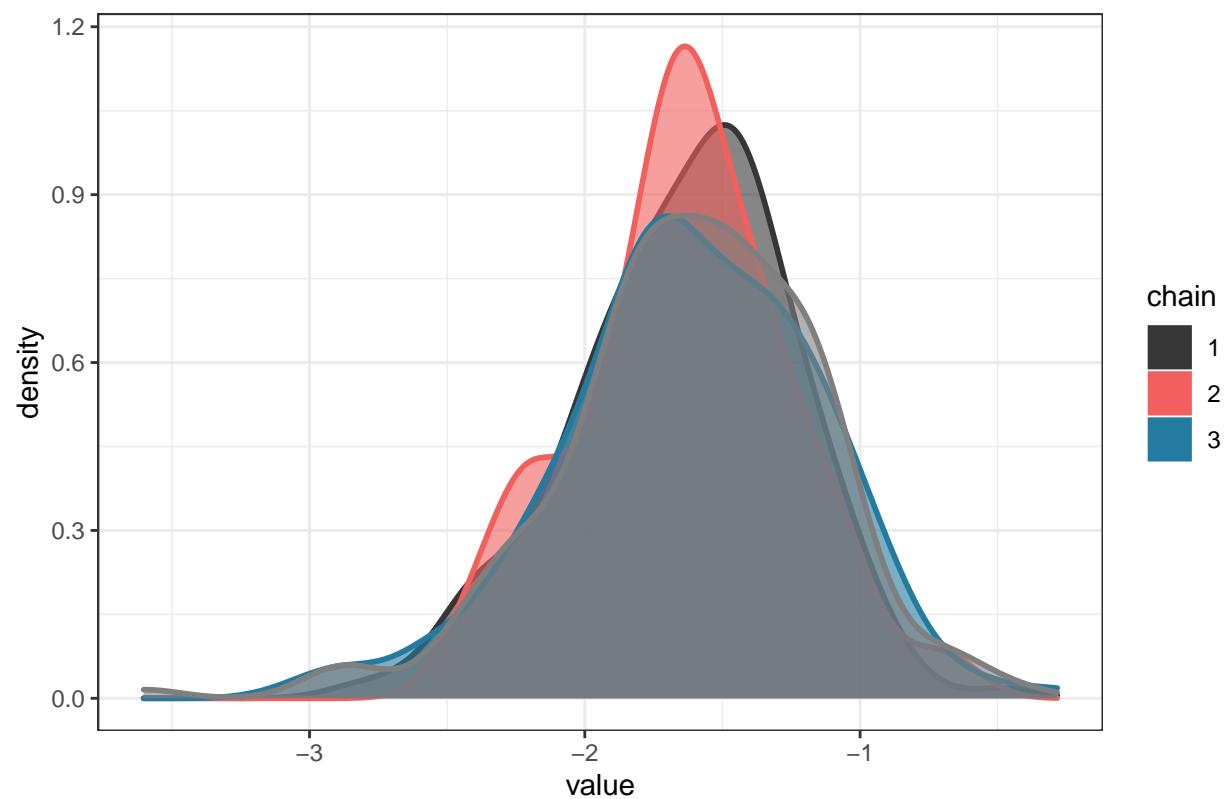
Density plot of black



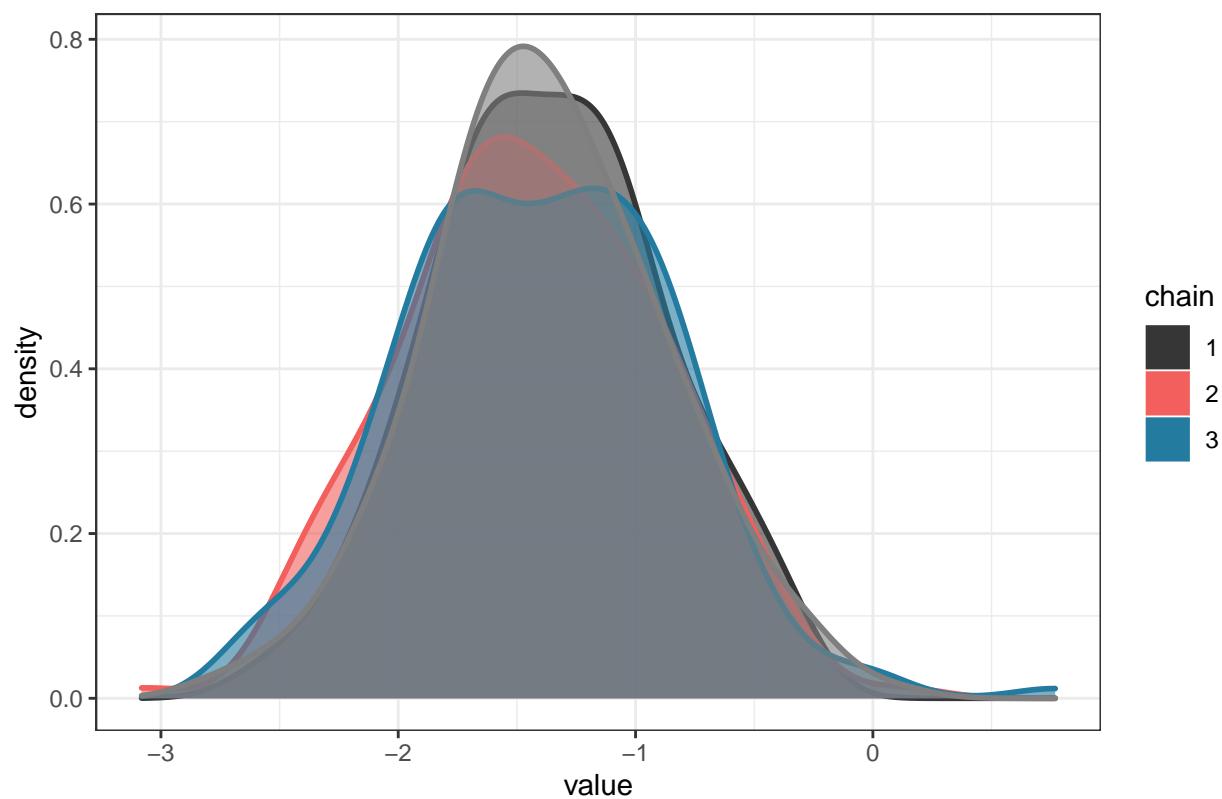
Density plot of hypertension



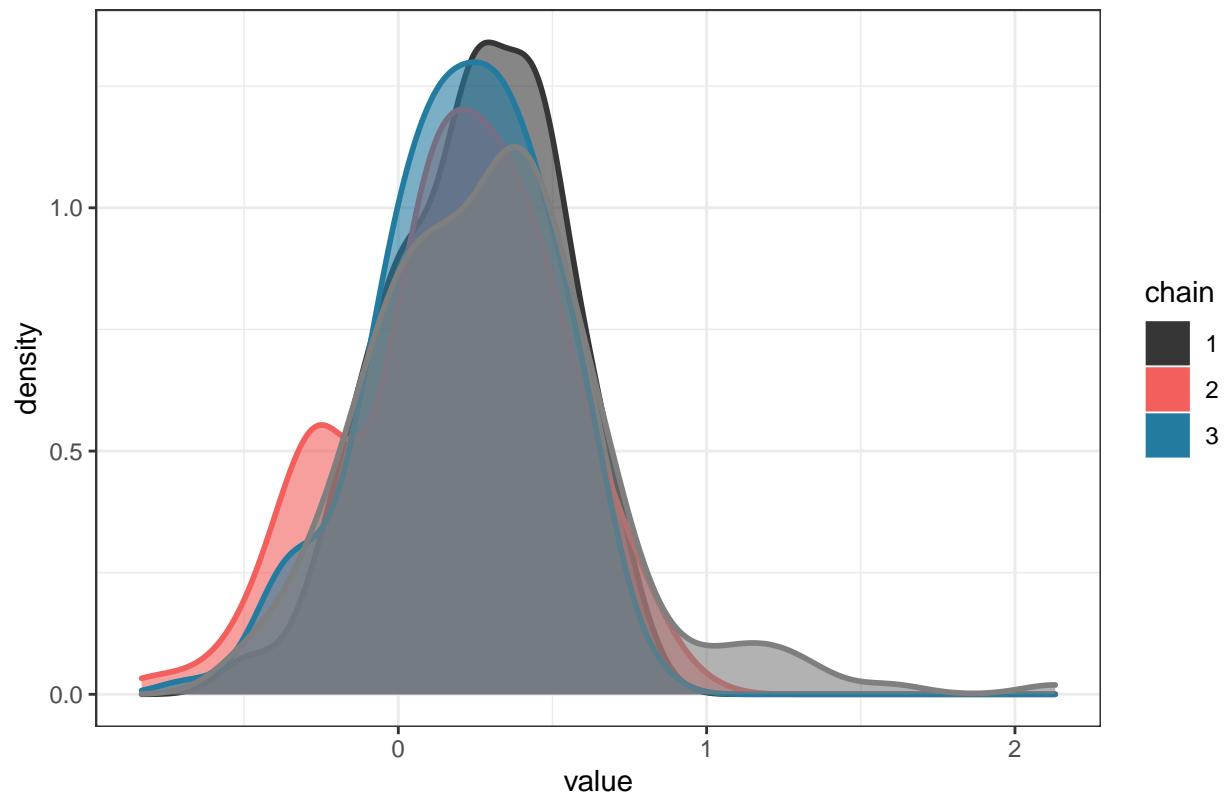
Density plot of mmf



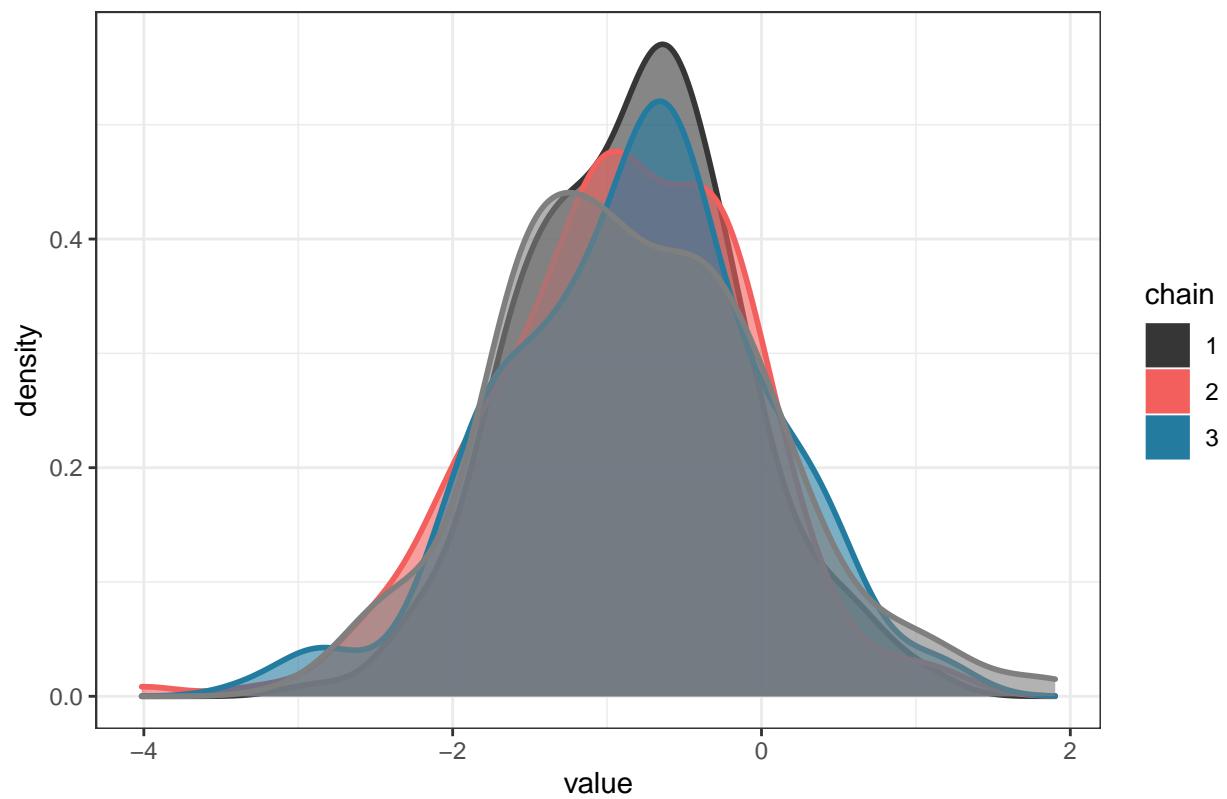
Density plot of cyc



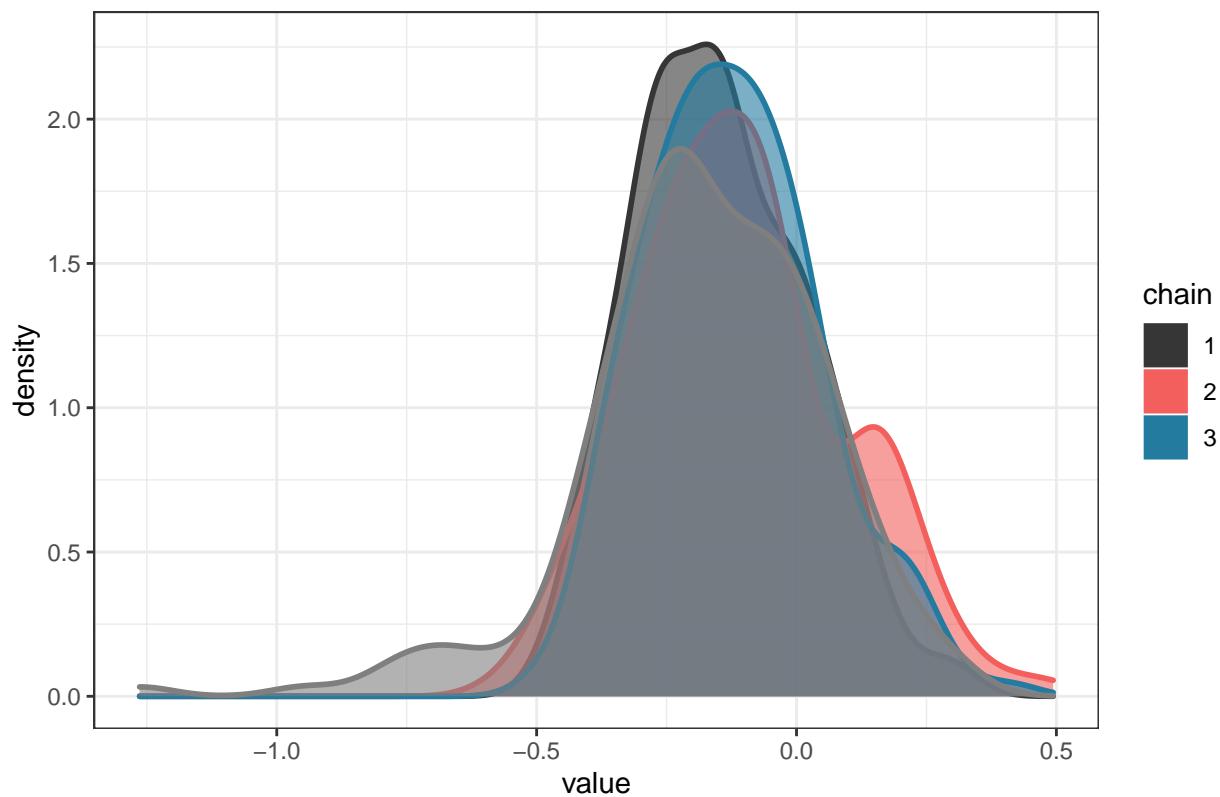
Density plot of slope(eGFR)



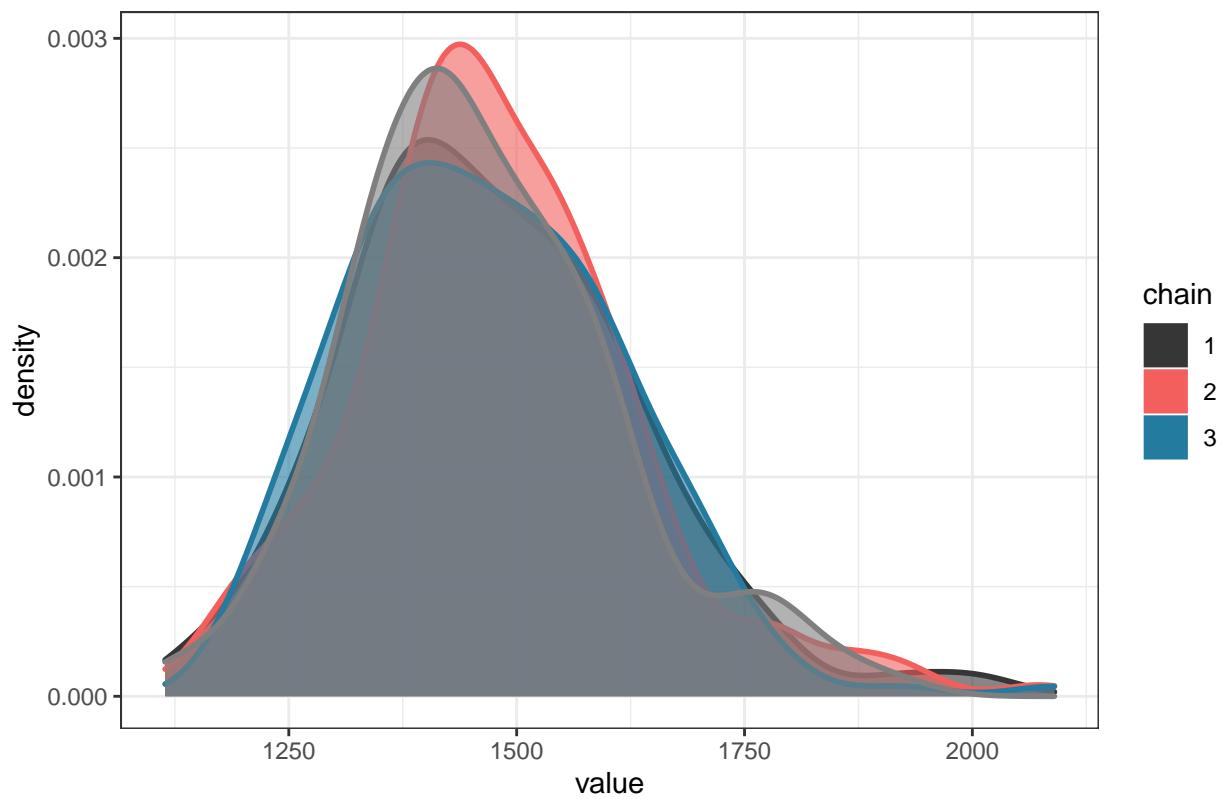
Density plot of



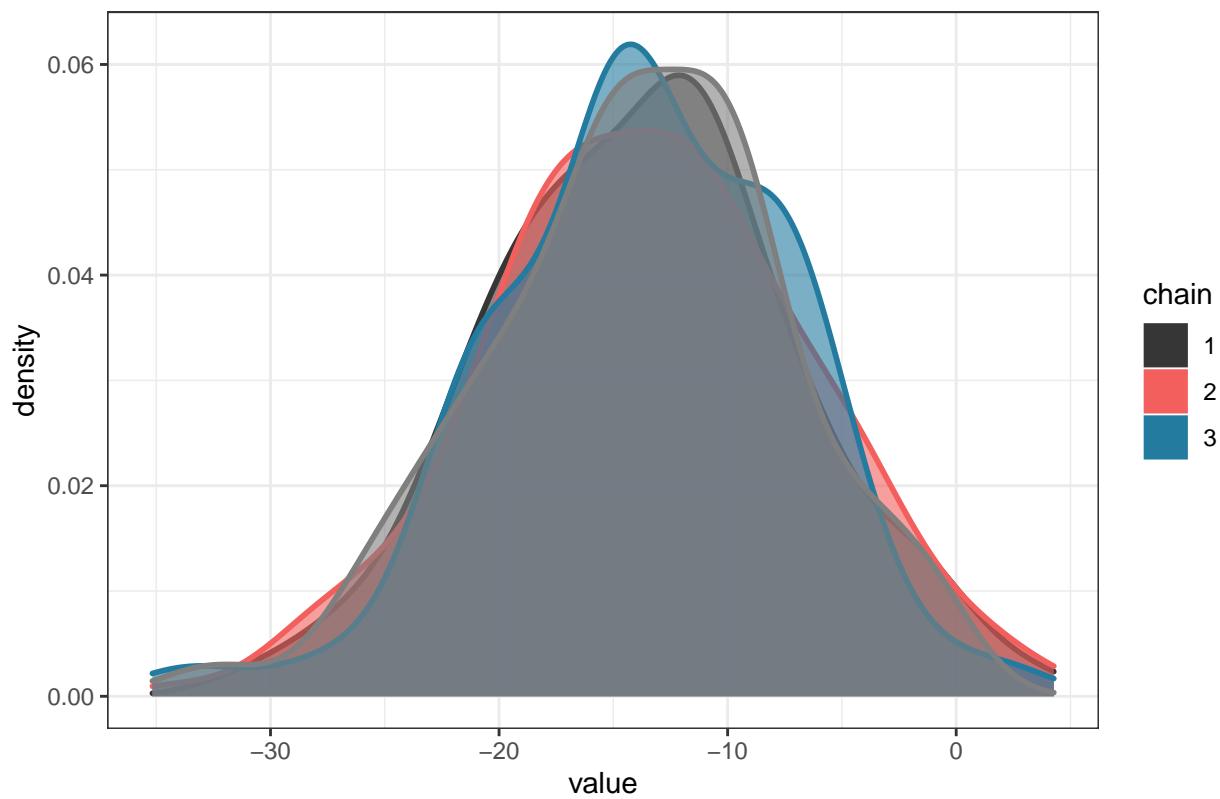
Density plot of .1



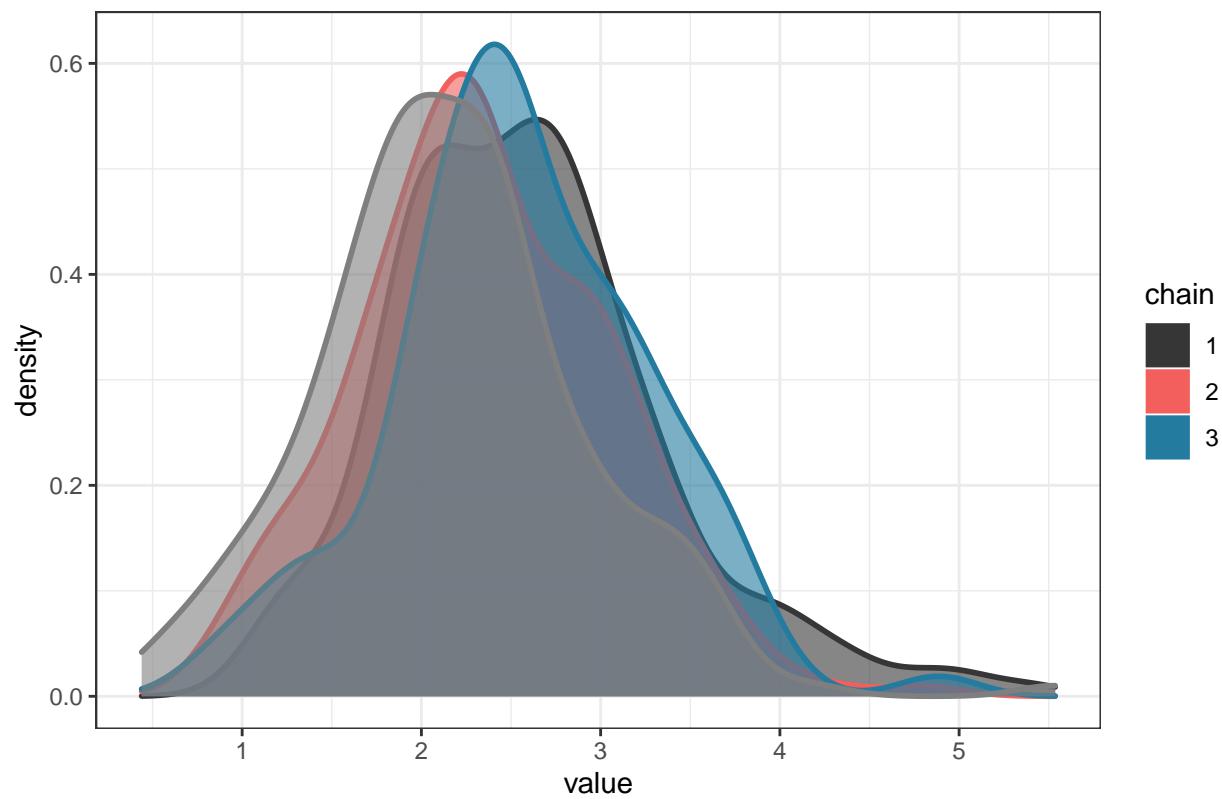
Density plot of $D[1, 1]$



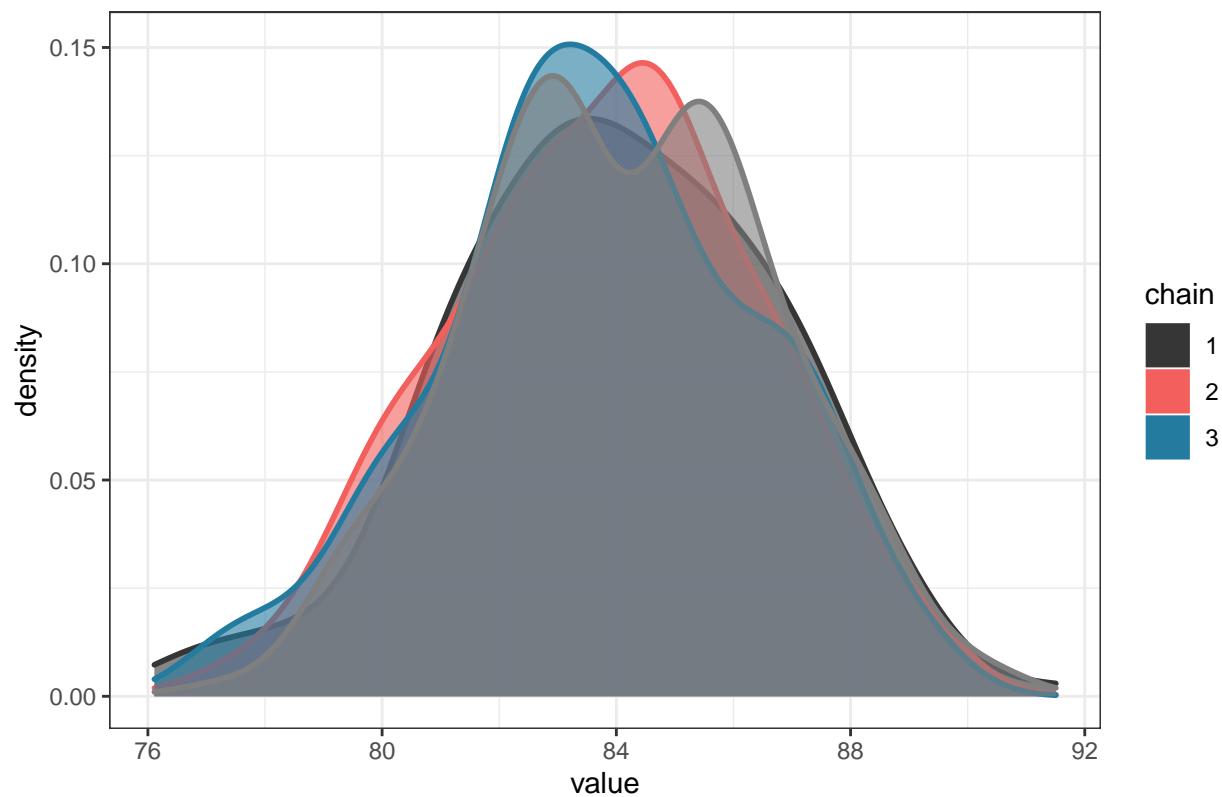
Density plot of $D[2, 1]$



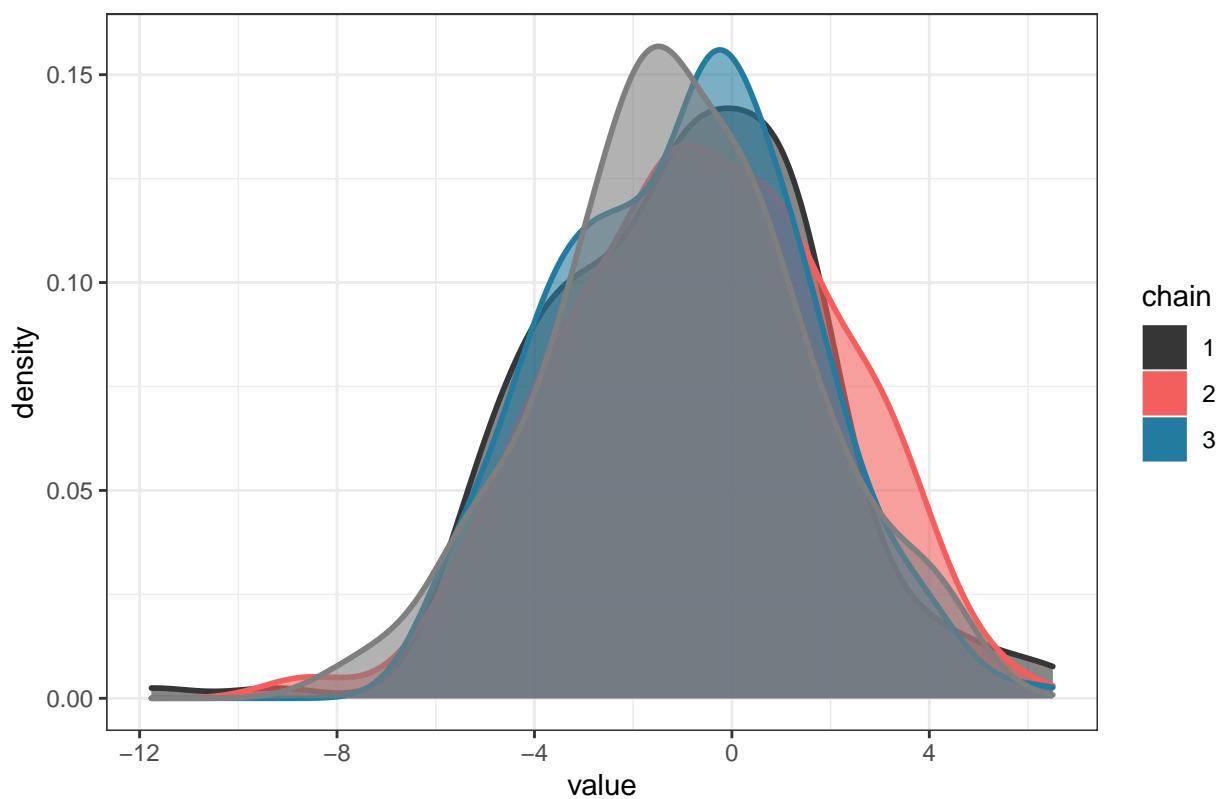
Density plot of $D[2, 2]$



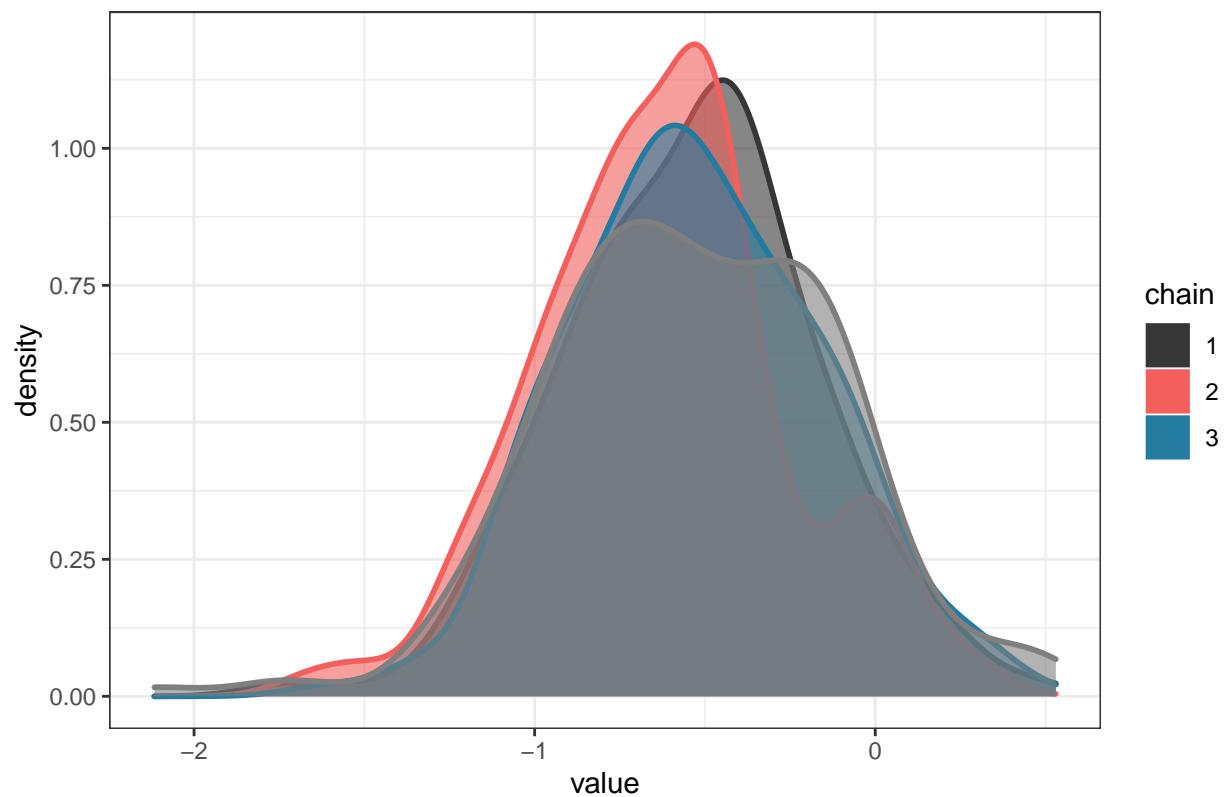
Density plot of (Intercept)



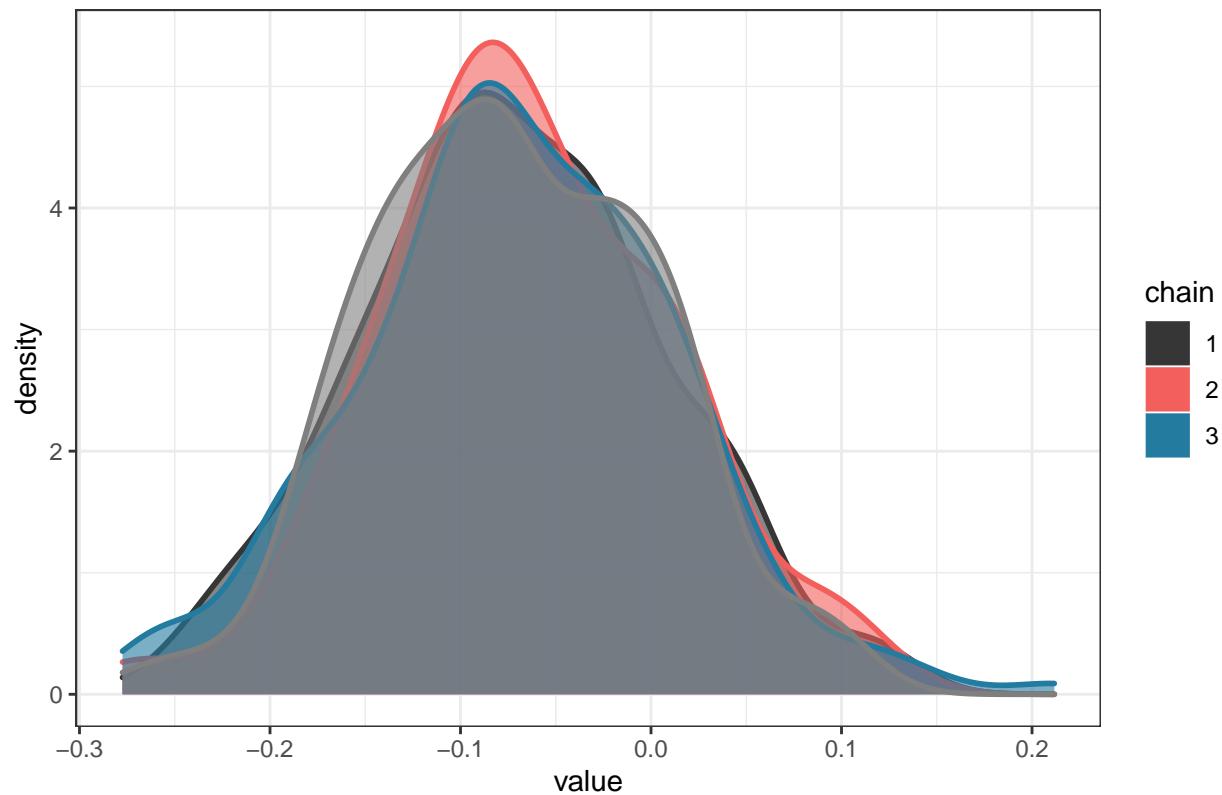
Density plot of LOWC31.1



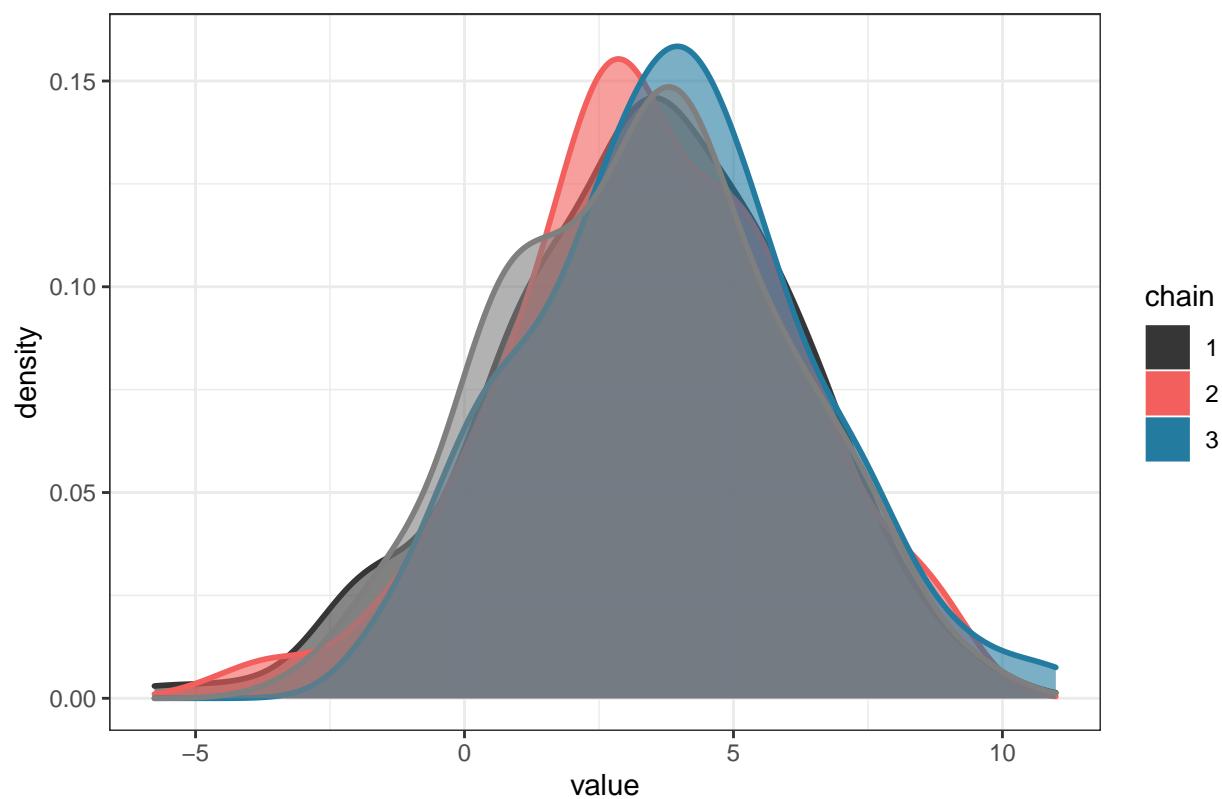
Density plot of time



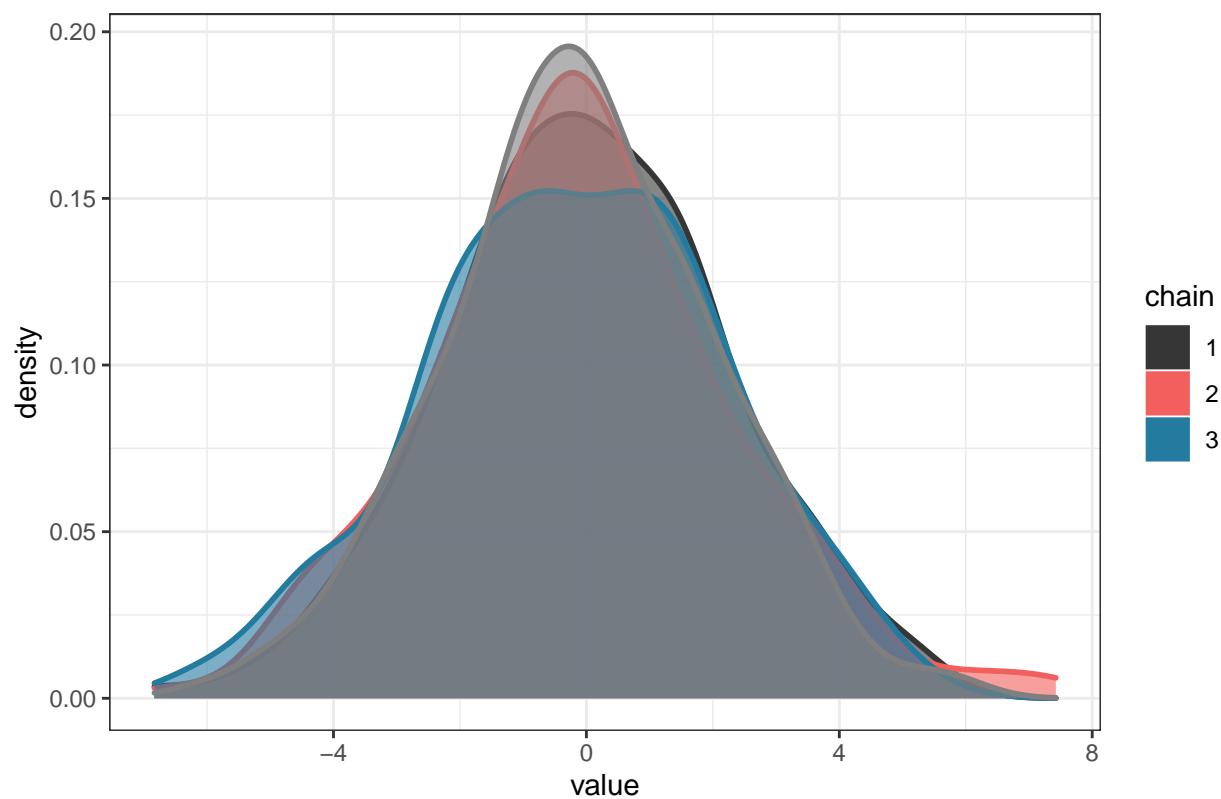
Density plot of ageatbiopsy.1



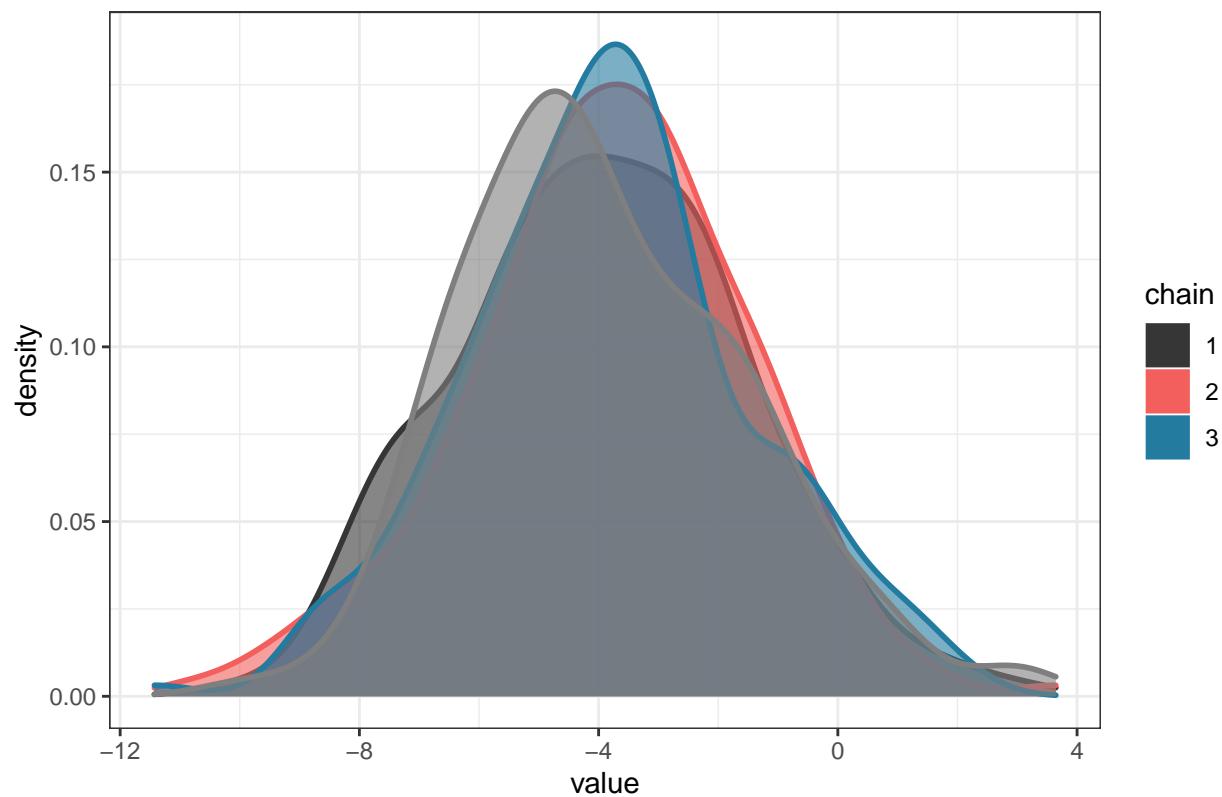
Density plot of sex.1



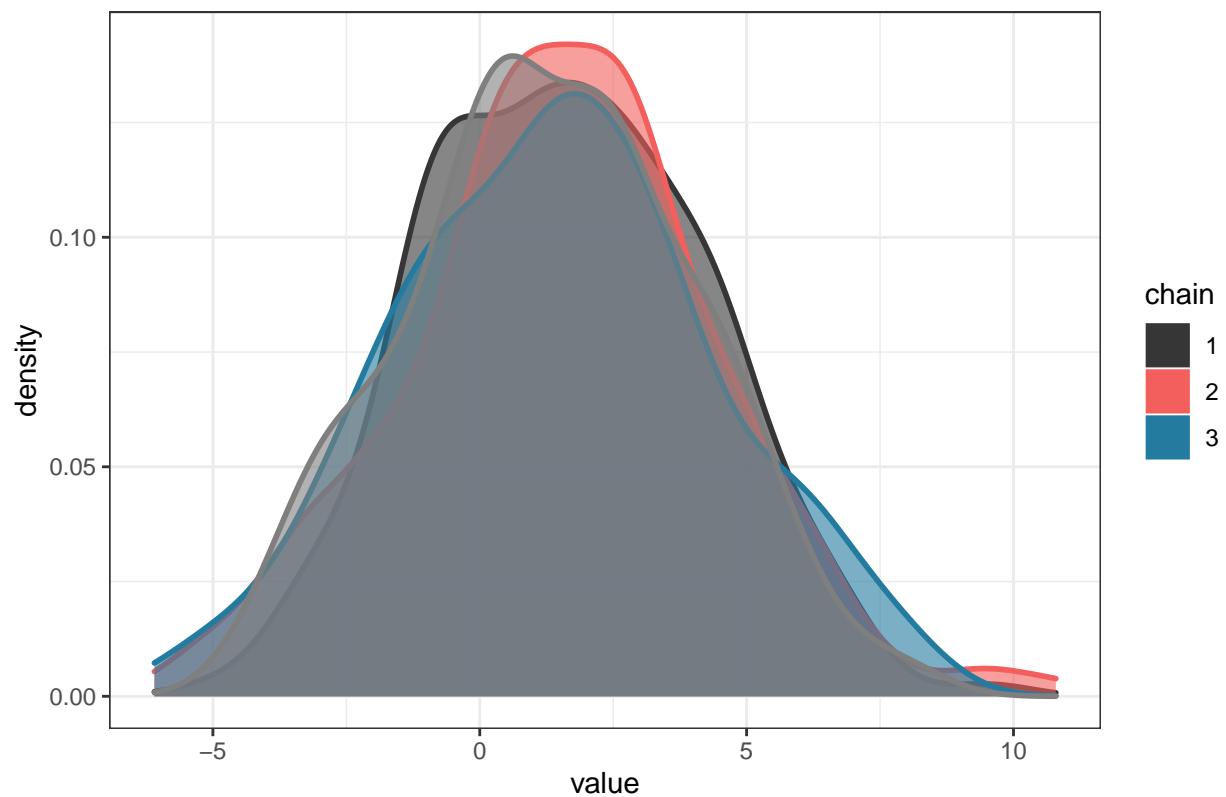
Density plot of black.1



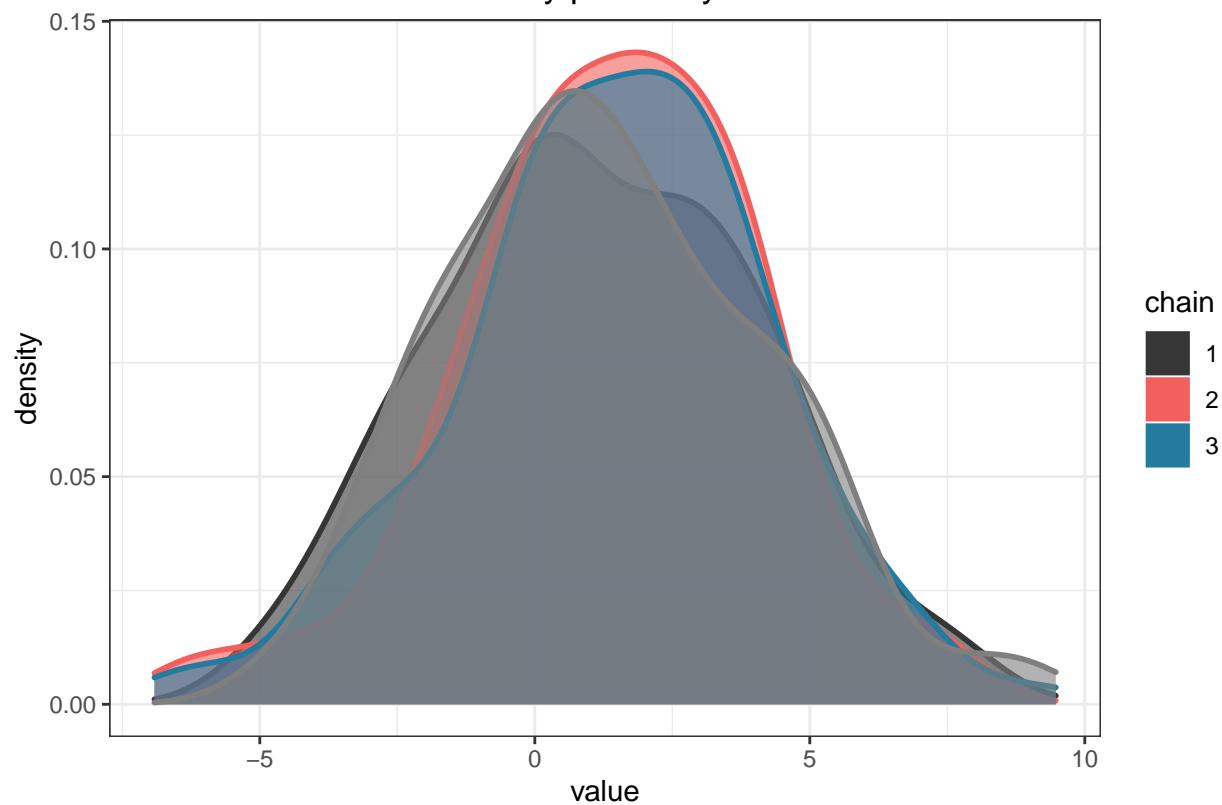
Density plot of hypertension.1



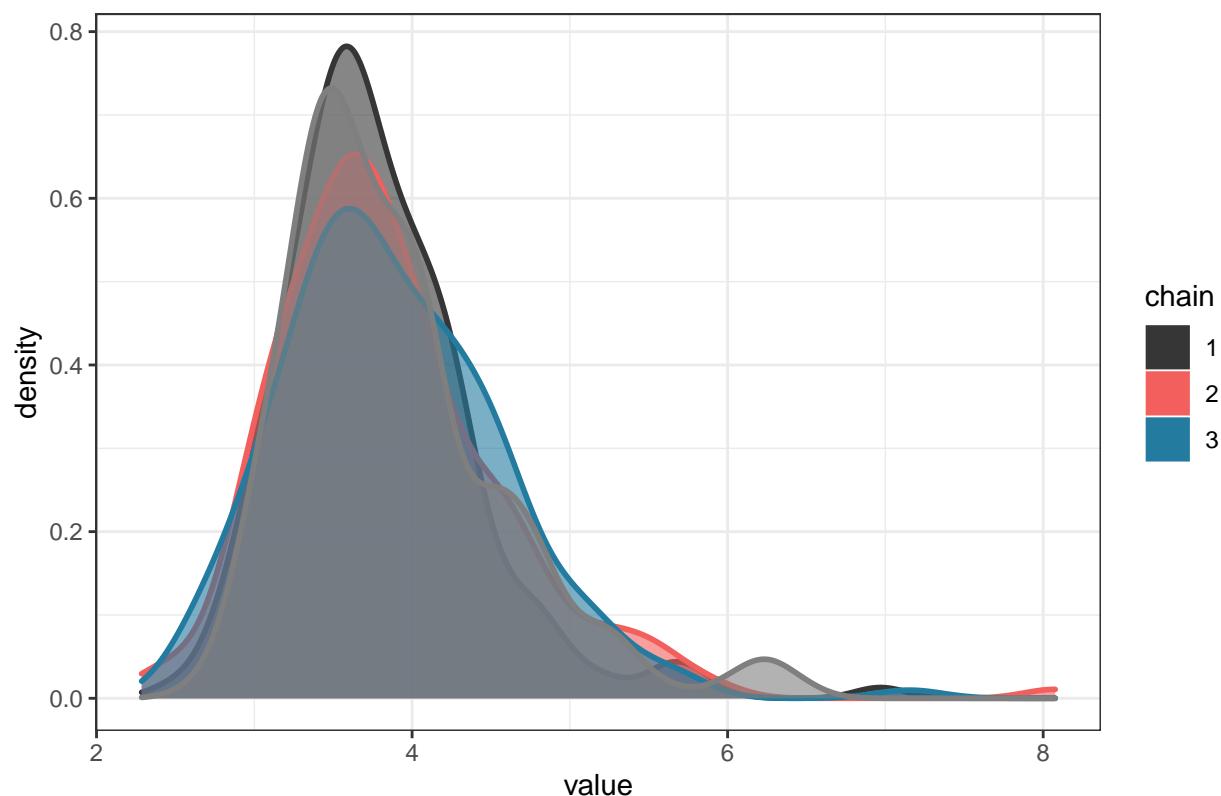
Density plot of mmf.1



Density plot of cyc.1

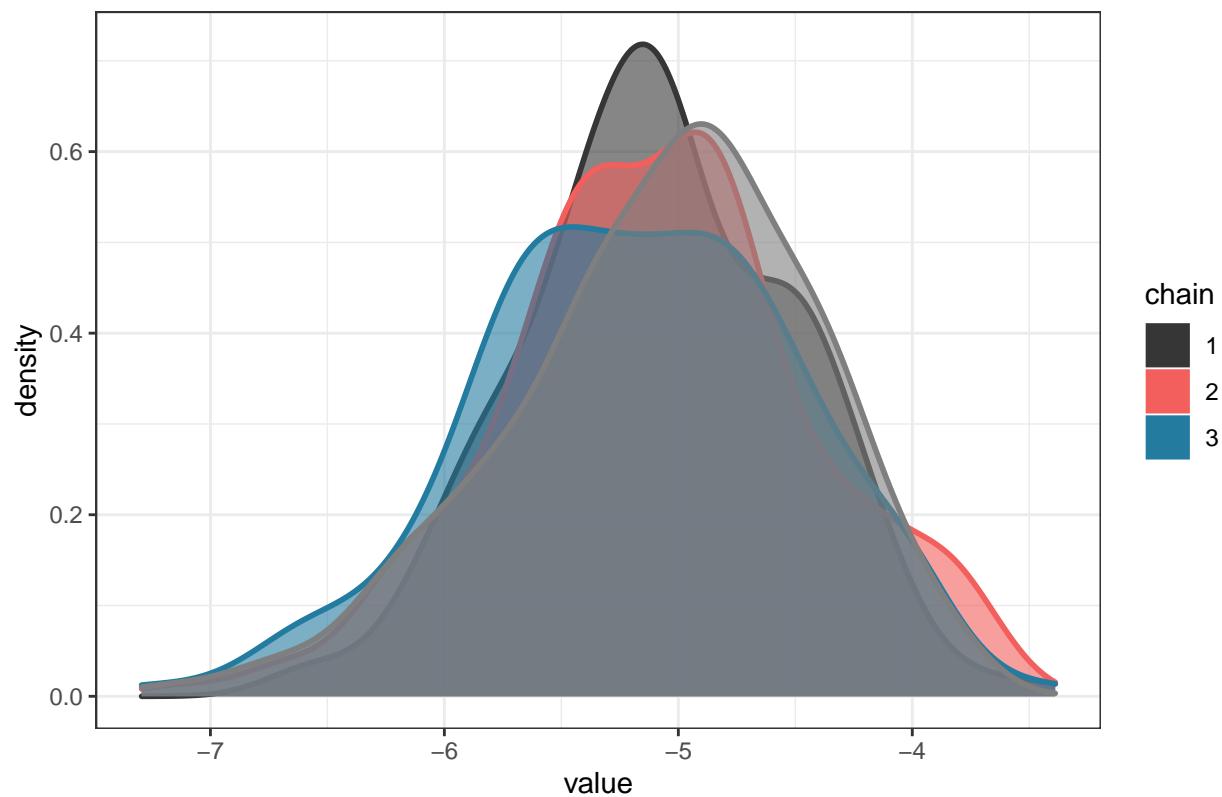


Density plot of sigmas_1

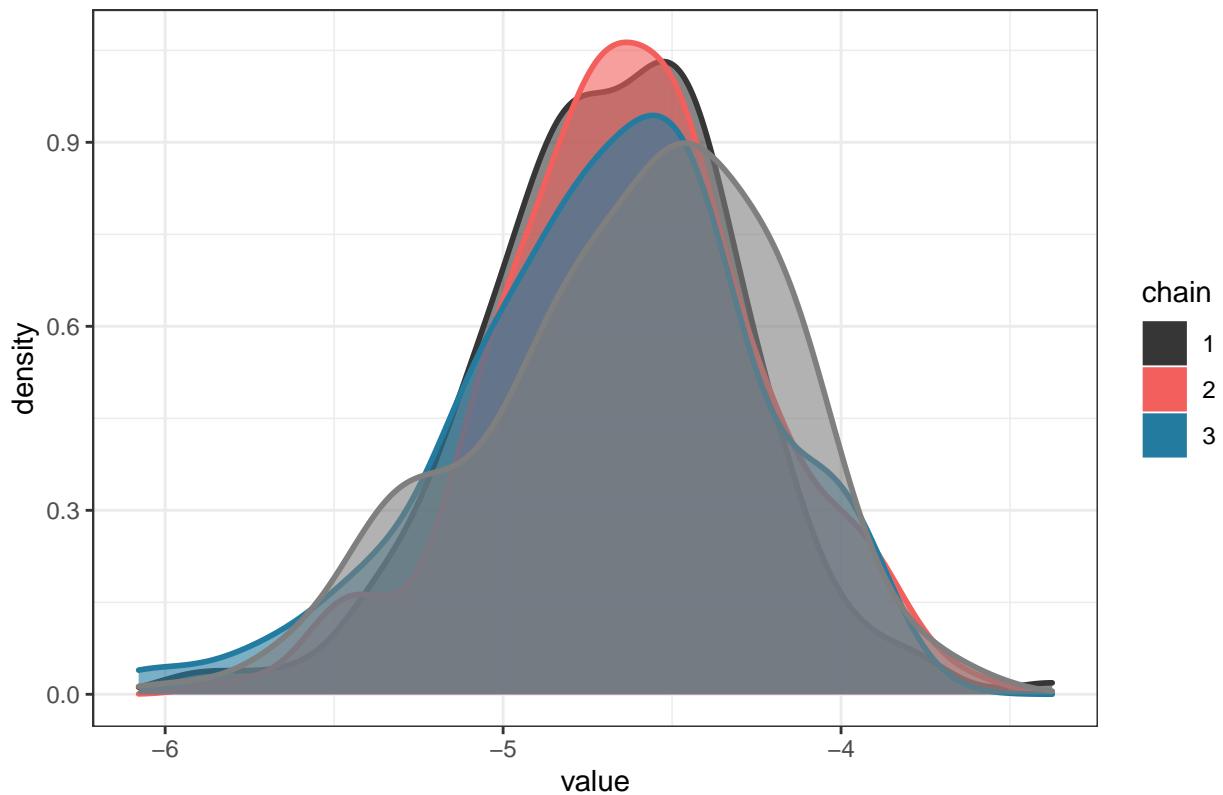


```
densplt2 <- ggdensityplot(jointFit2)
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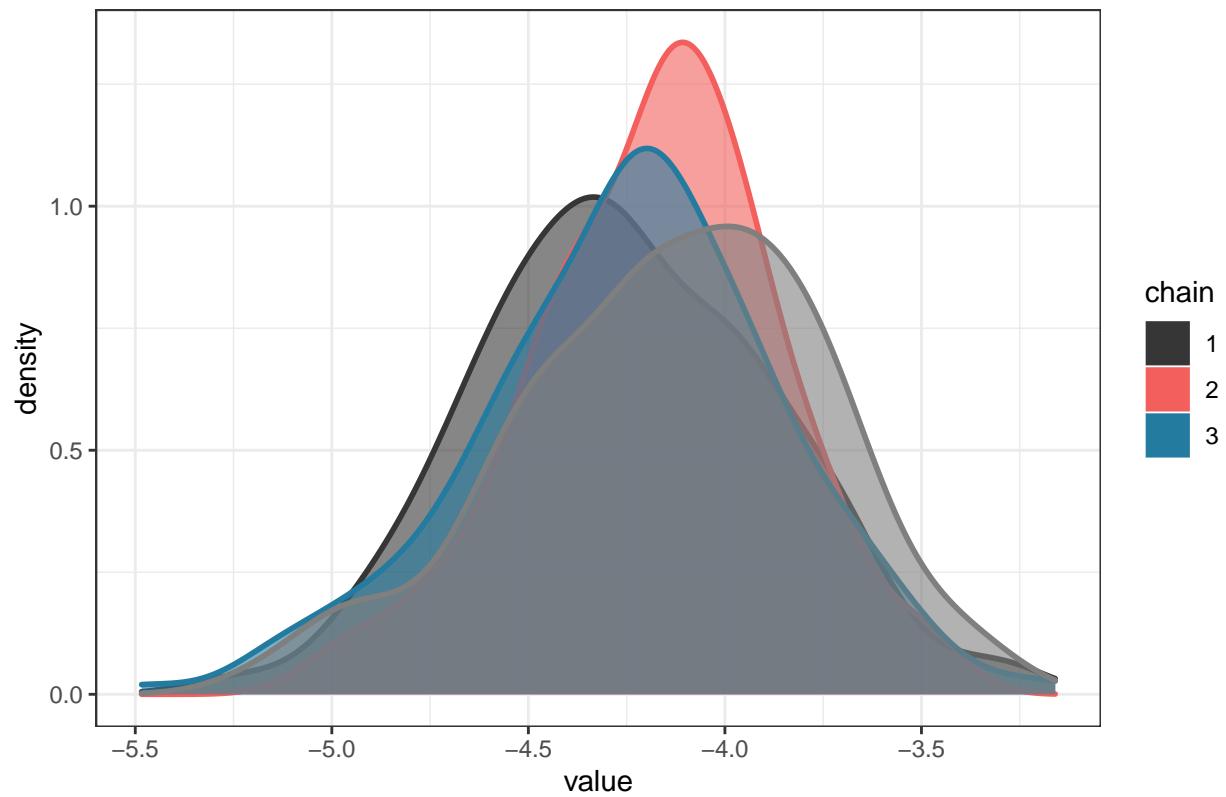
Density plot of bs_gammas_1



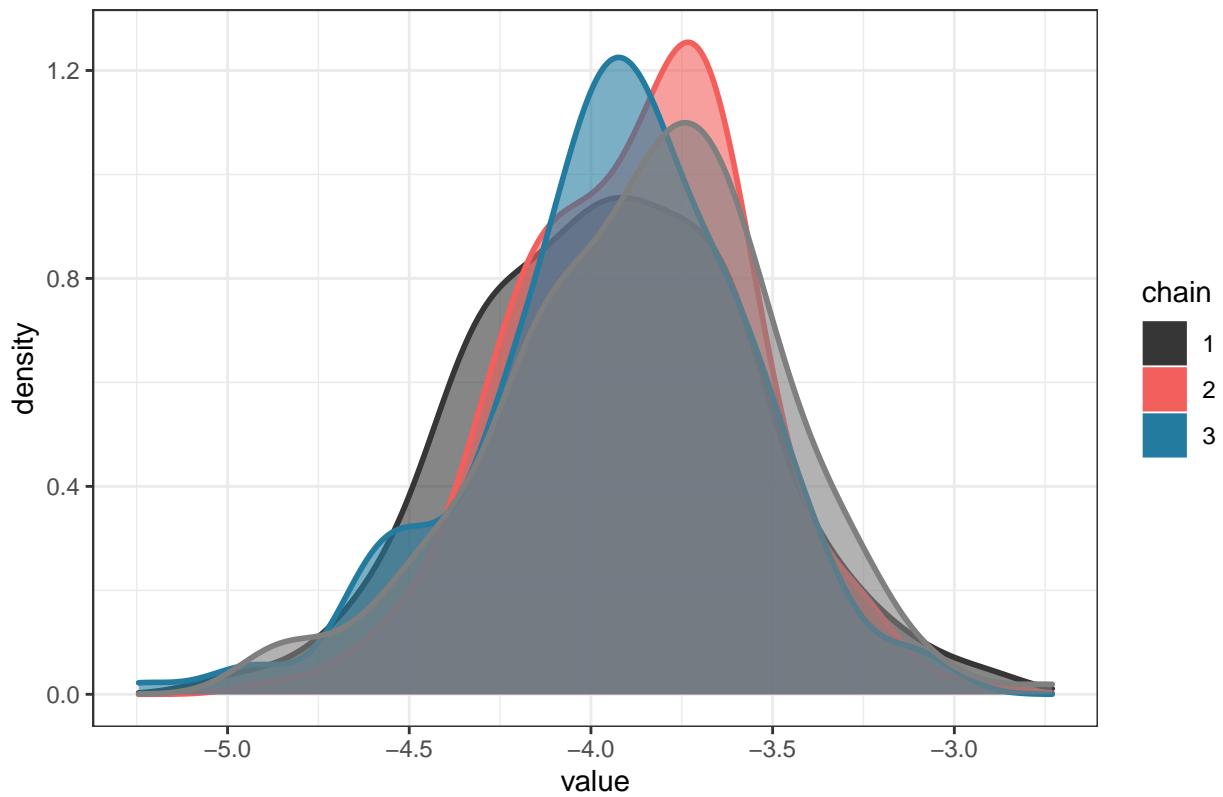
Density plot of bs_gammas_2



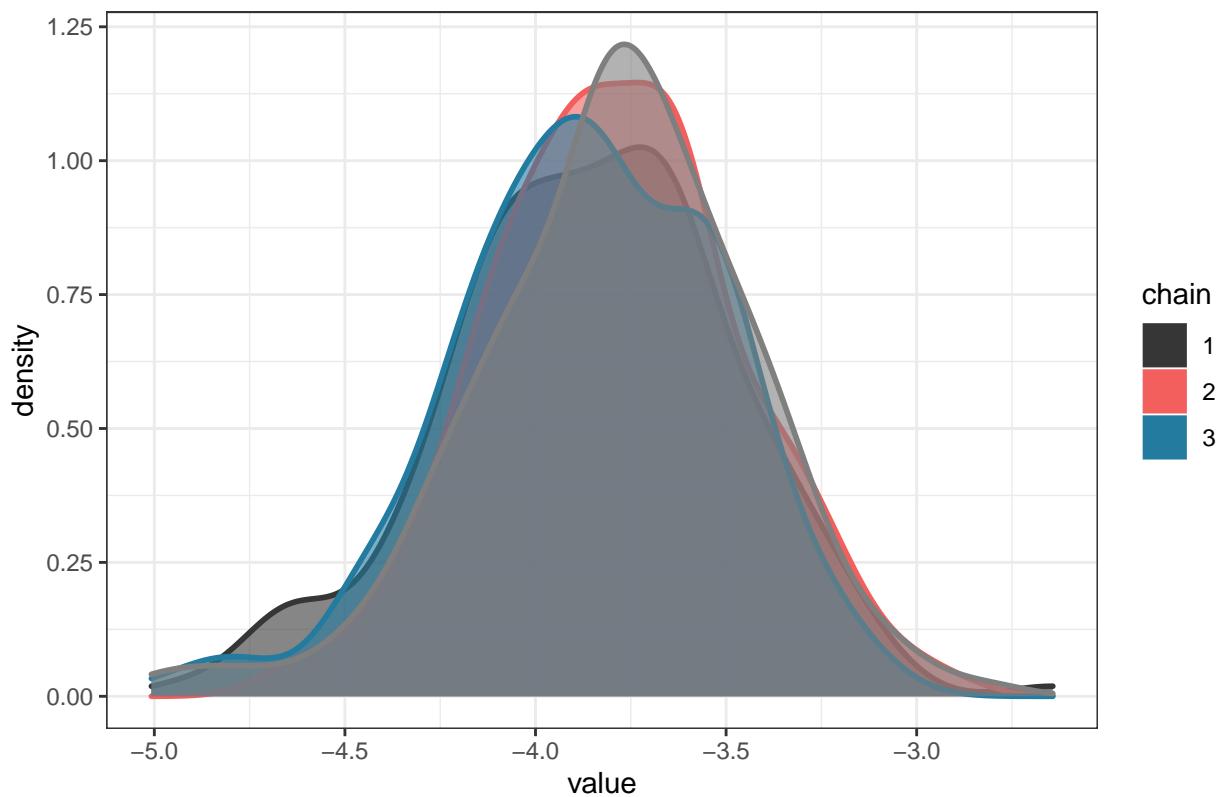
Density plot of bs_gammas_3



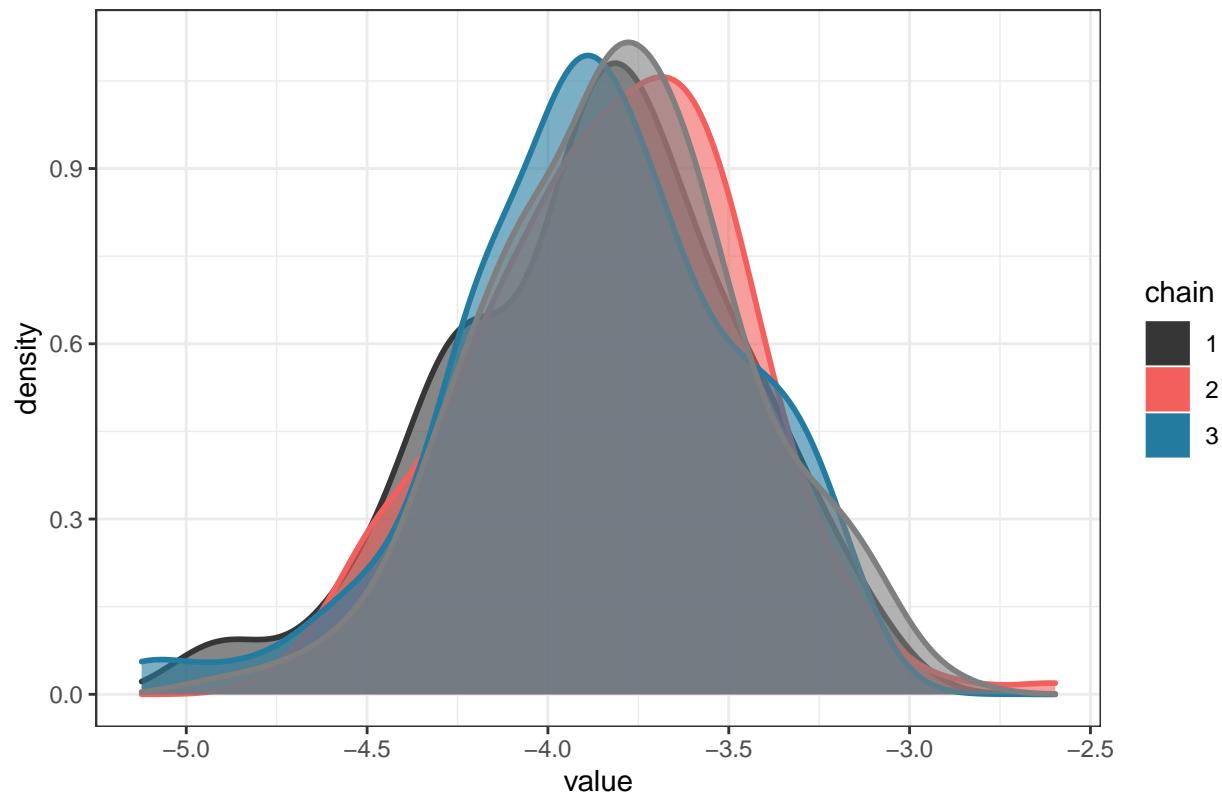
Density plot of bs_gammas_4



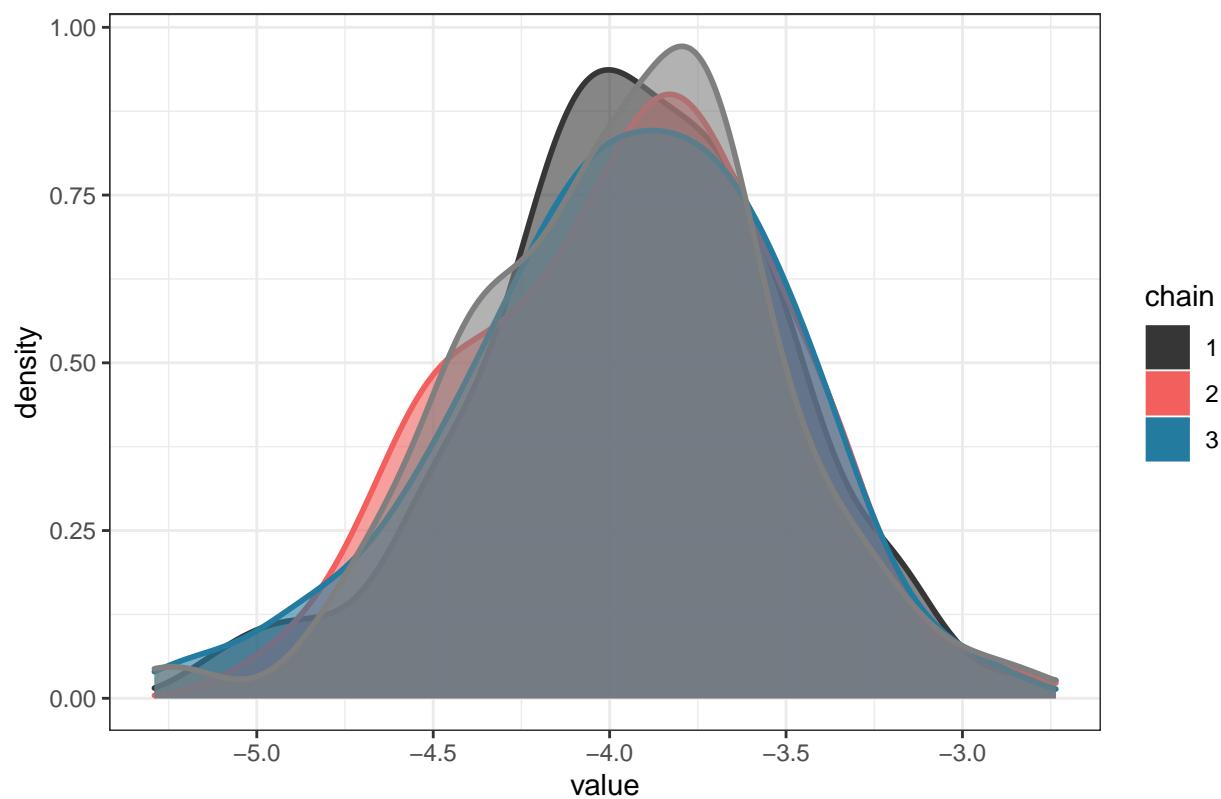
Density plot of bs_gammas_5



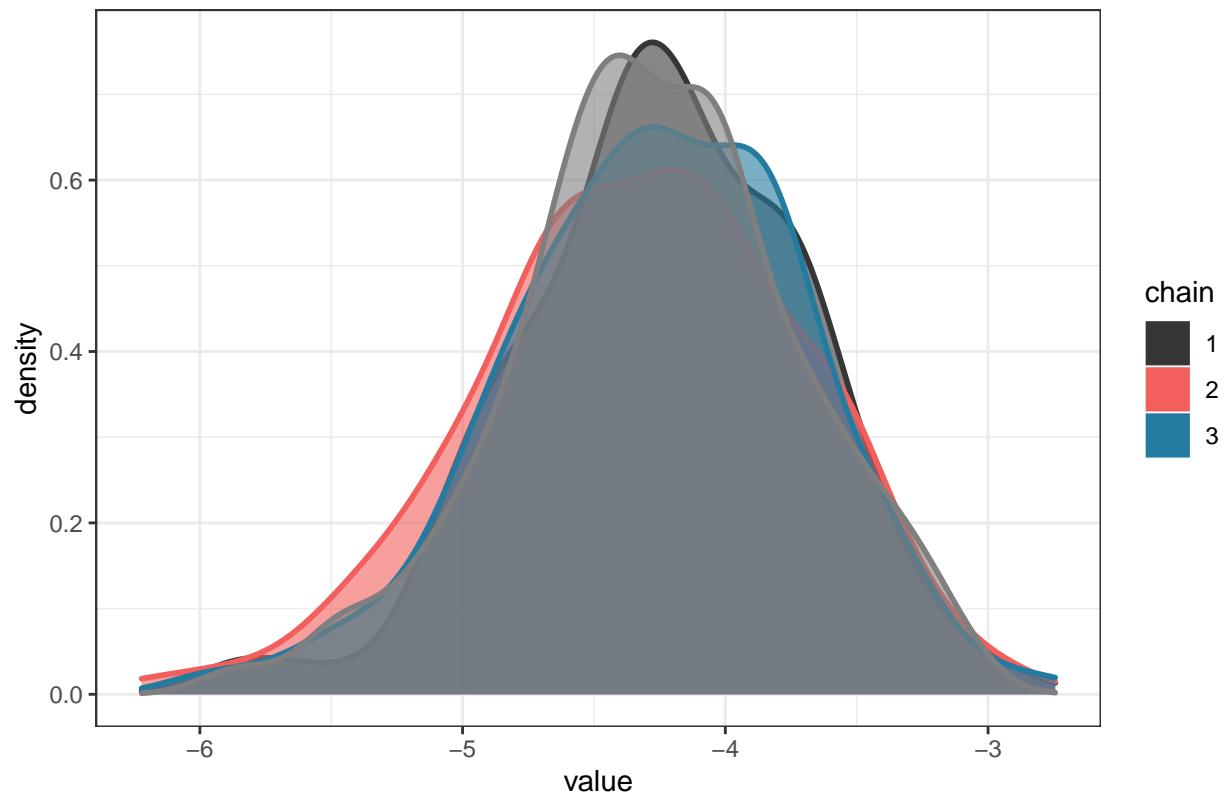
Density plot of bs_gammas_6



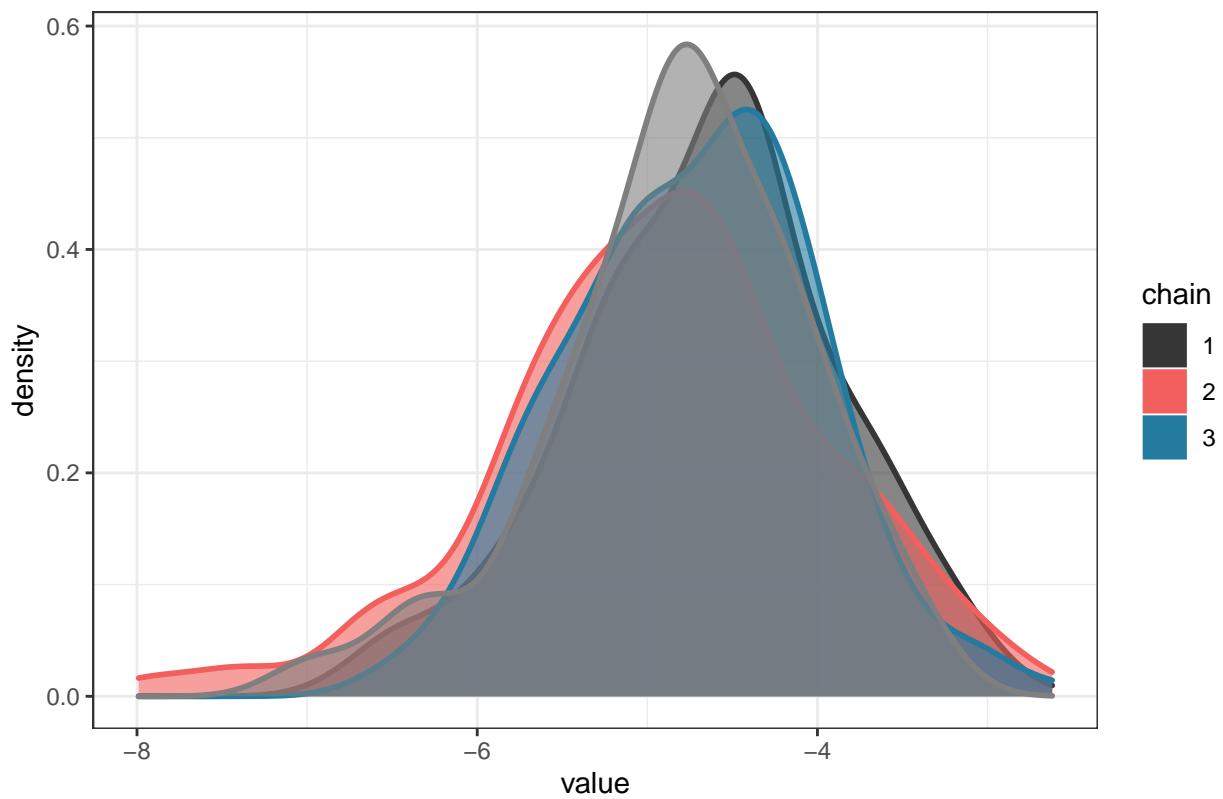
Density plot of bs_gammas_7



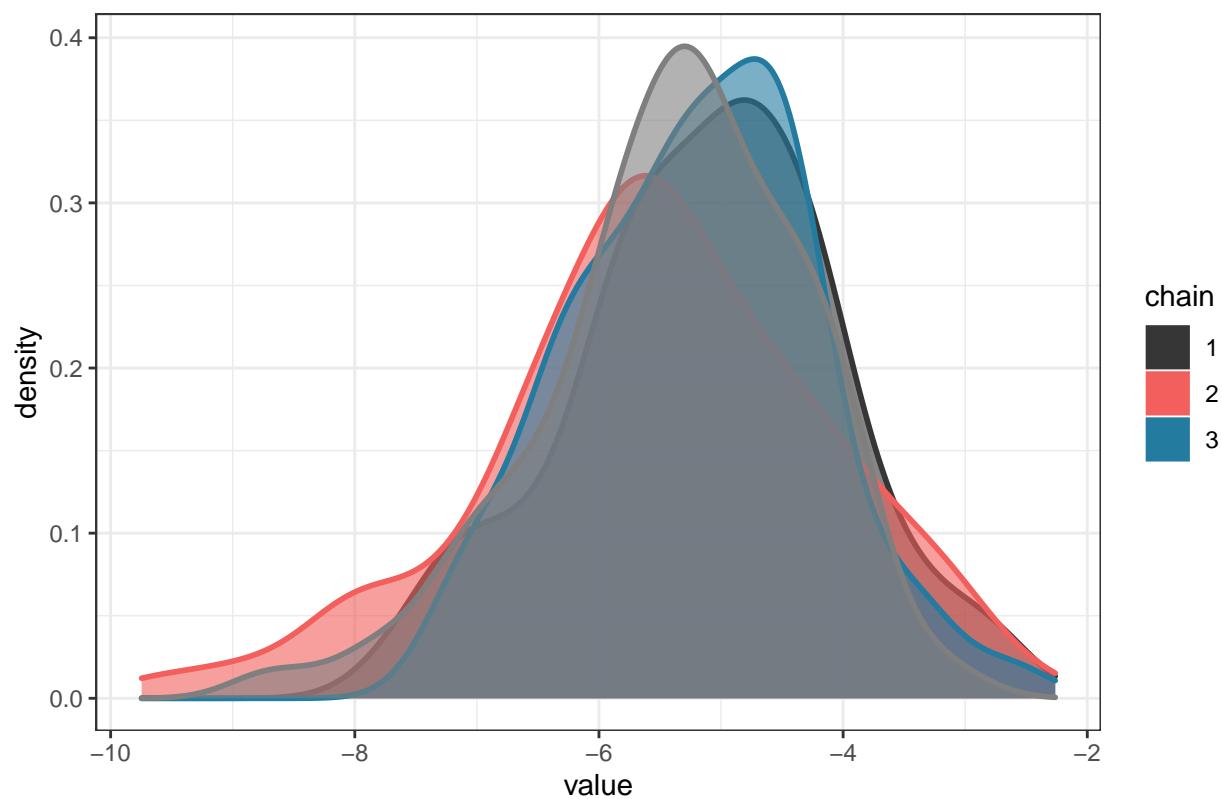
Density plot of bs_gammas_8



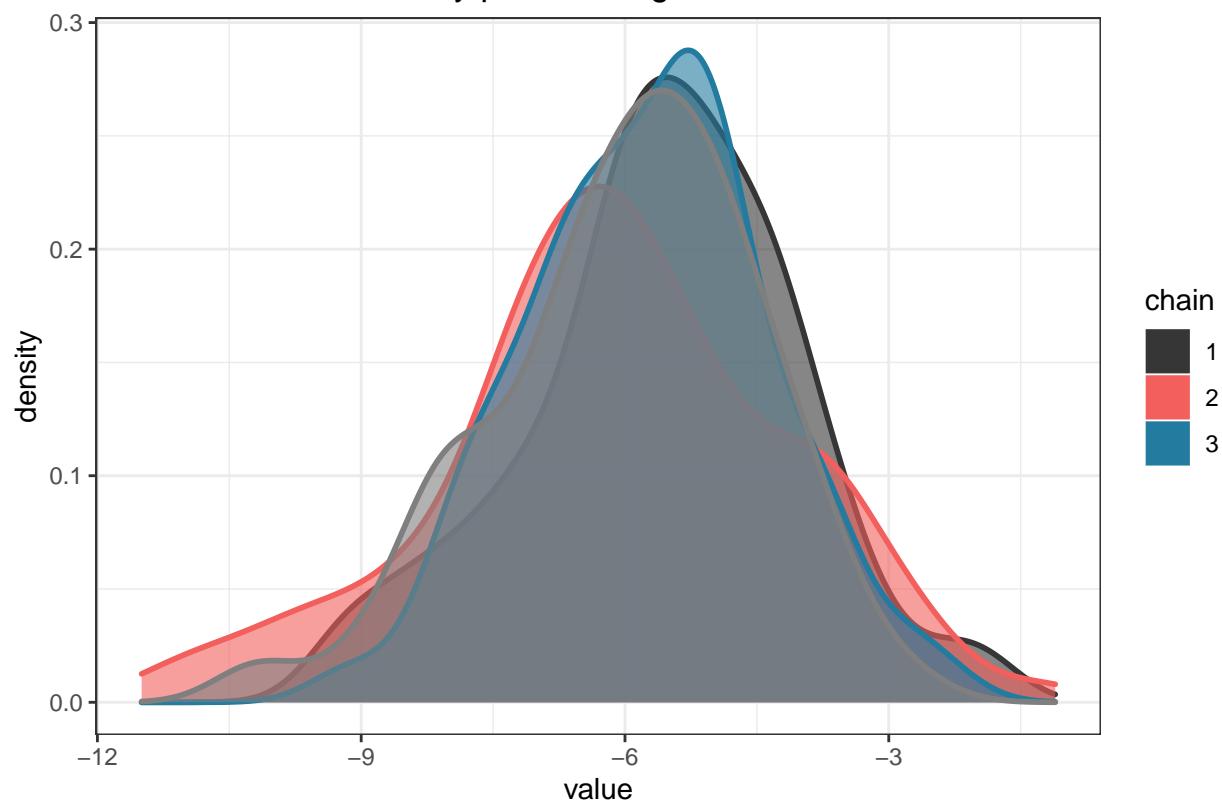
Density plot of bs_gammas_9



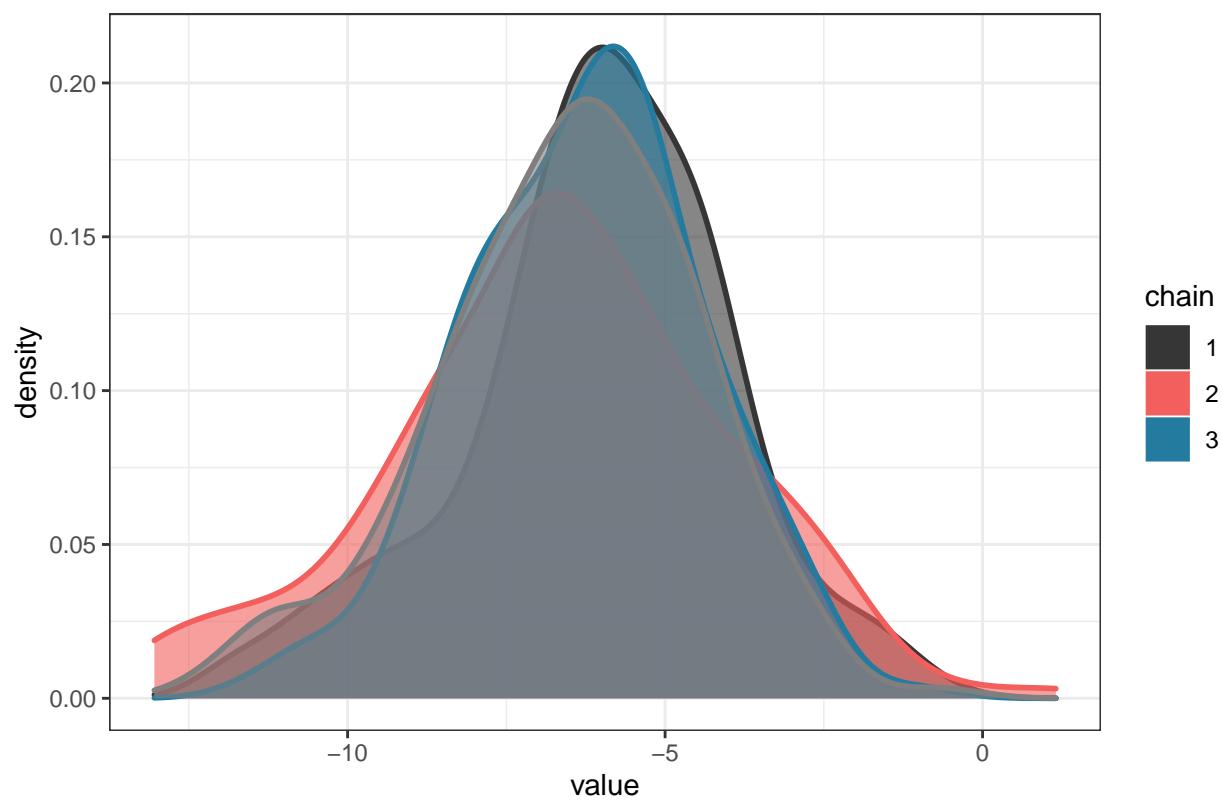
Density plot of bs_gammas_10



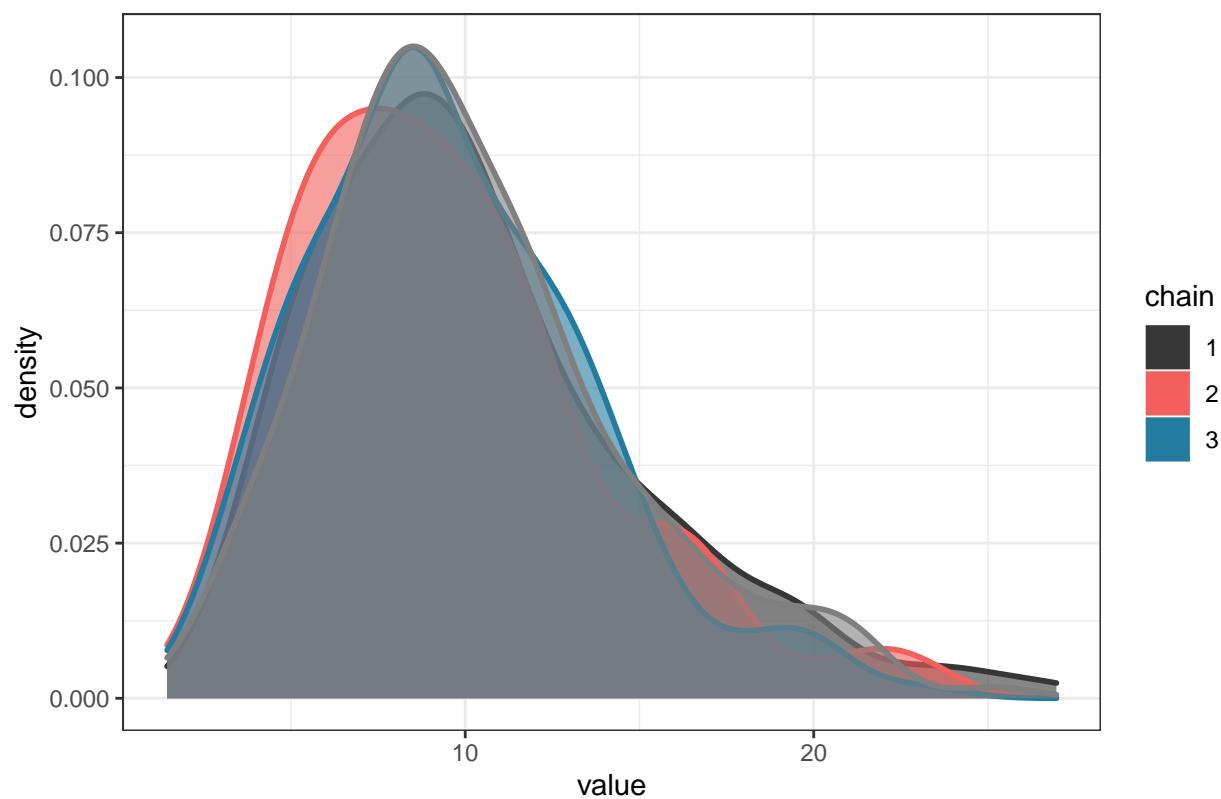
Density plot of bs_gammas_11



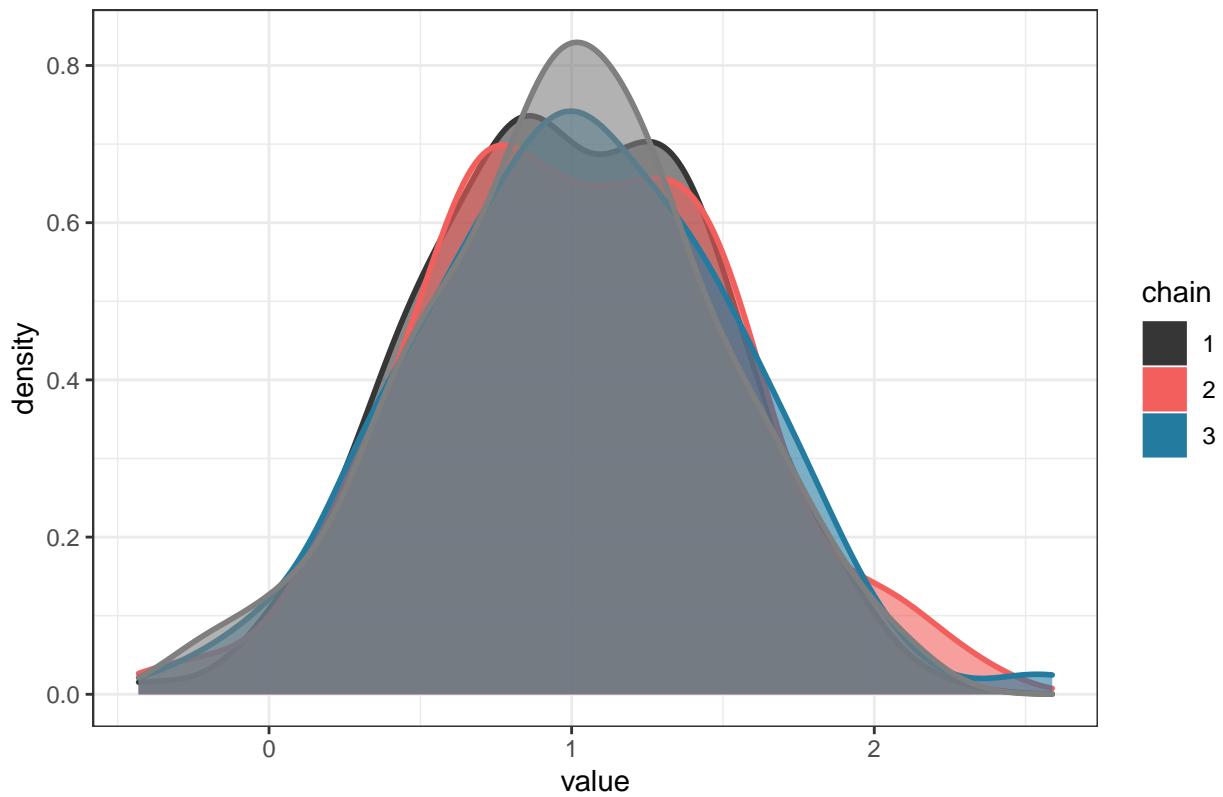
Density plot of bs_gammas_12



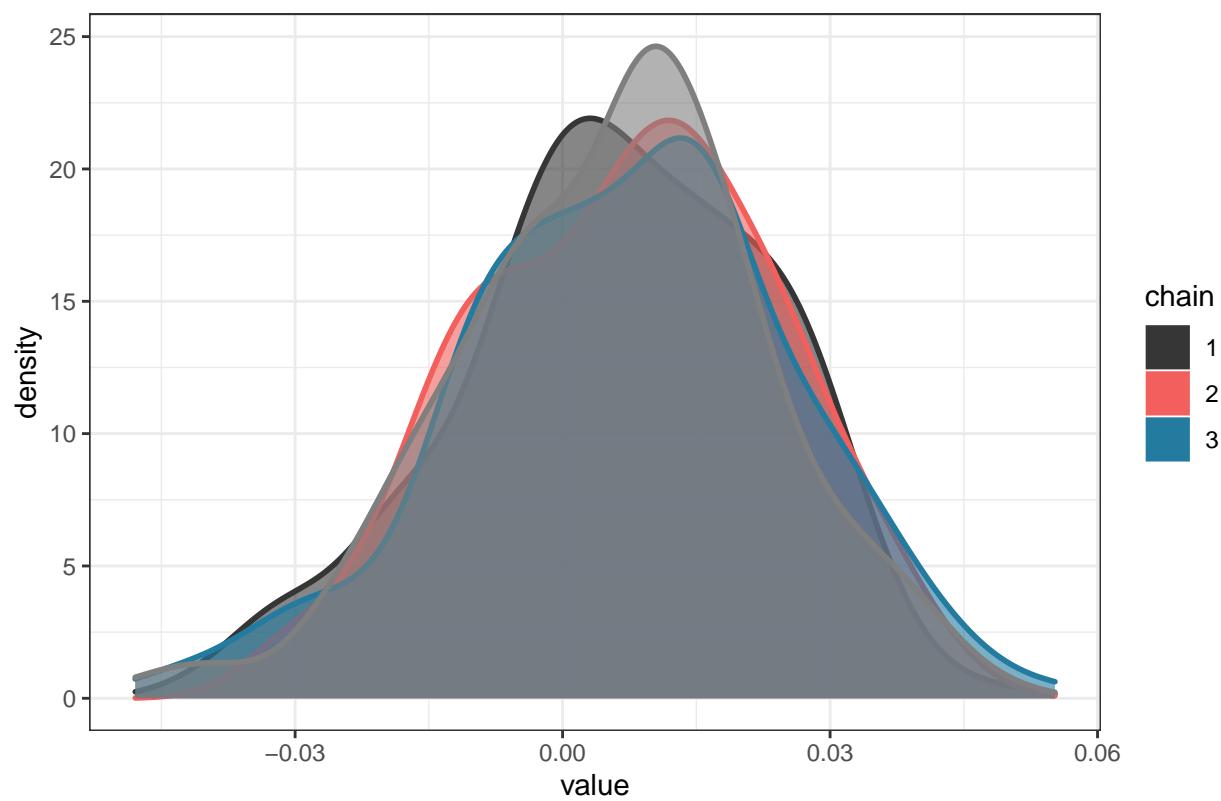
Density plot of tau_bs_gammas



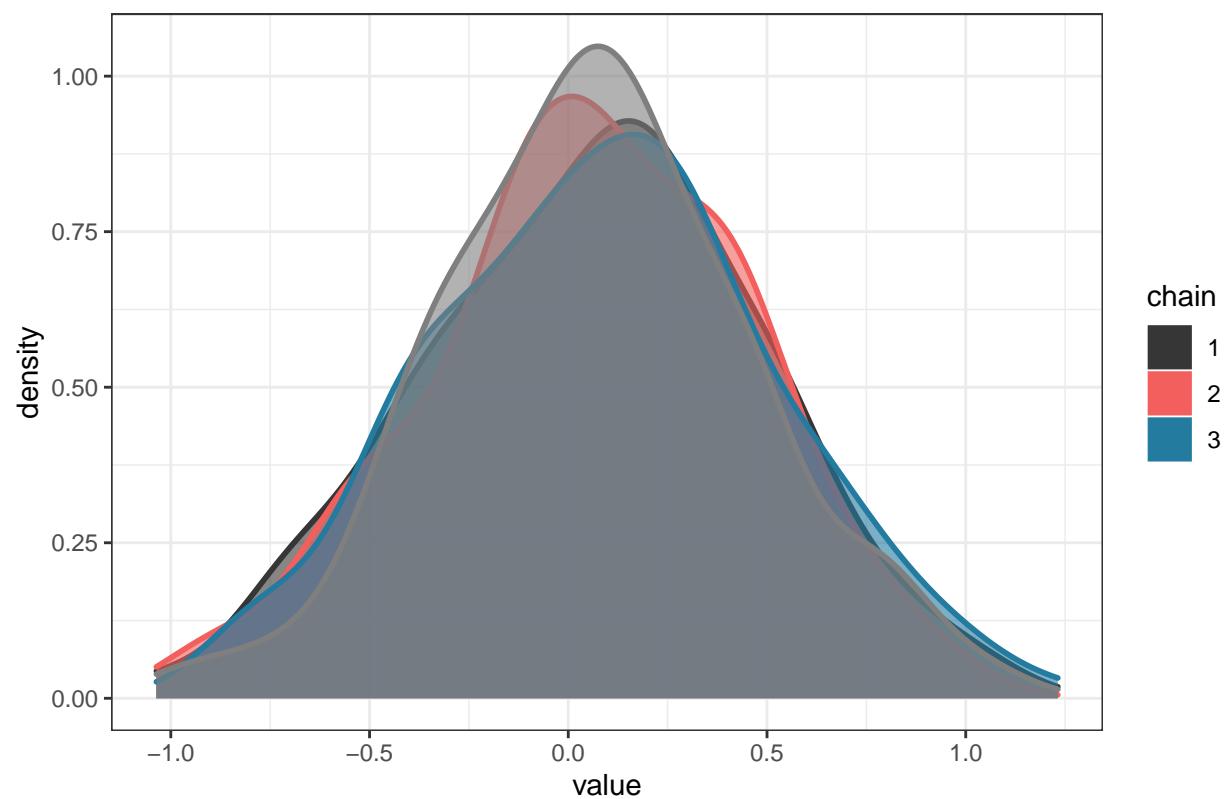
Density plot of LOWC31



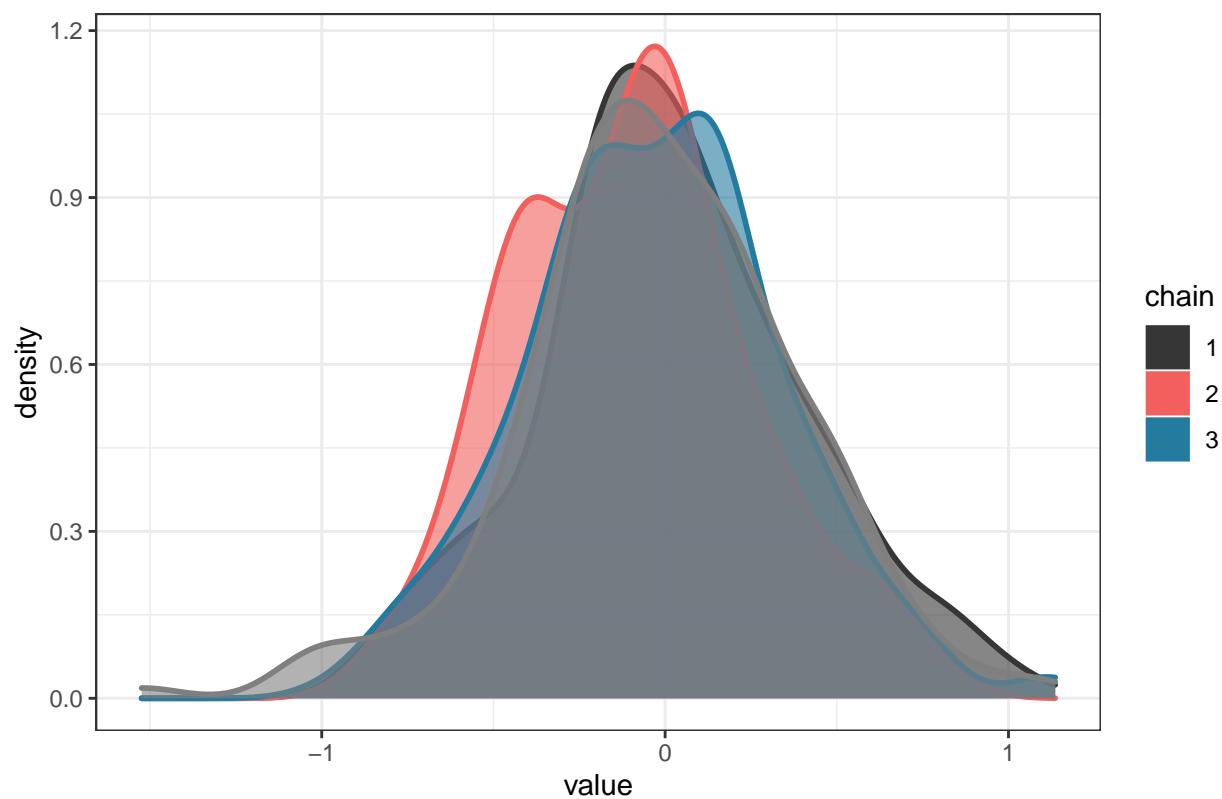
Density plot of ageatbiopsy



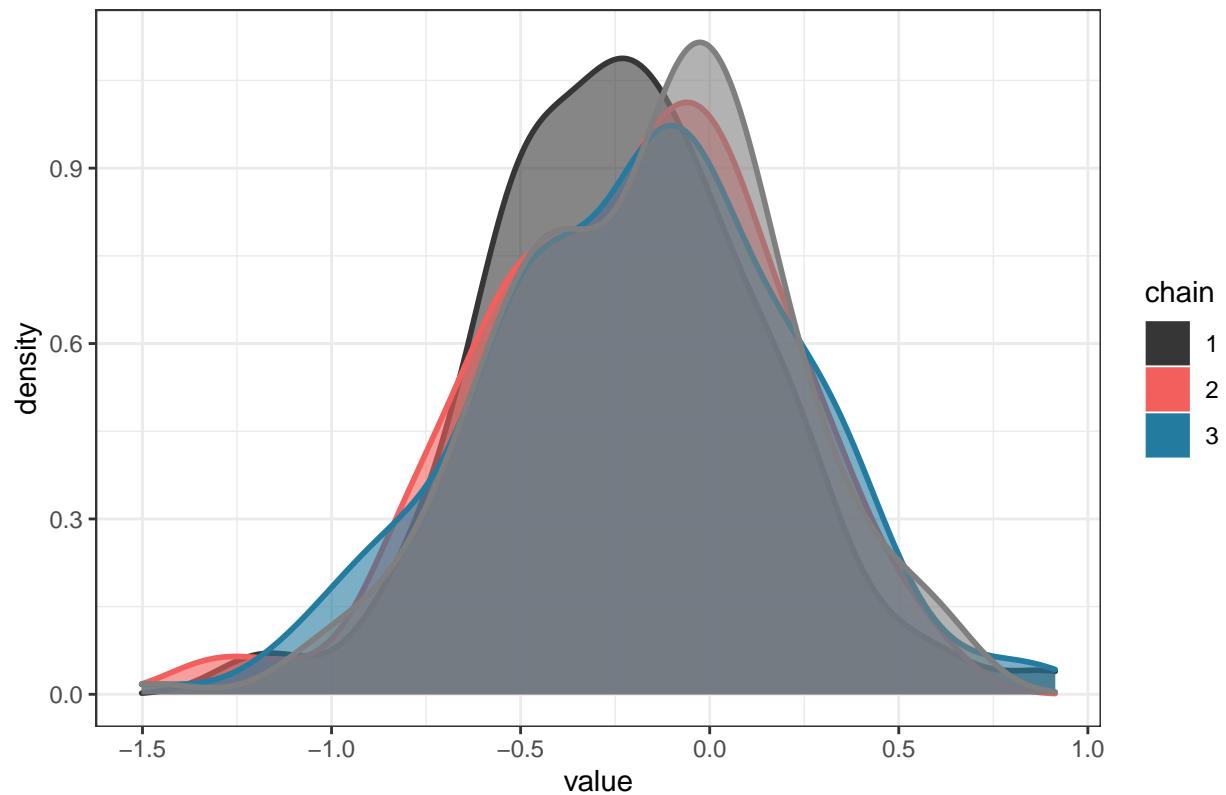
Density plot of sex



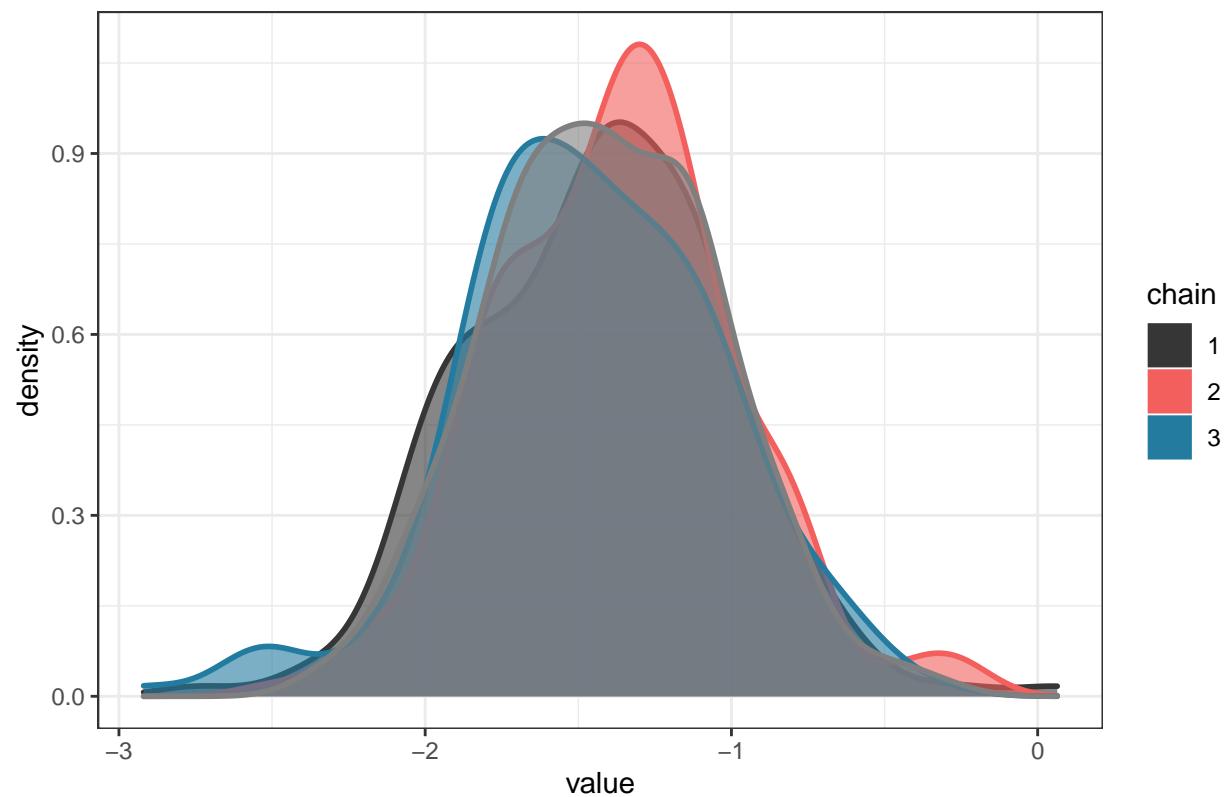
Density plot of black



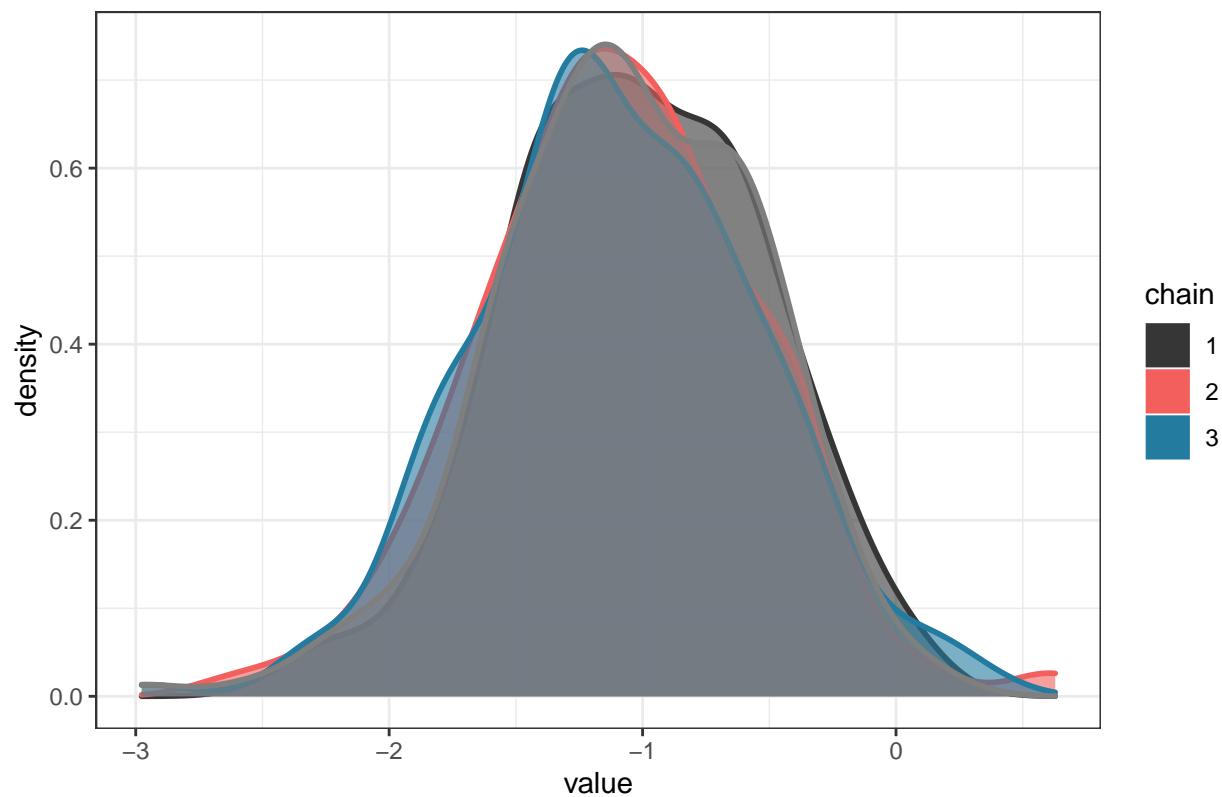
Density plot of hypertension



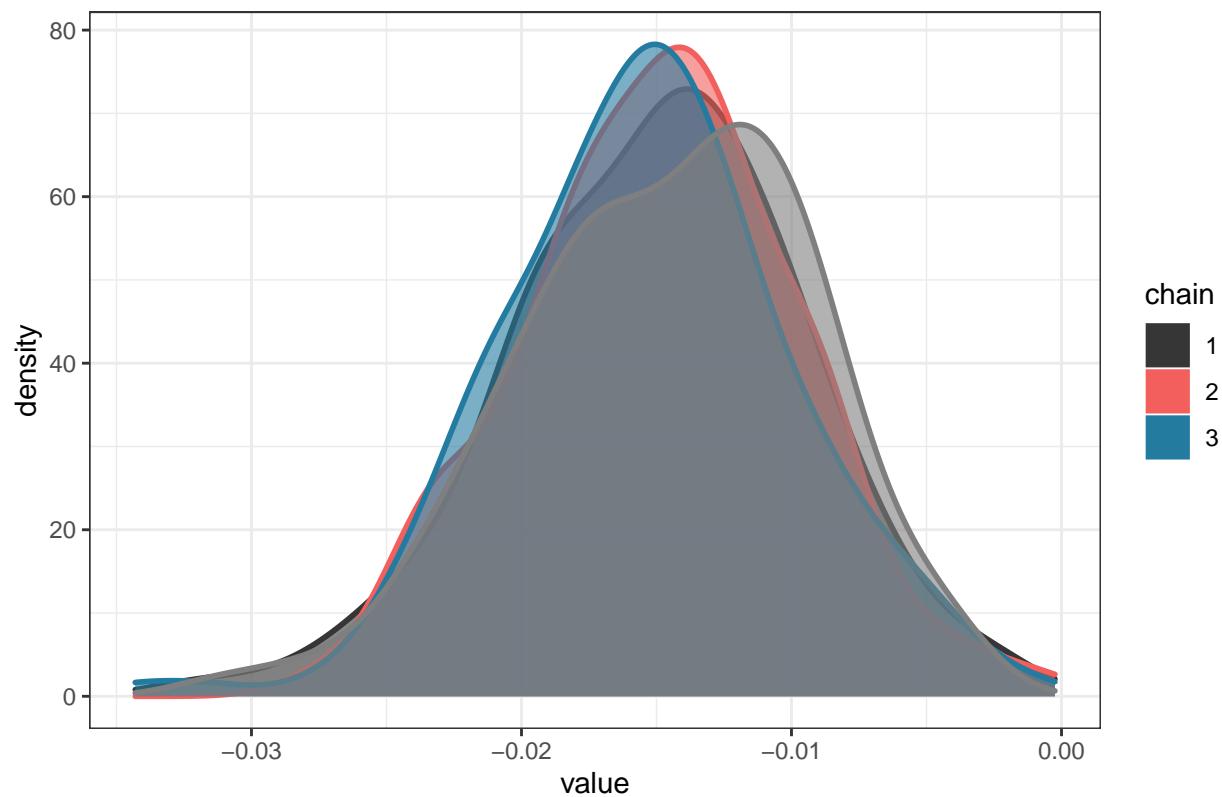
Density plot of mmf



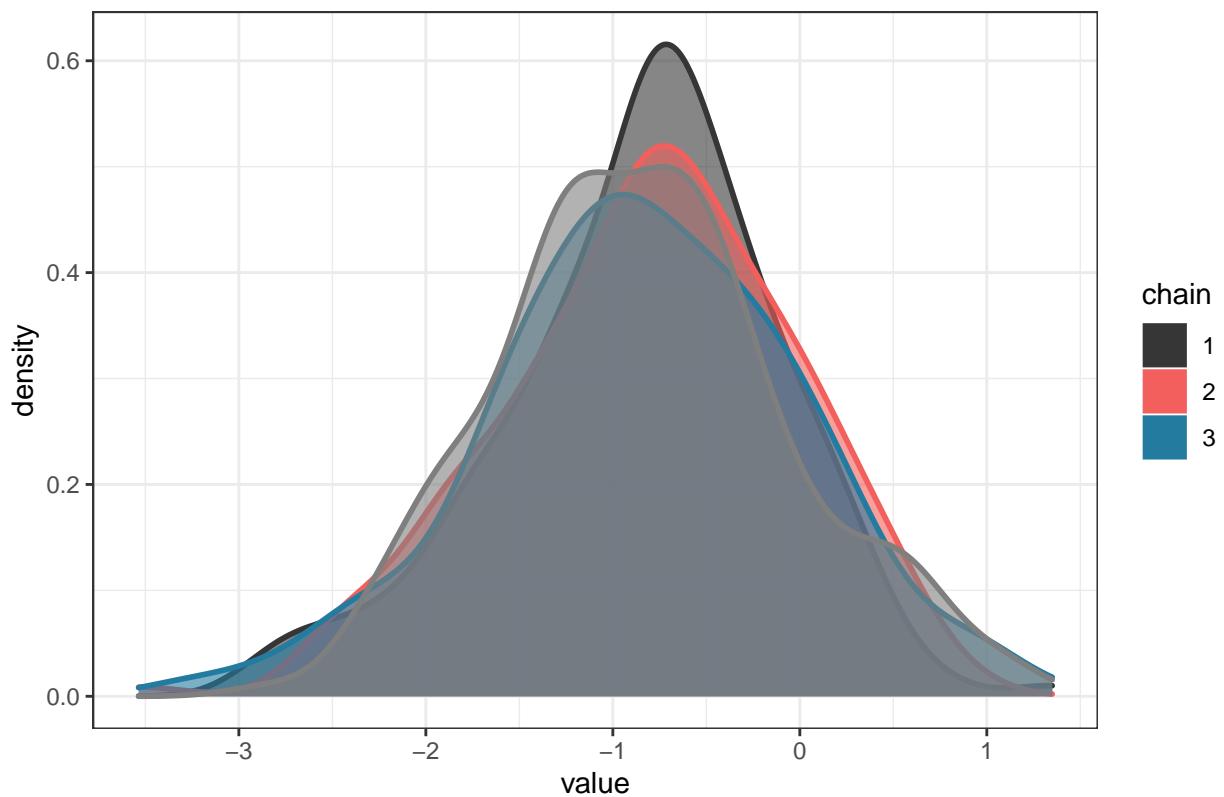
Density plot of cyc



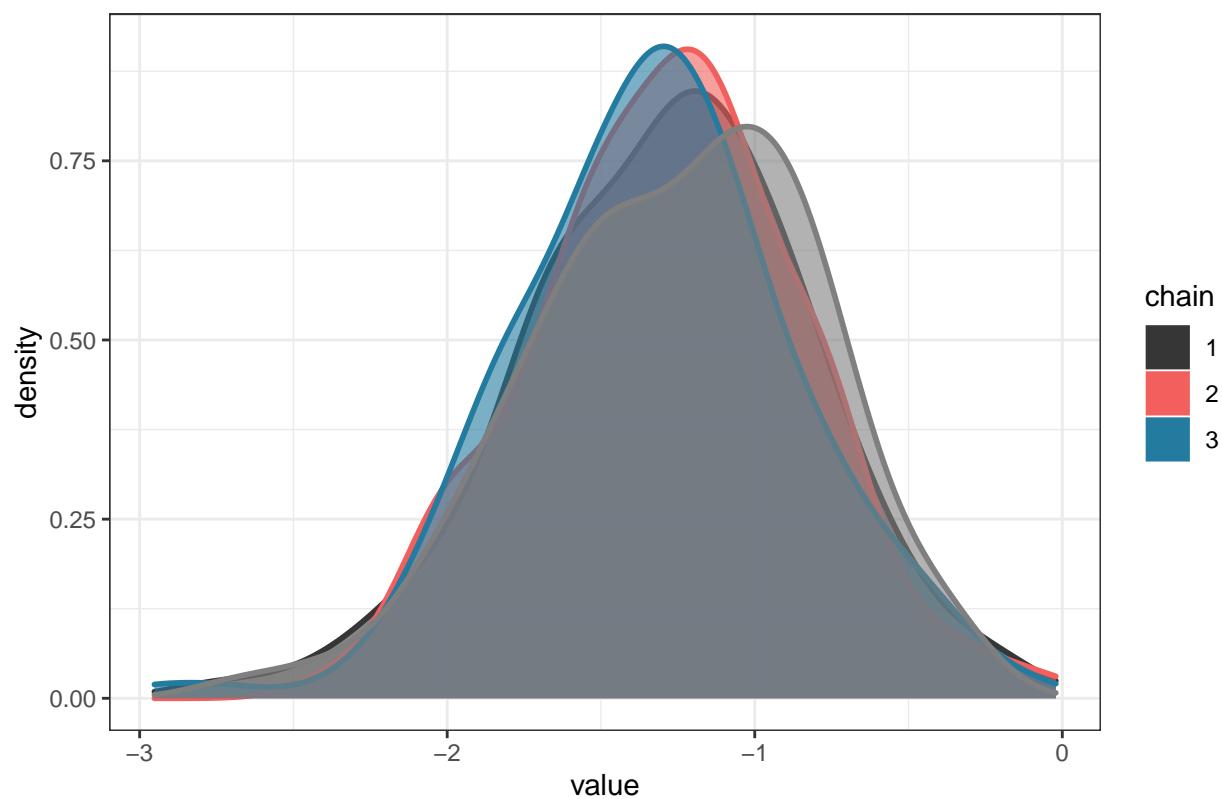
Density plot of area(eGFR)



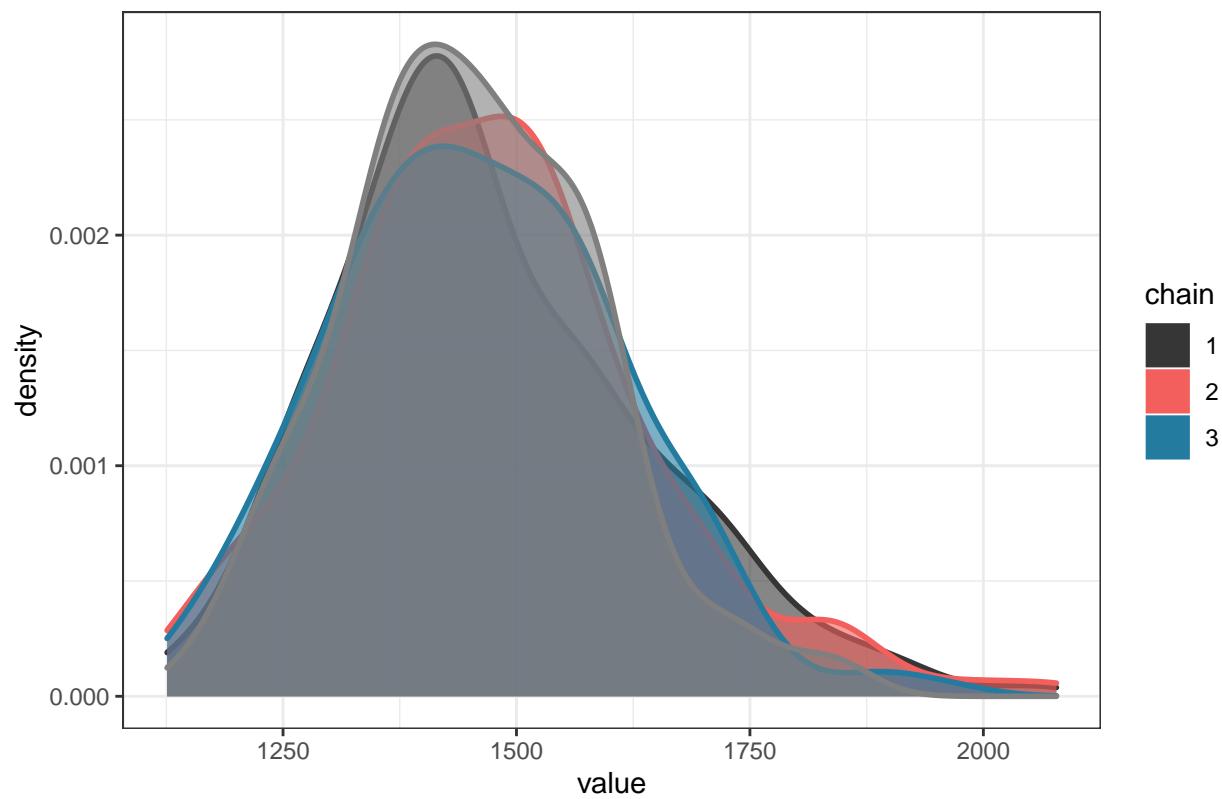
Density plot of



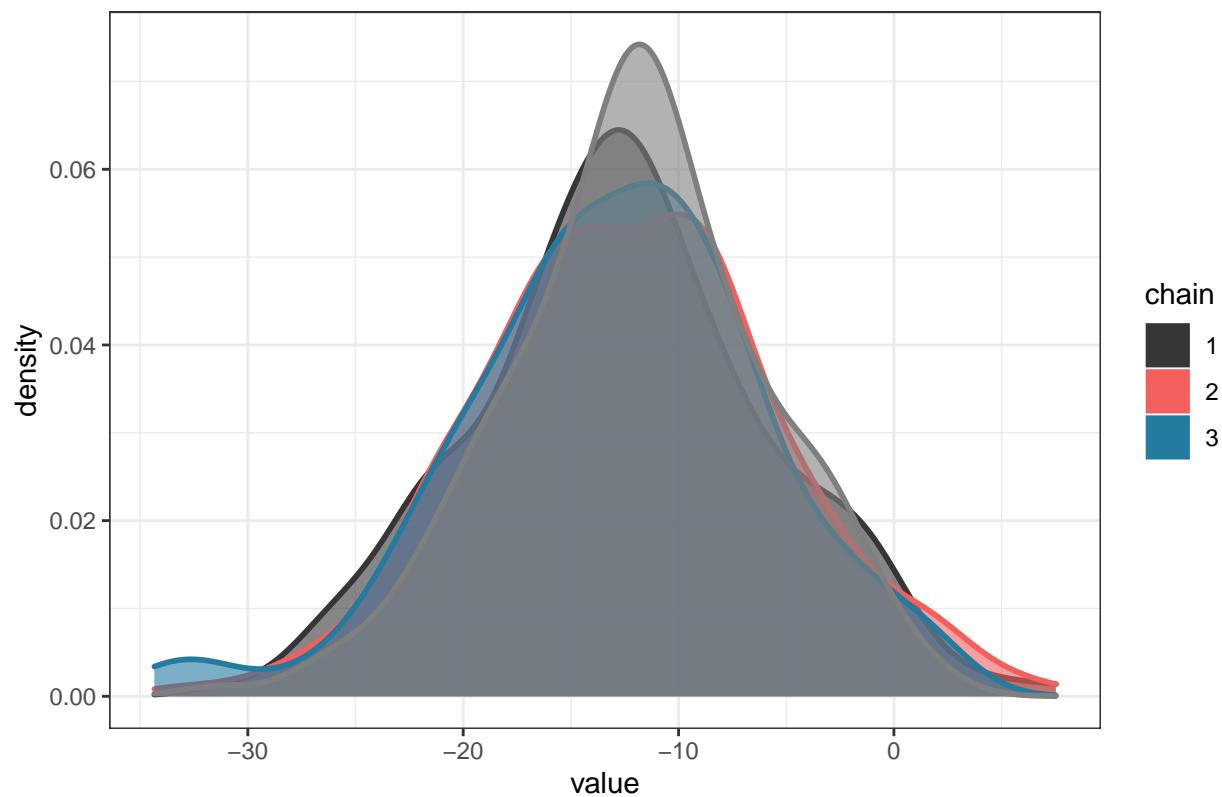
Density plot of .1



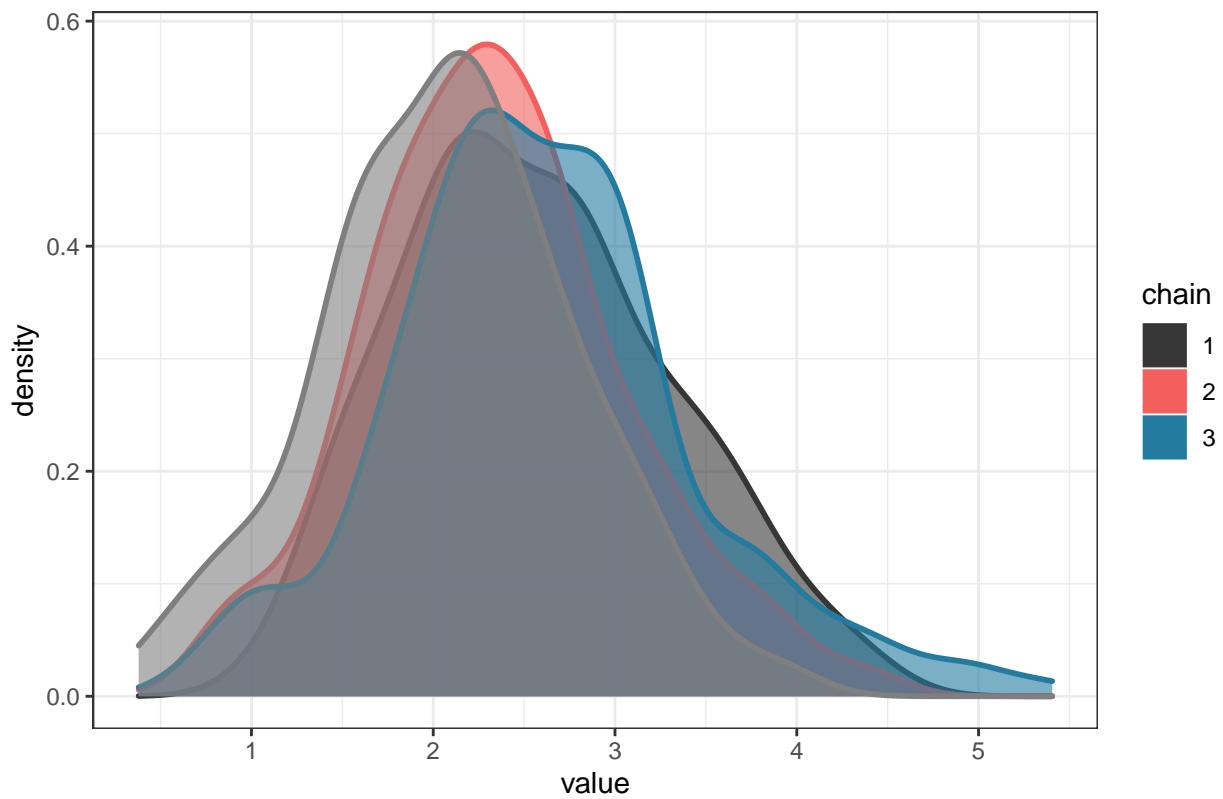
Density plot of $D[1, 1]$



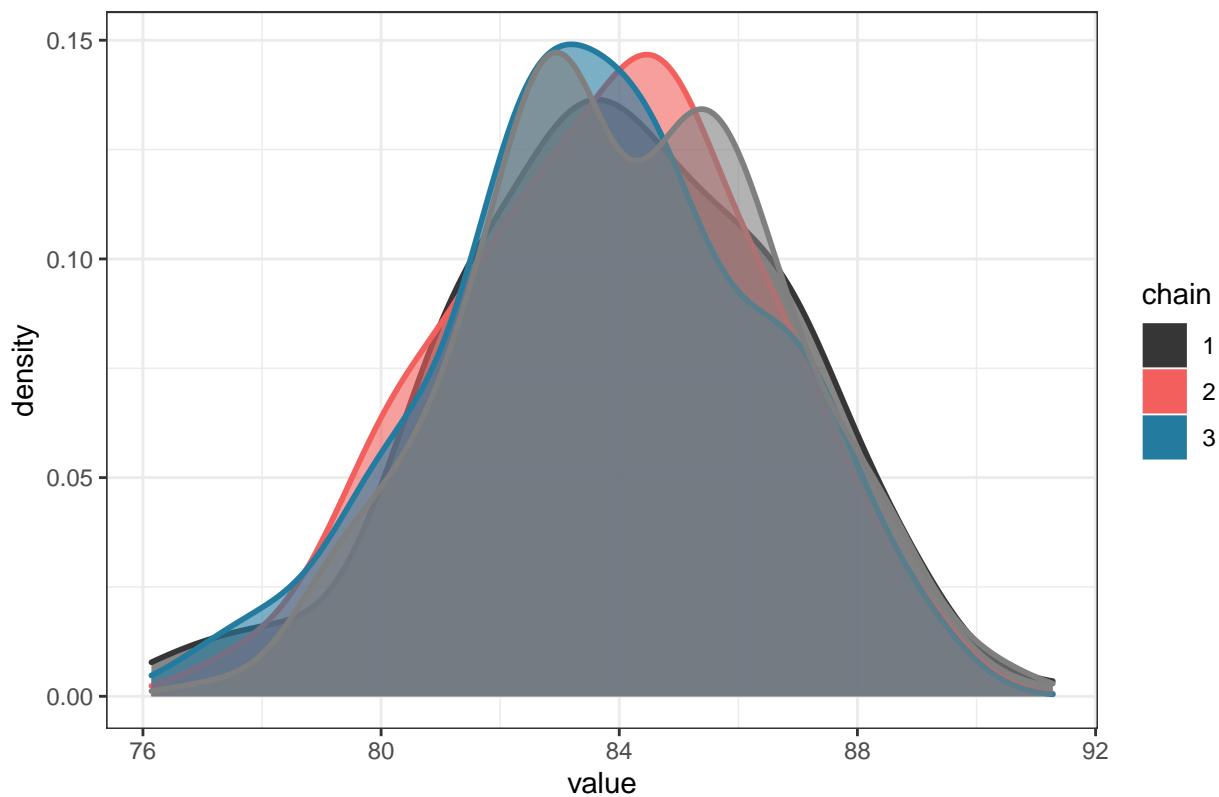
Density plot of $D[2, 1]$



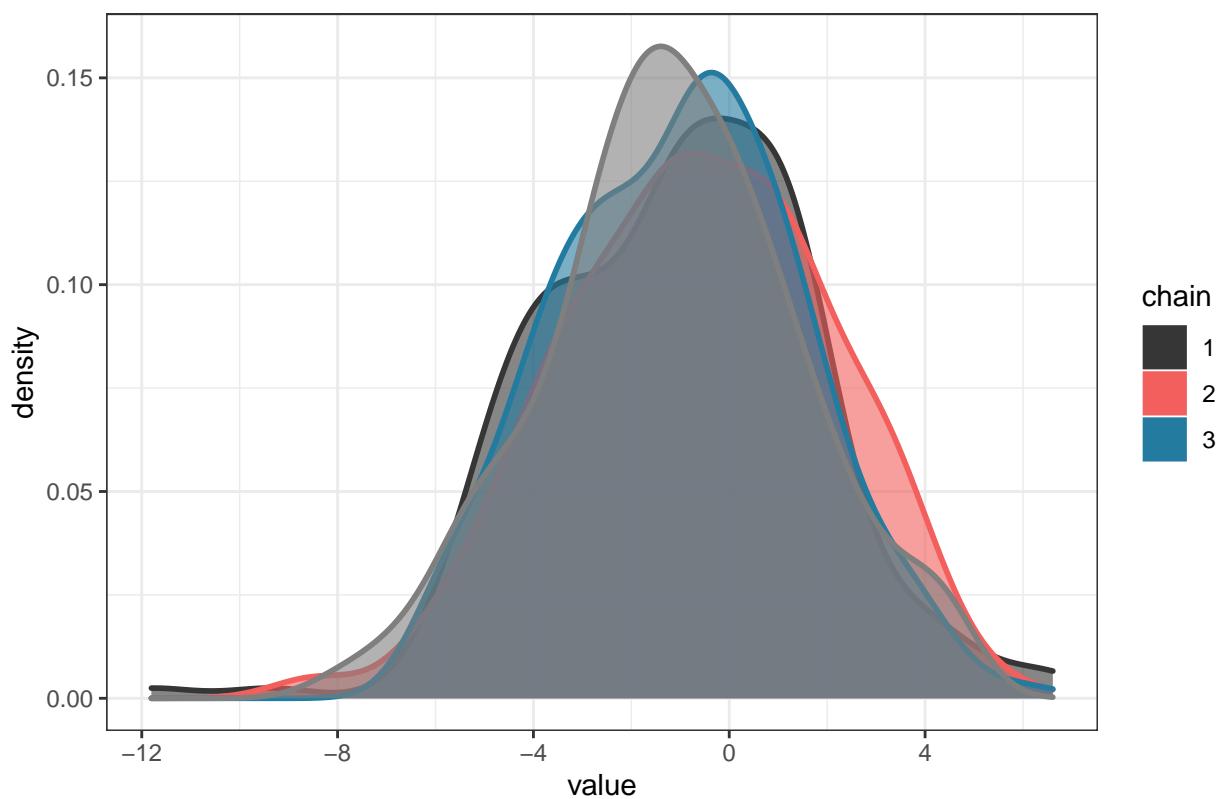
Density plot of $D[2, 2]$



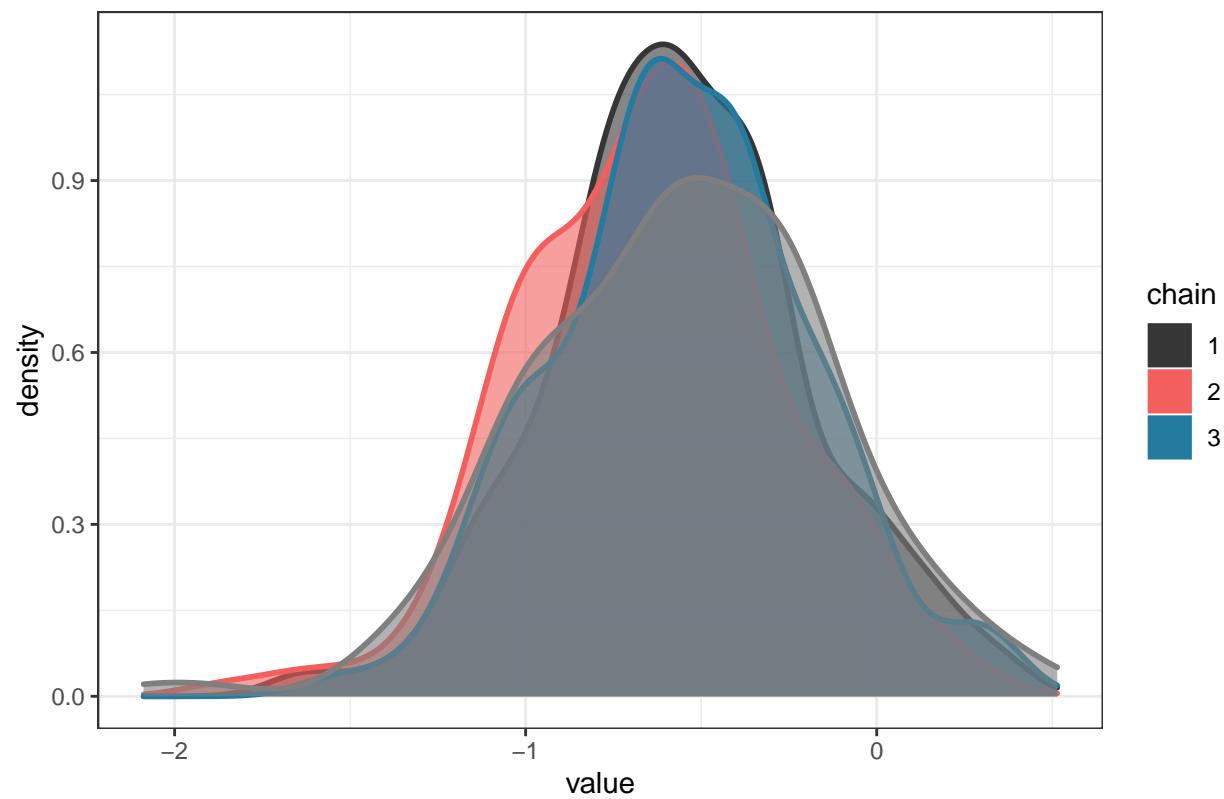
Density plot of (Intercept)



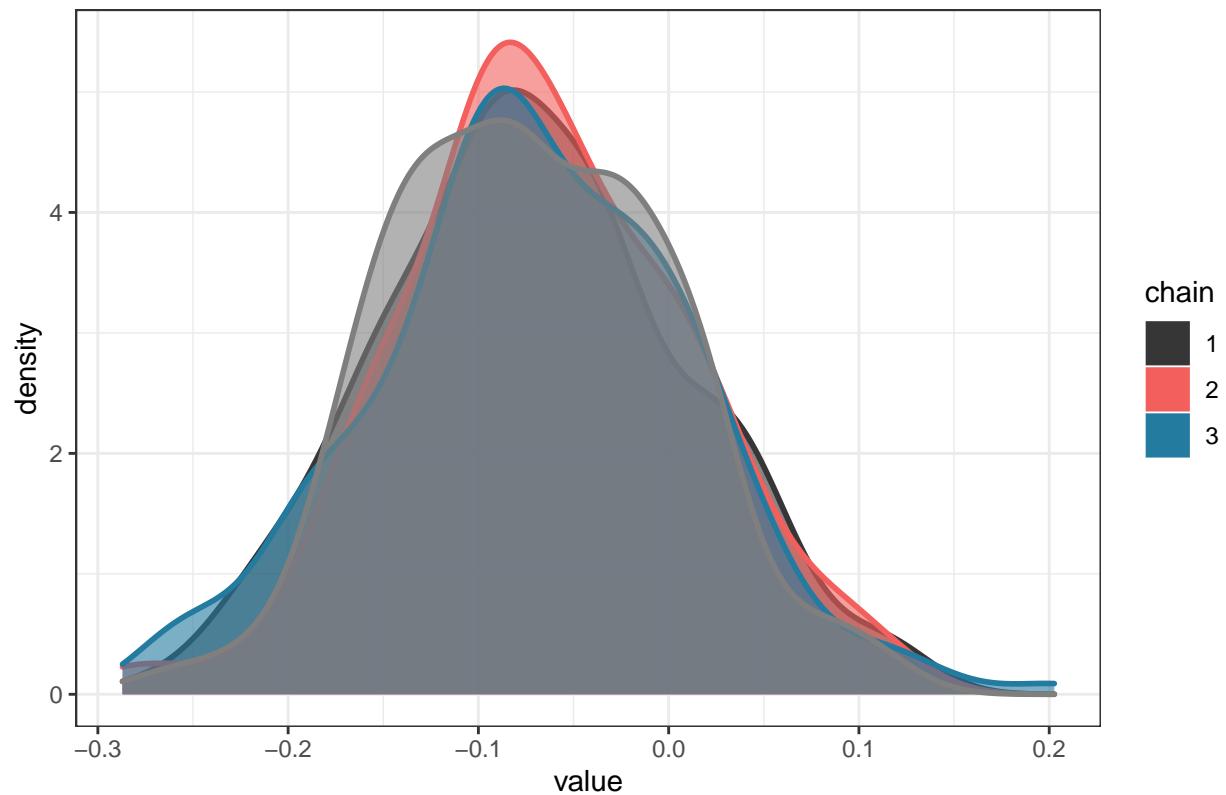
Density plot of LOWC31.1



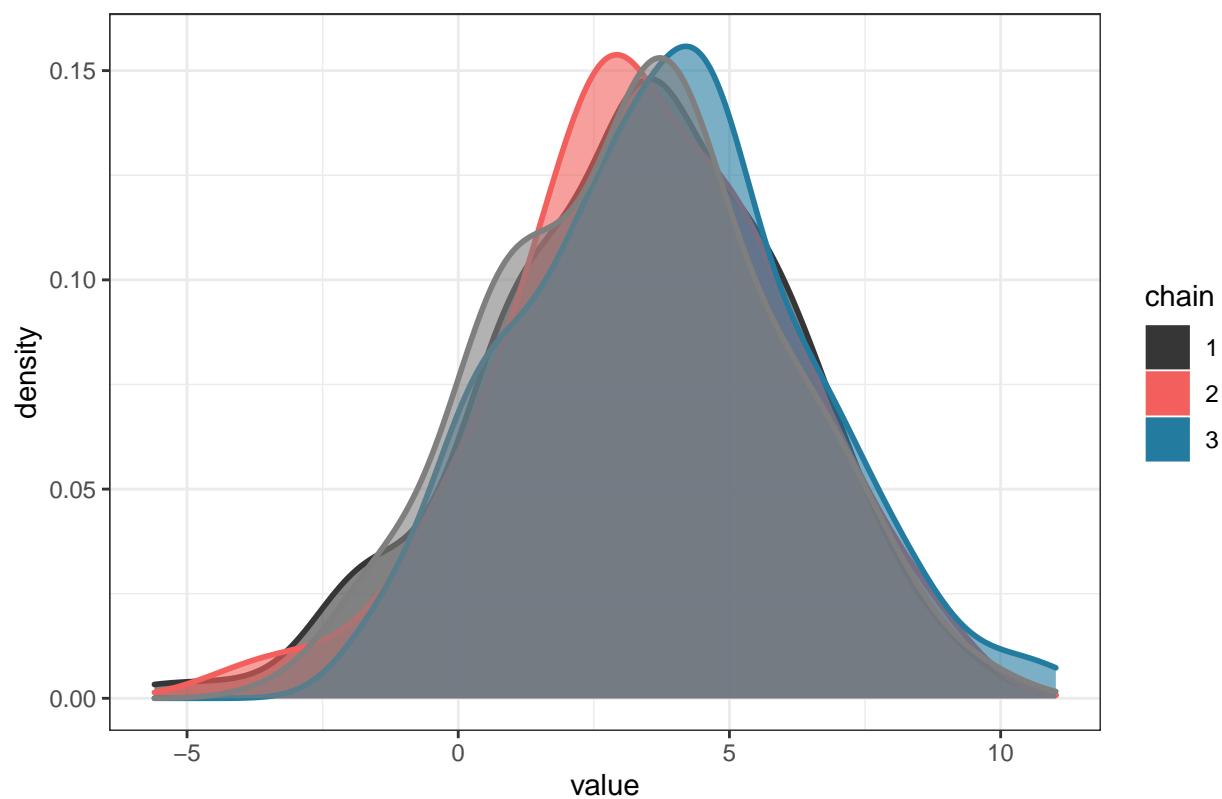
Density plot of time



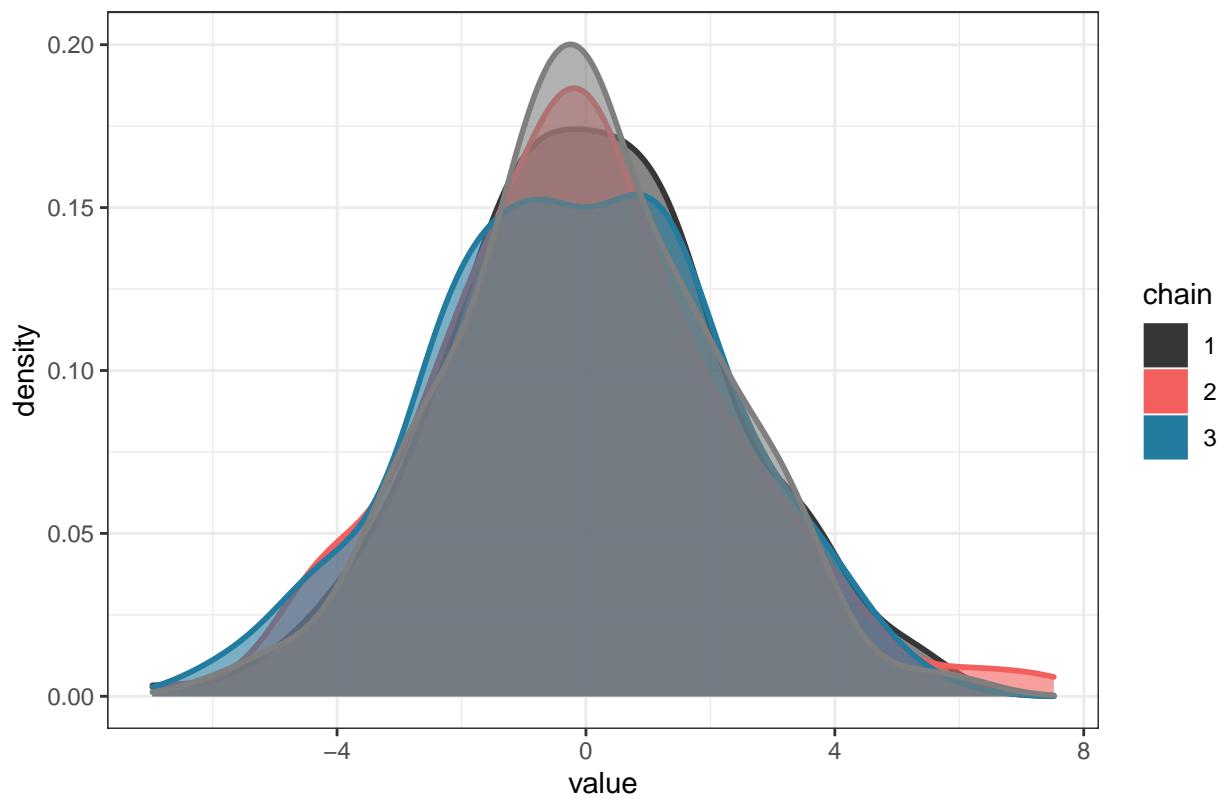
Density plot of ageatbiopsy.1



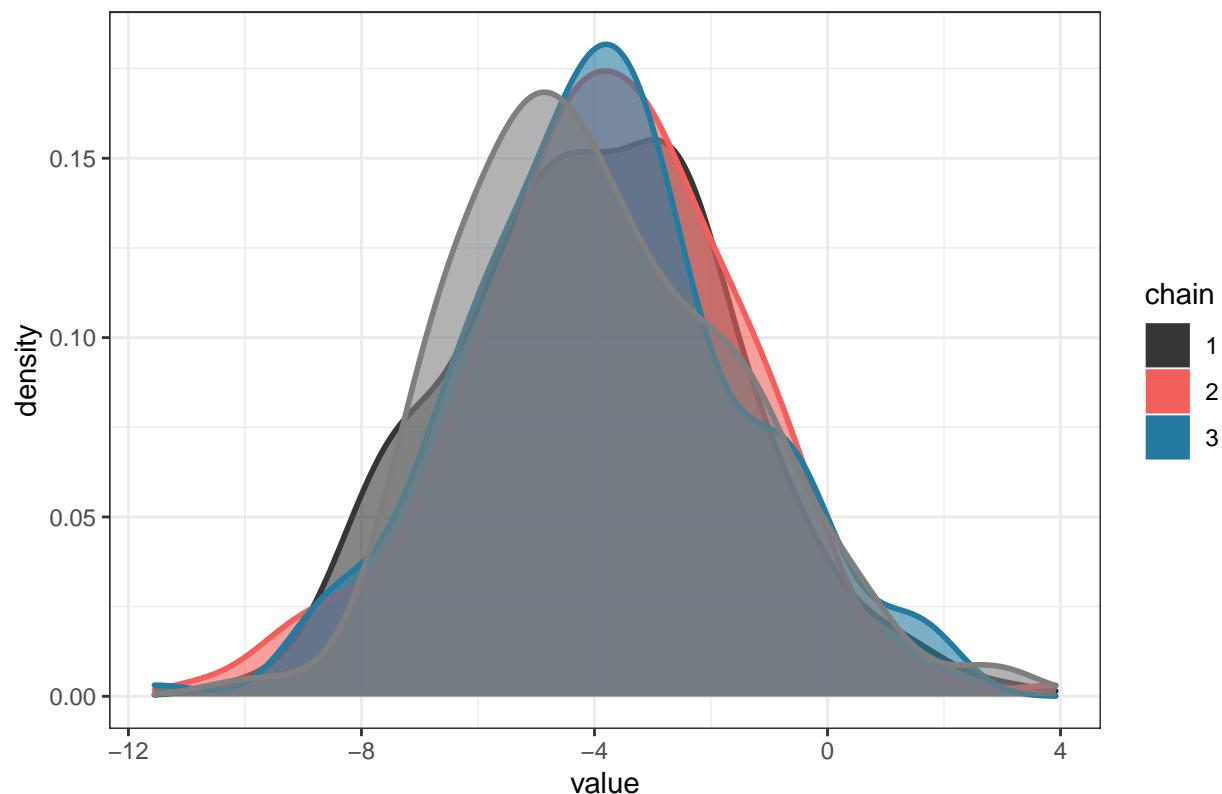
Density plot of sex.1



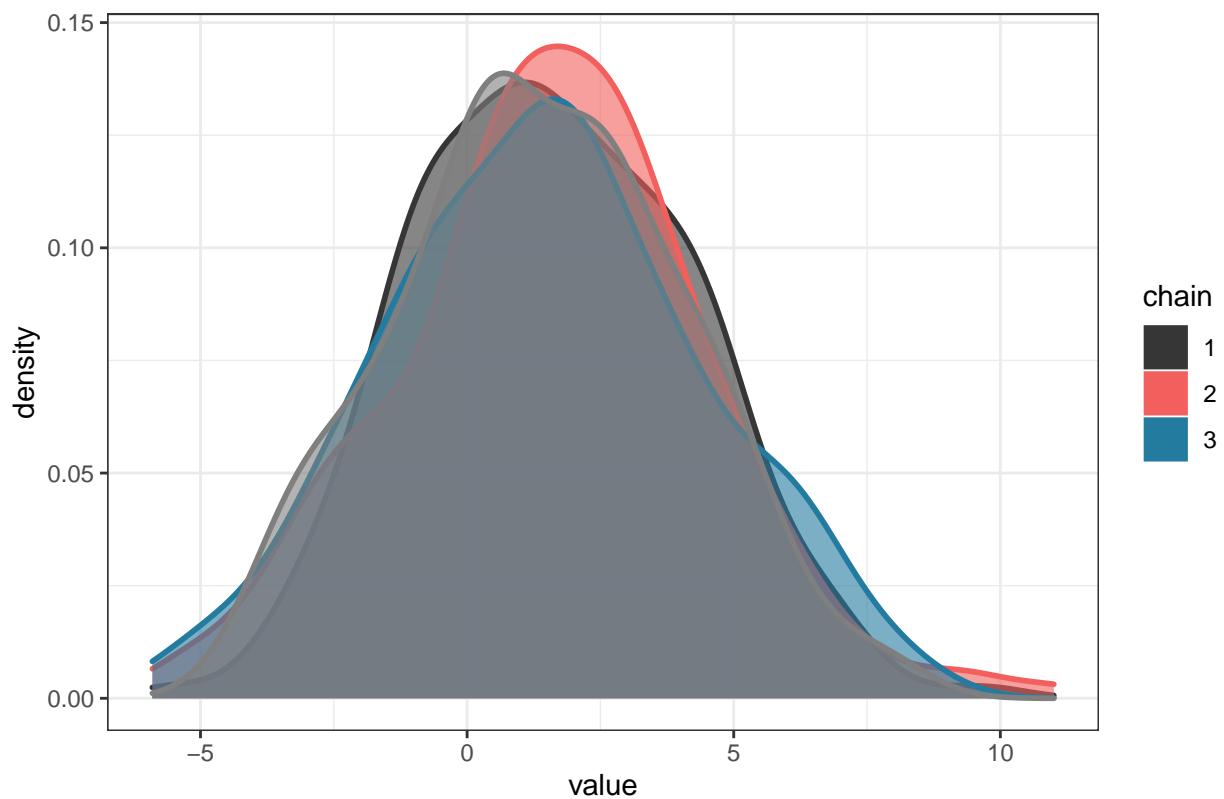
Density plot of black.1



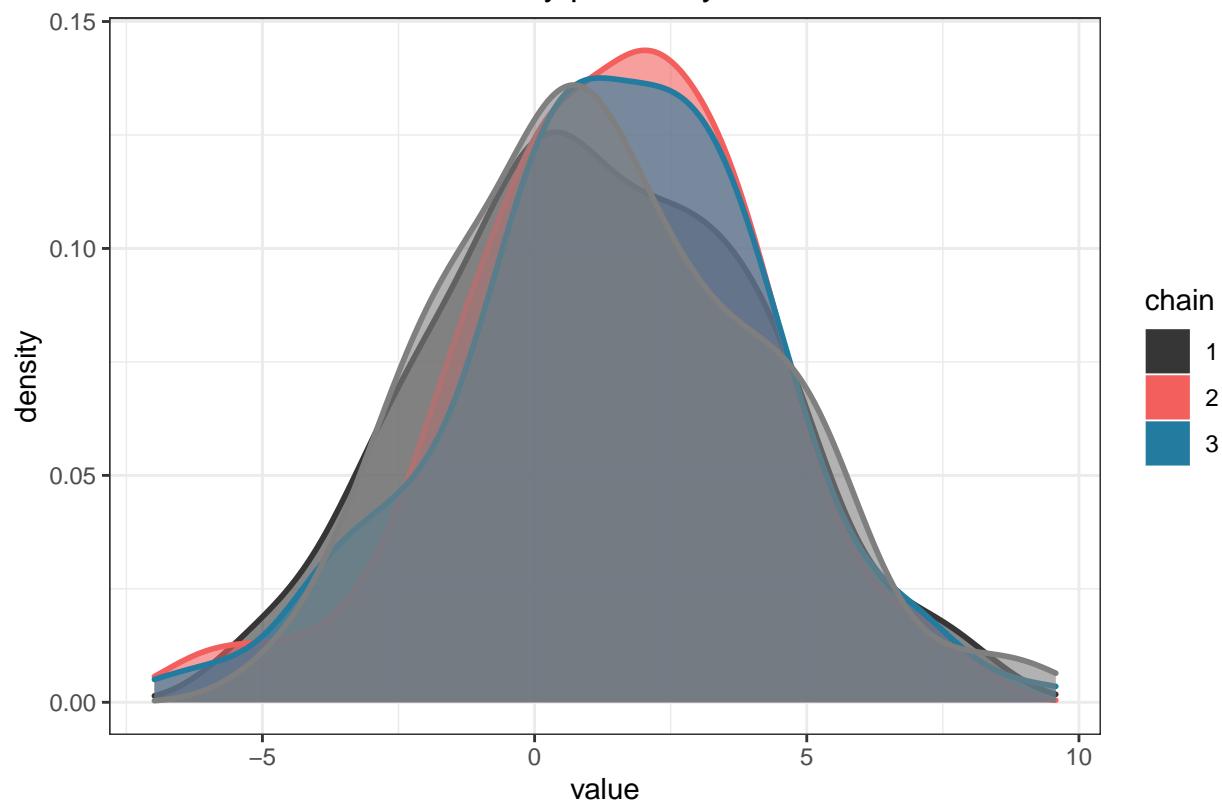
Density plot of hypertension.1



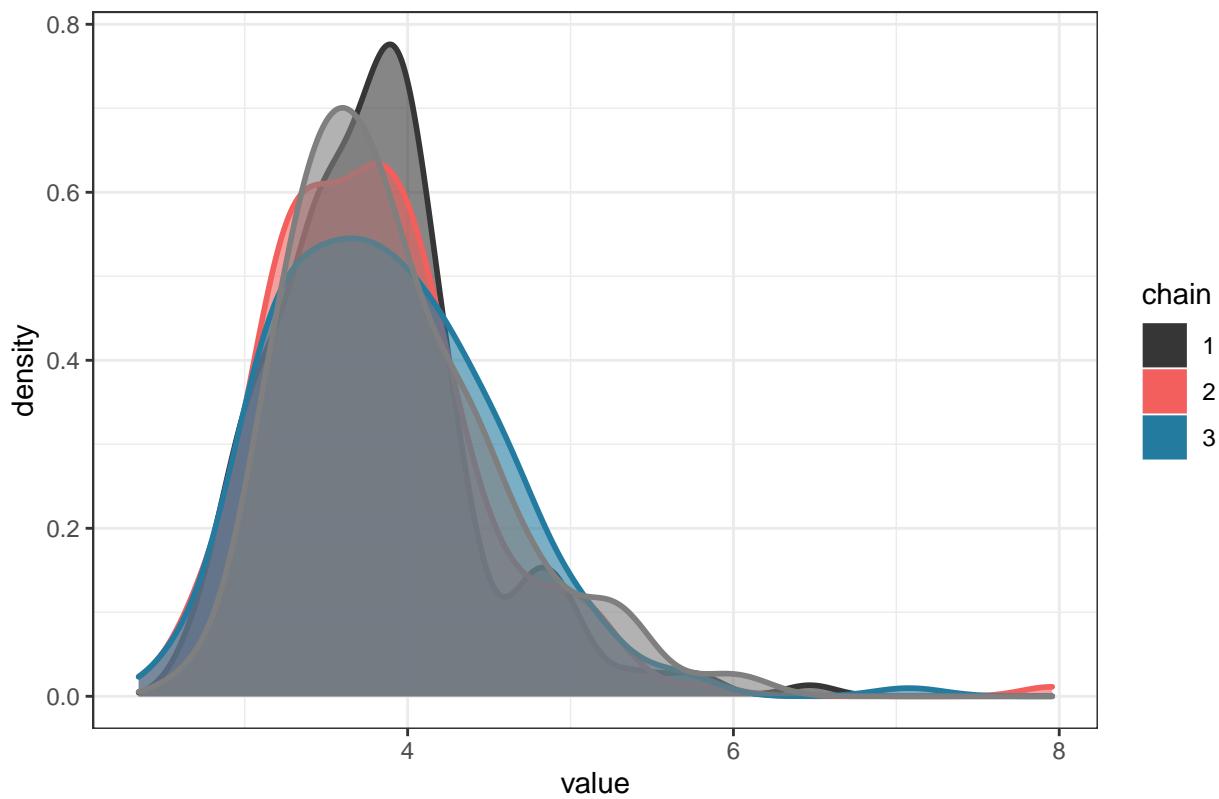
Density plot of mmf.1



Density plot of cyc.1



Density plot of sigmas_1



```
## ADJUSTED
```

```
densplt
```

```
## NULL
```

```
densplt1
```

```
## NULL
```

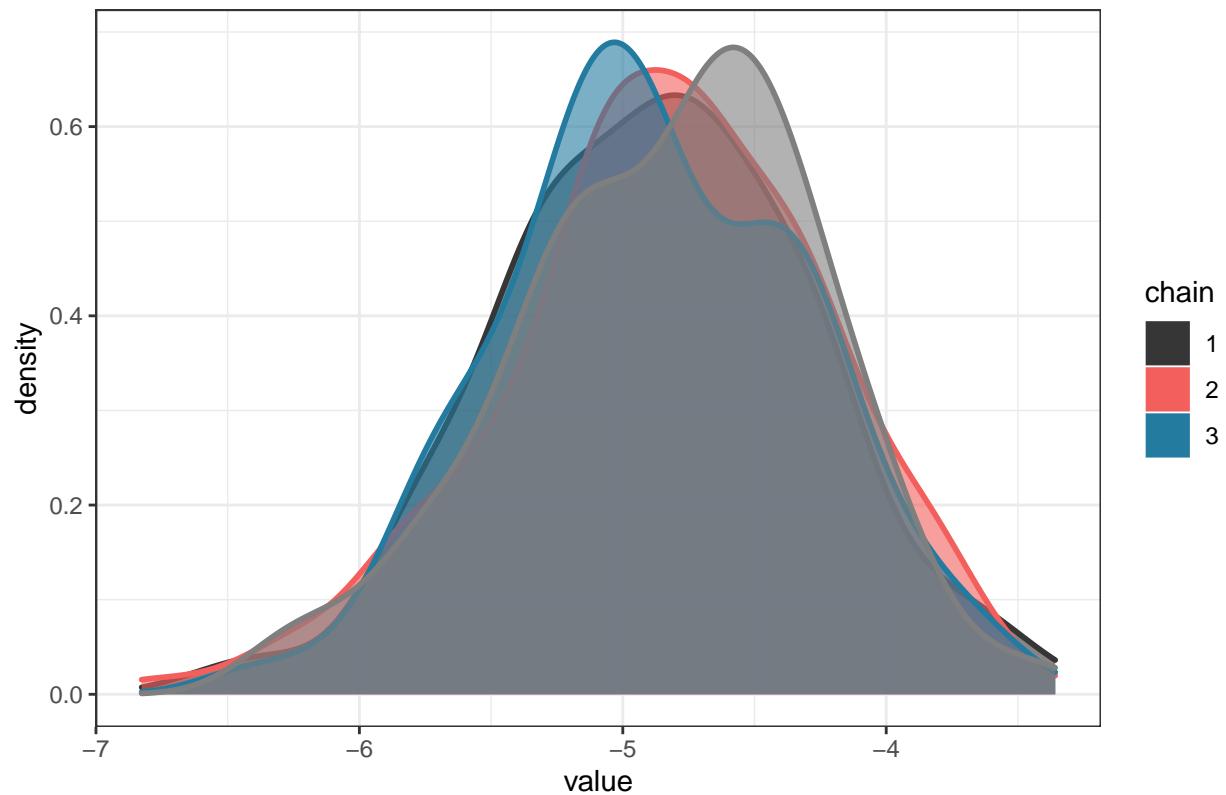
```
densplt2
```

```
## NULL
```

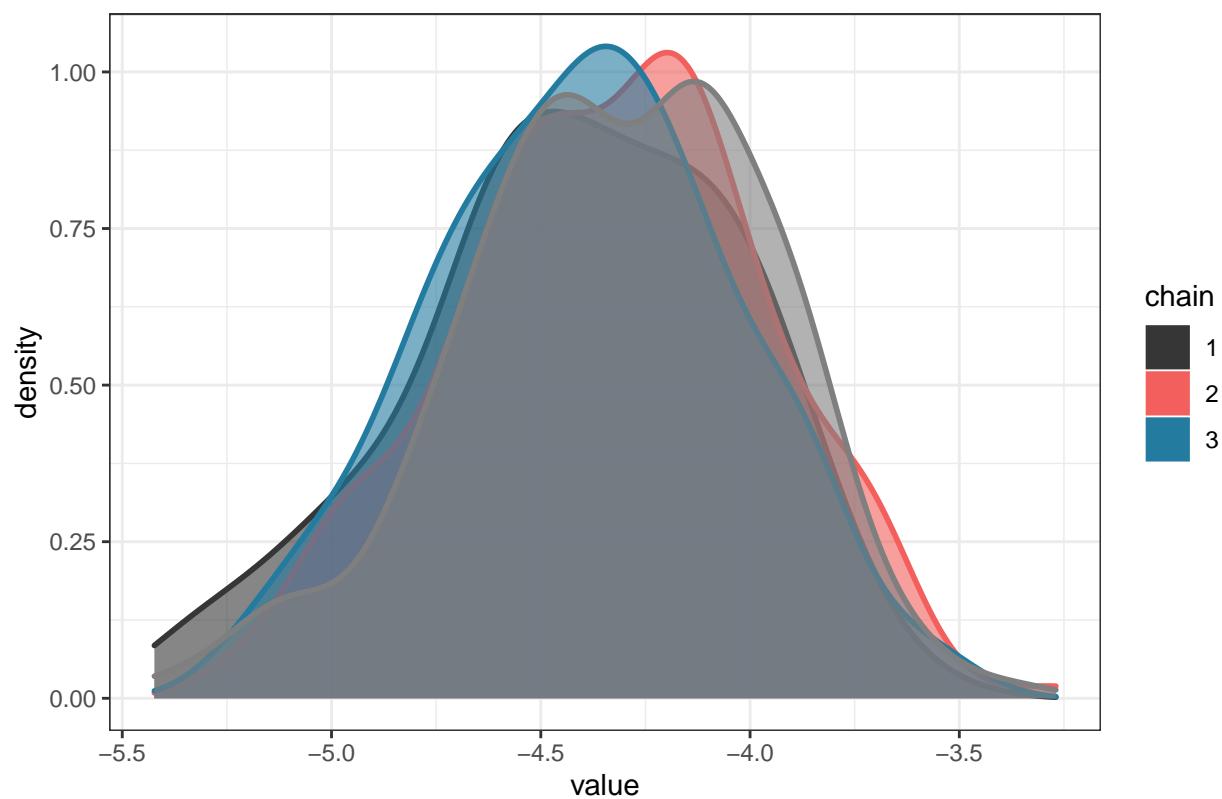
CRUDE

```
densCplt <- ggdensityplot(jointCFit)
```

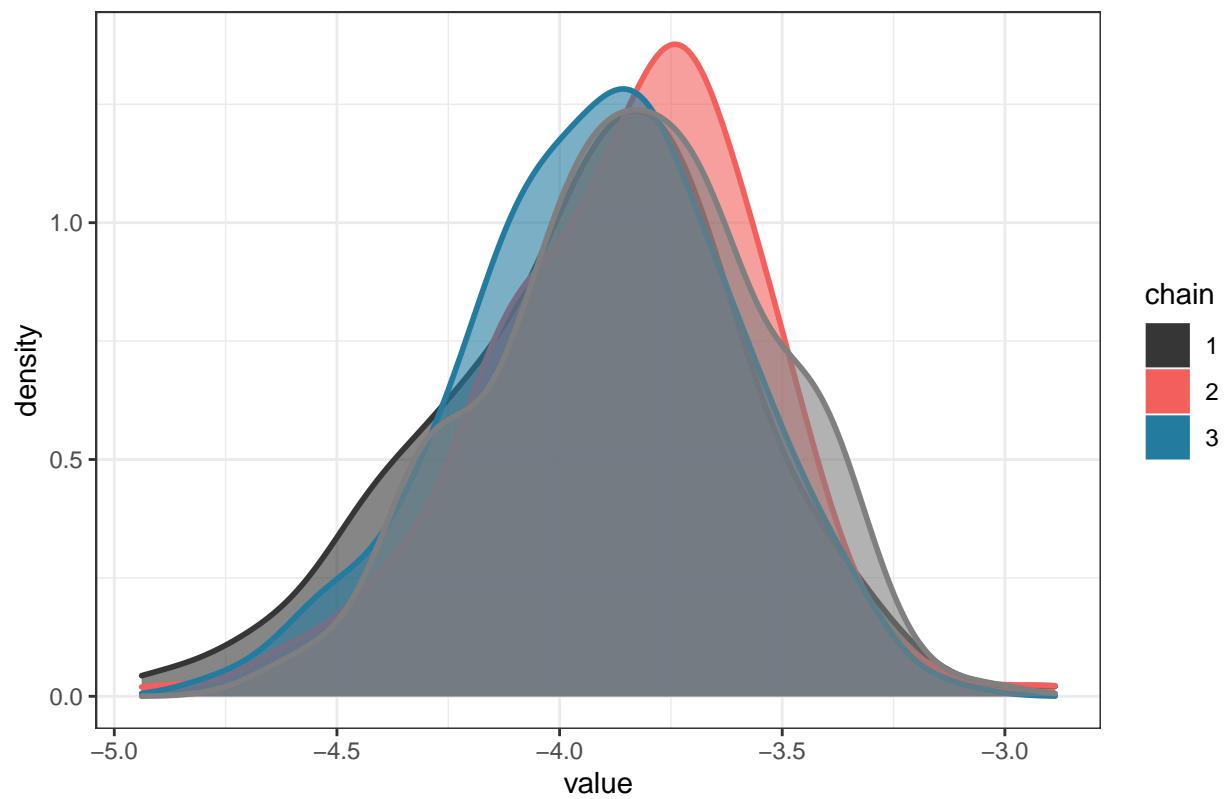
Density plot of bs_gammas_1



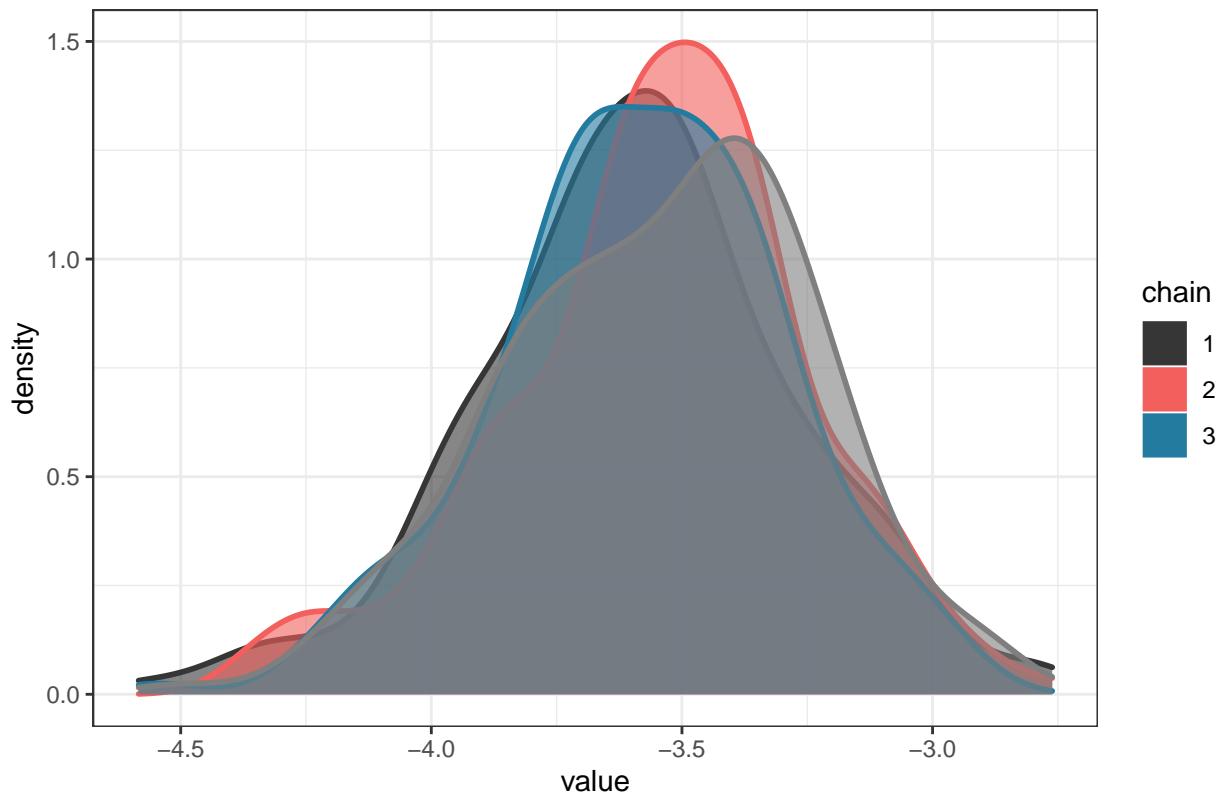
Density plot of bs_gammas_2



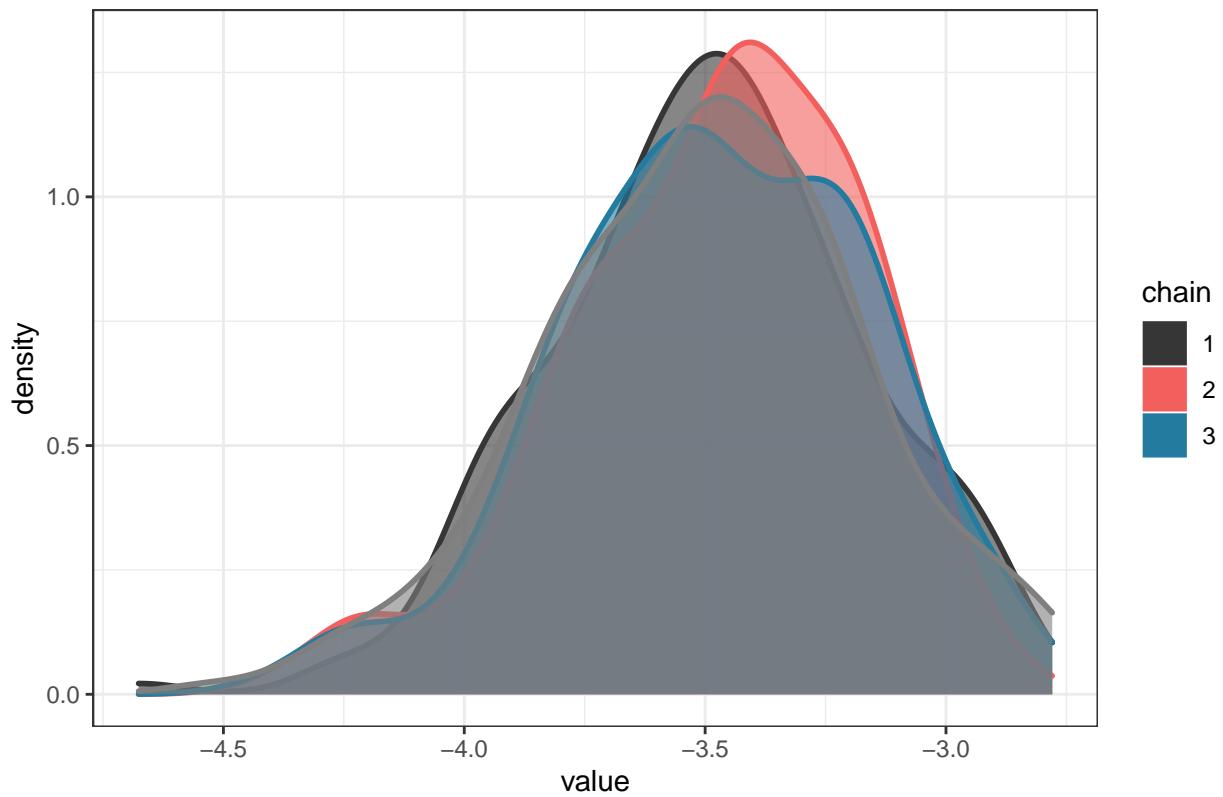
Density plot of bs_gammas_3



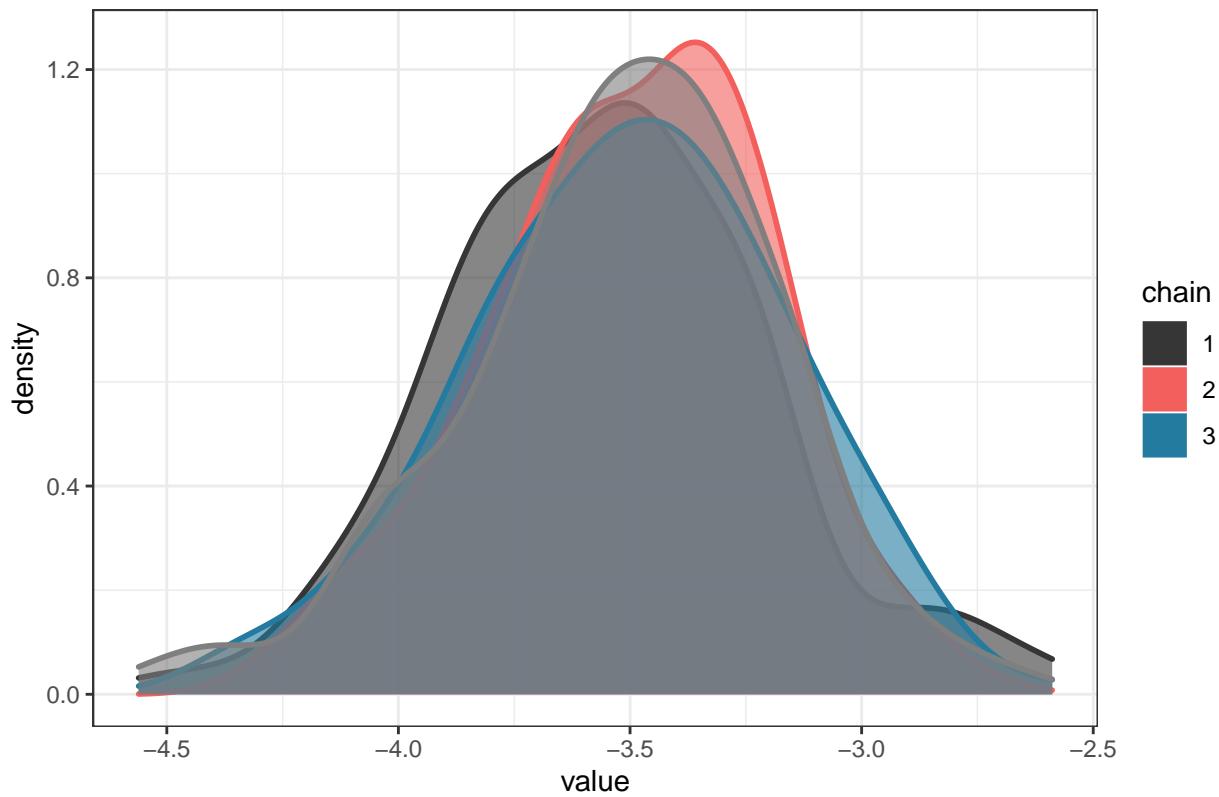
Density plot of bs_gammas_4



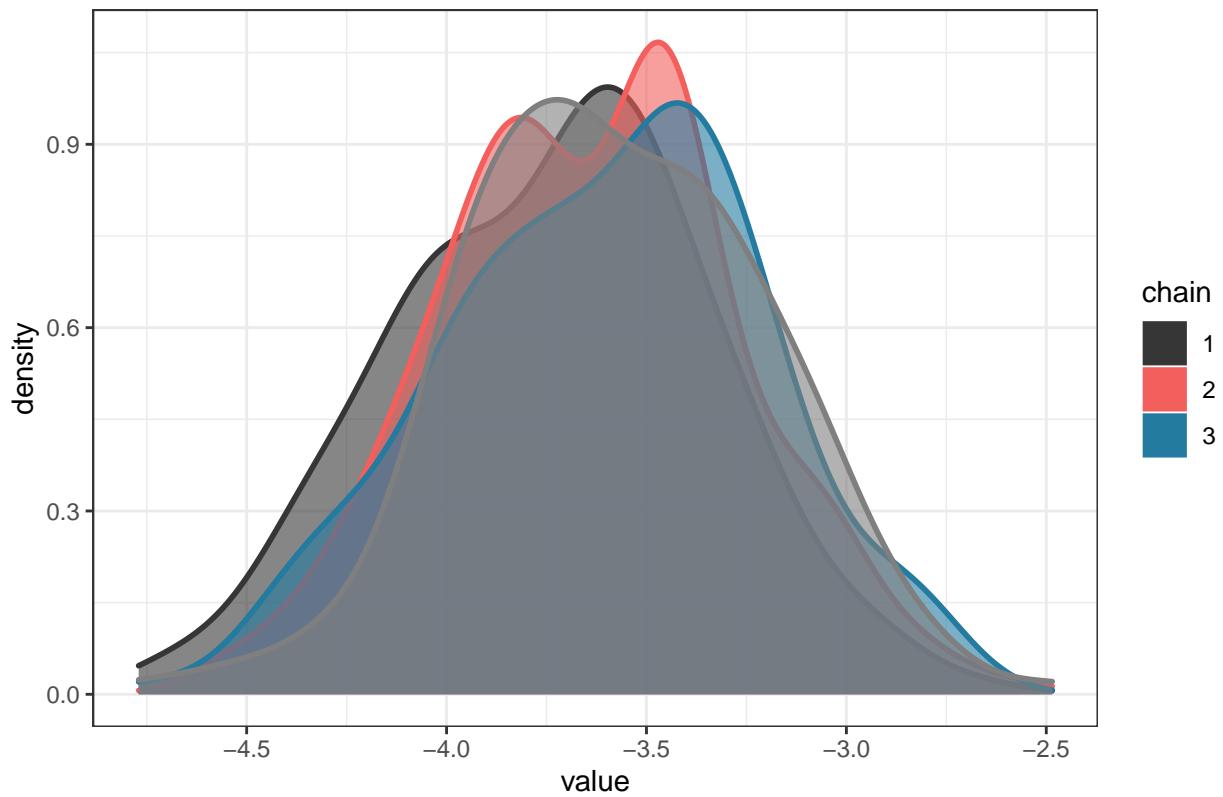
Density plot of bs_gammas_5



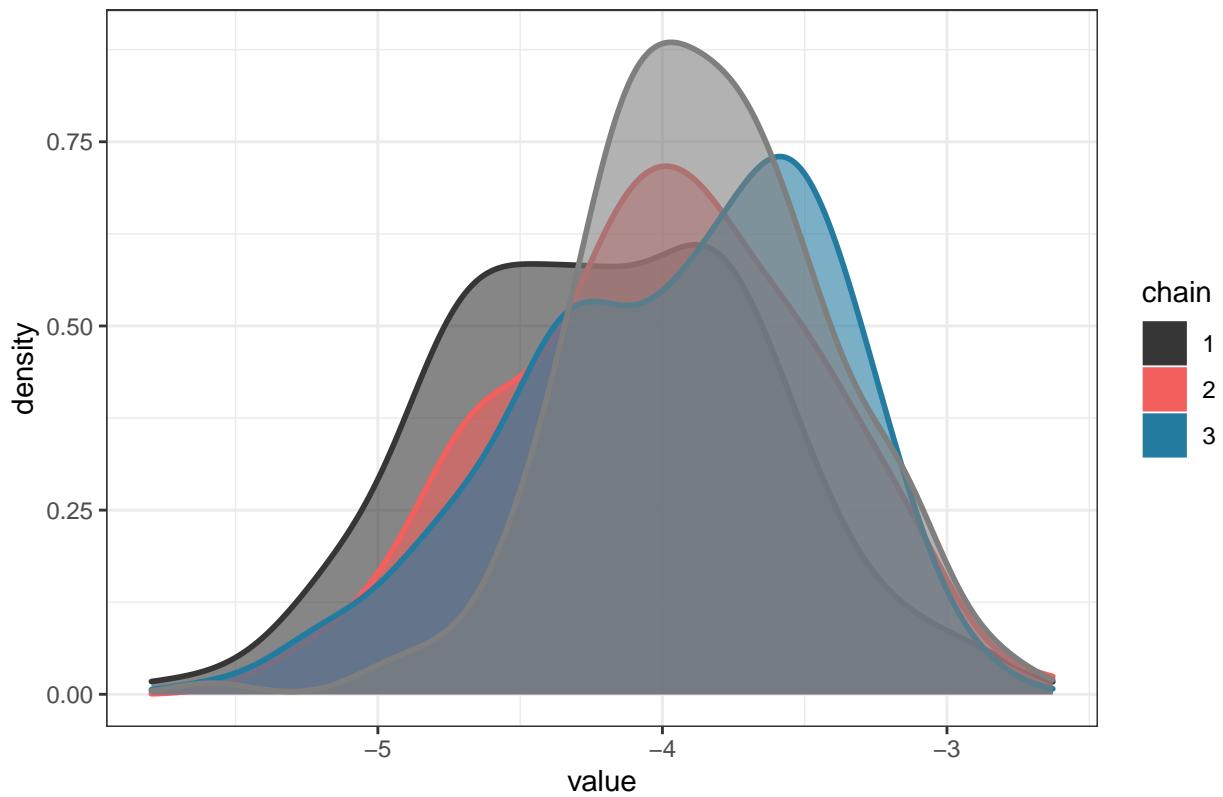
Density plot of bs_gammas_6



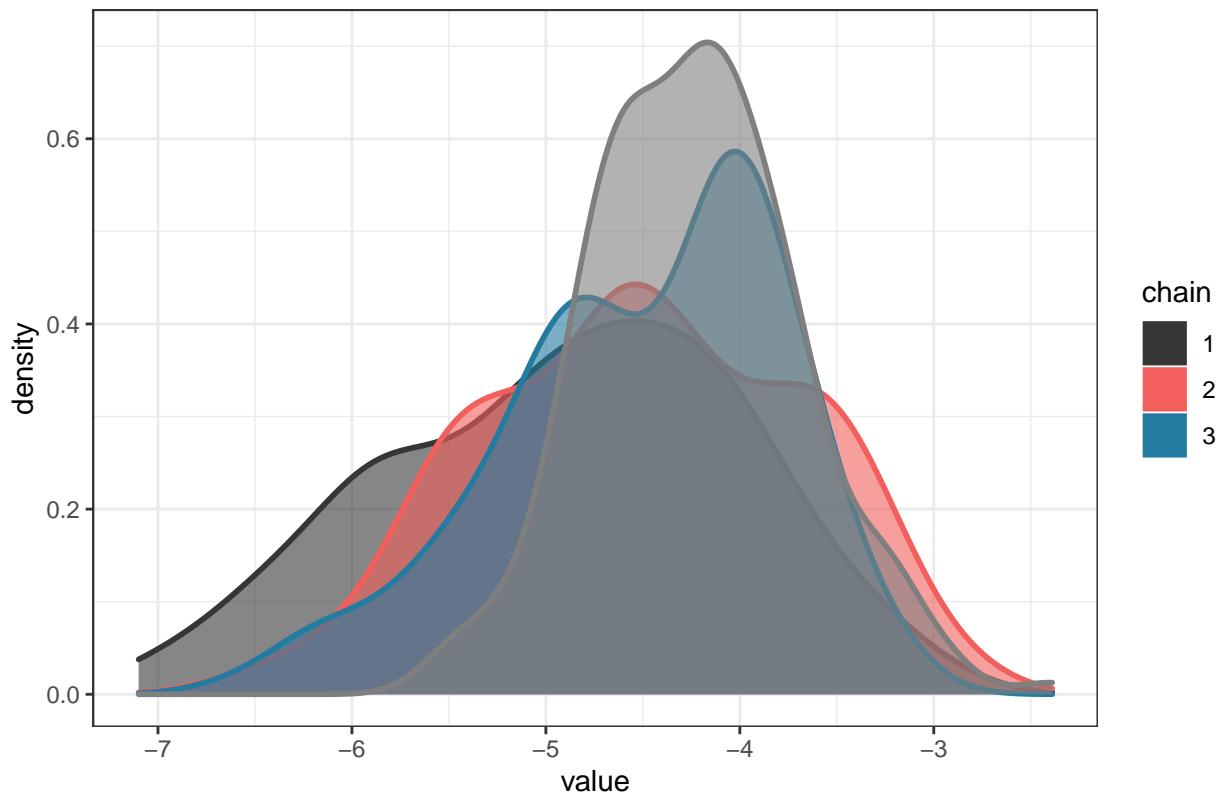
Density plot of bs_gammas_7



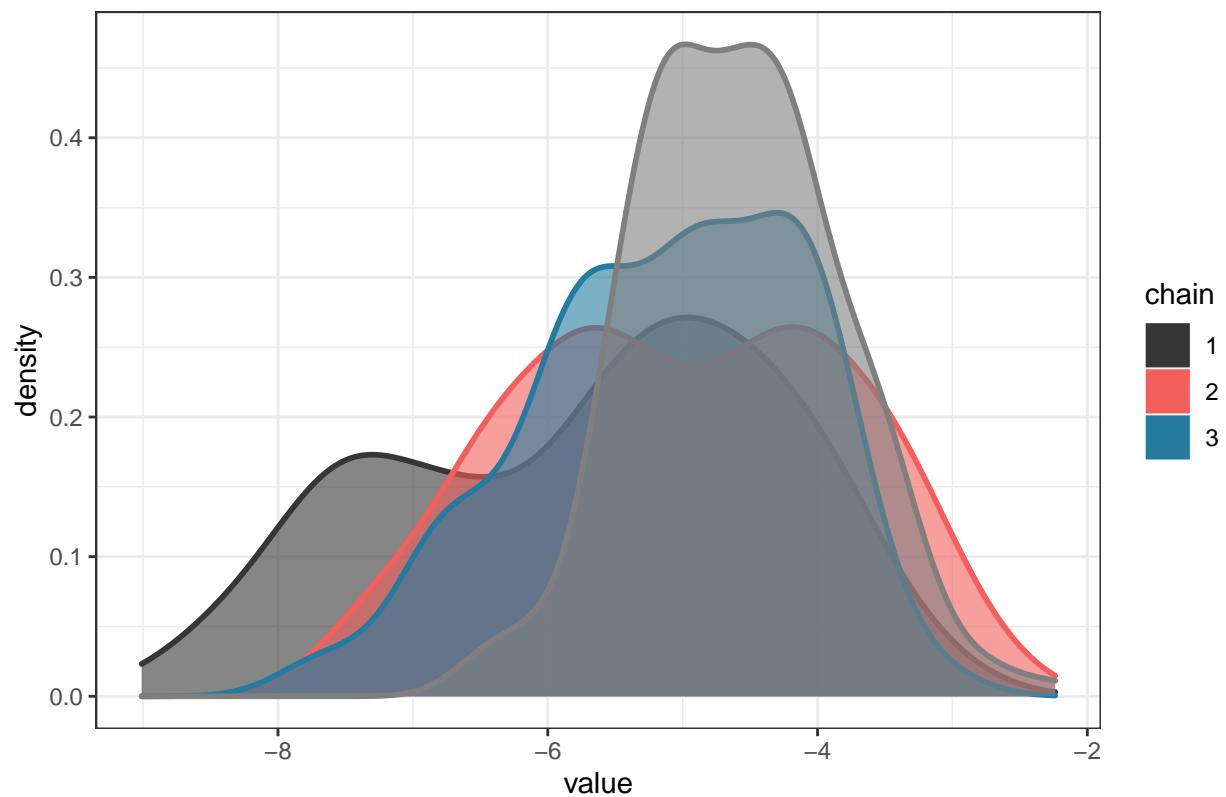
Density plot of bs_gammas_8



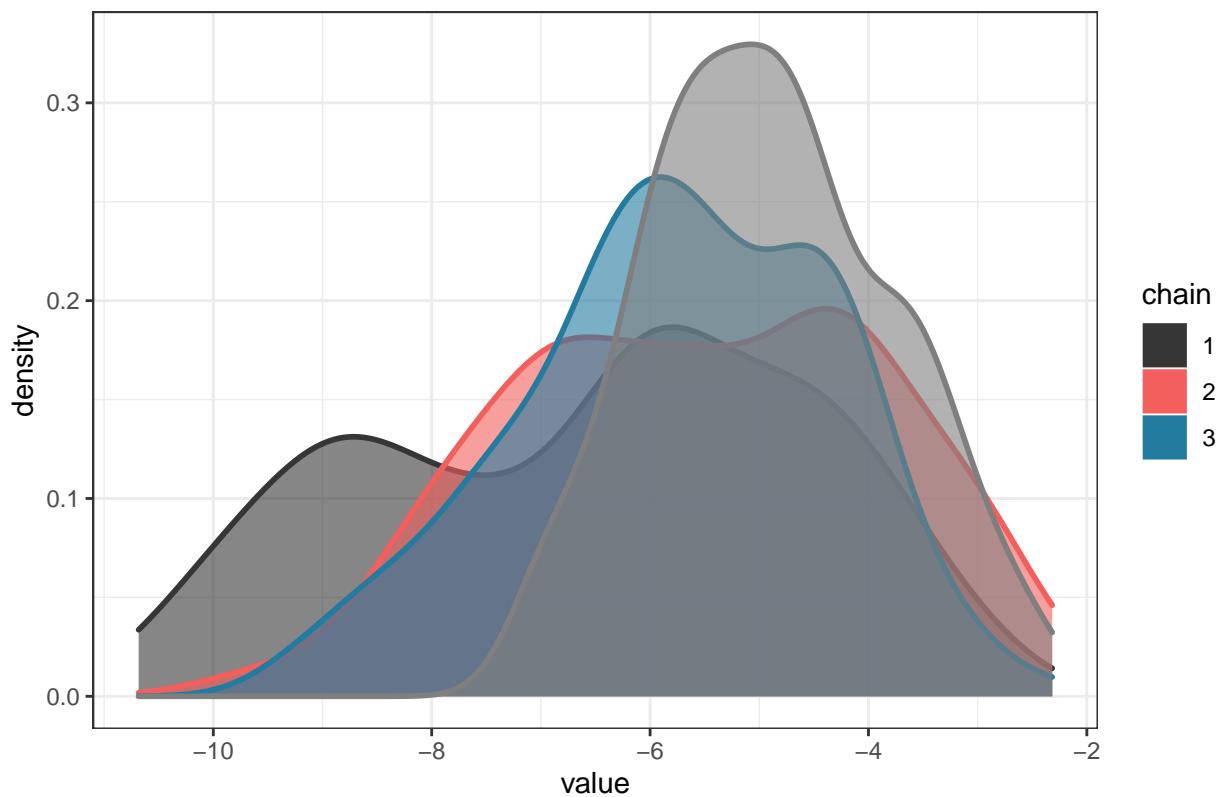
Density plot of bs_gammas_9



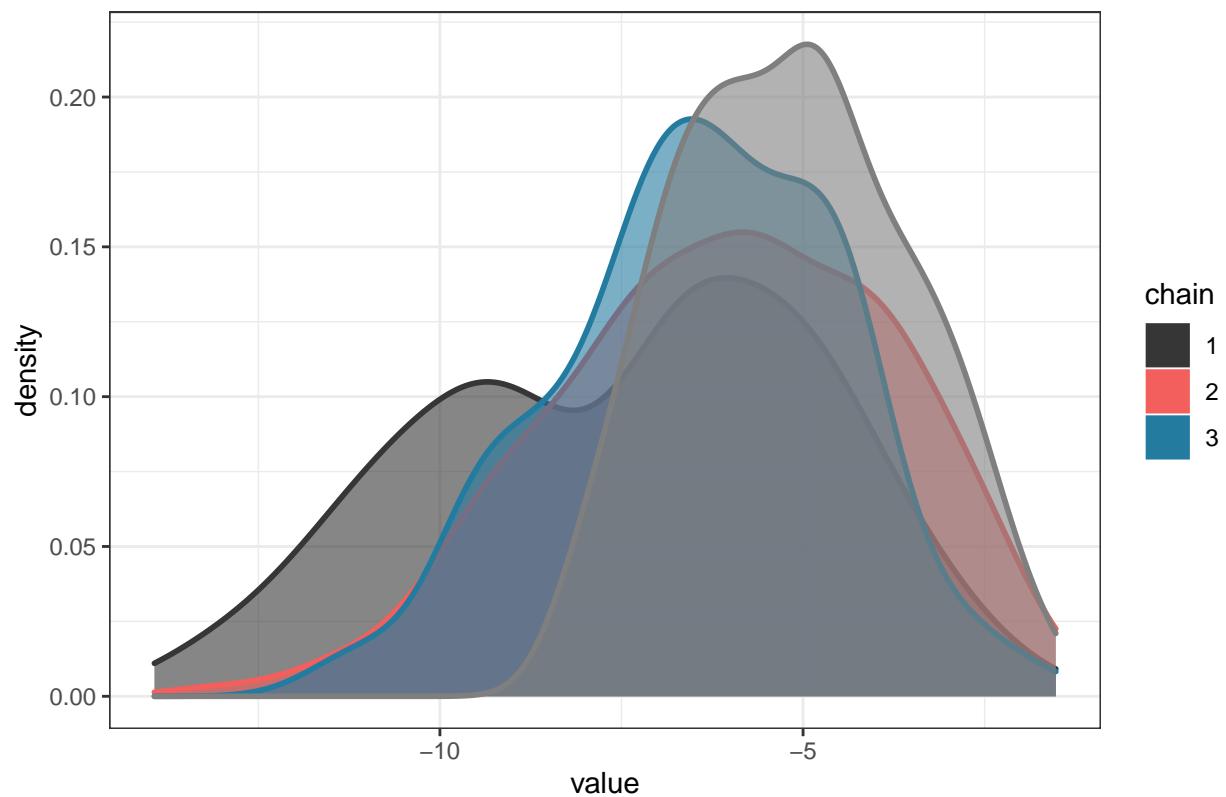
Density plot of bs_gammas_10



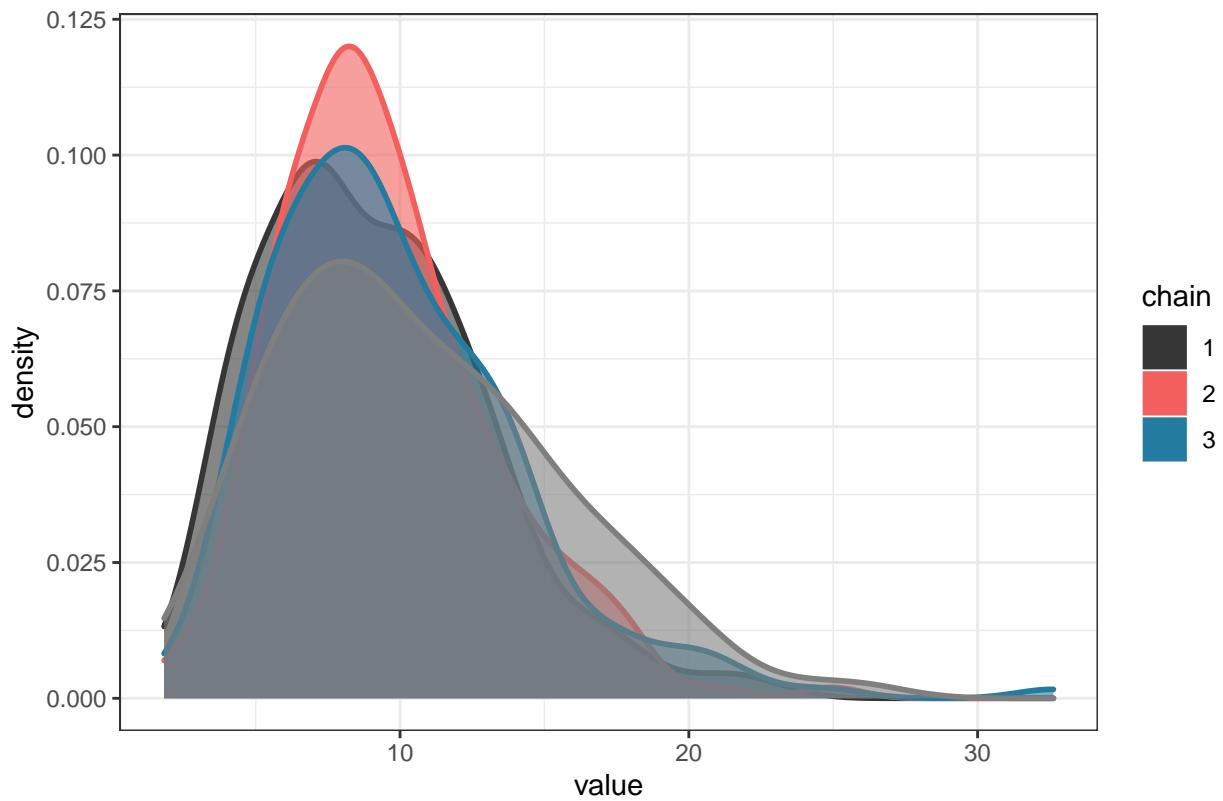
Density plot of bs_gammas_11



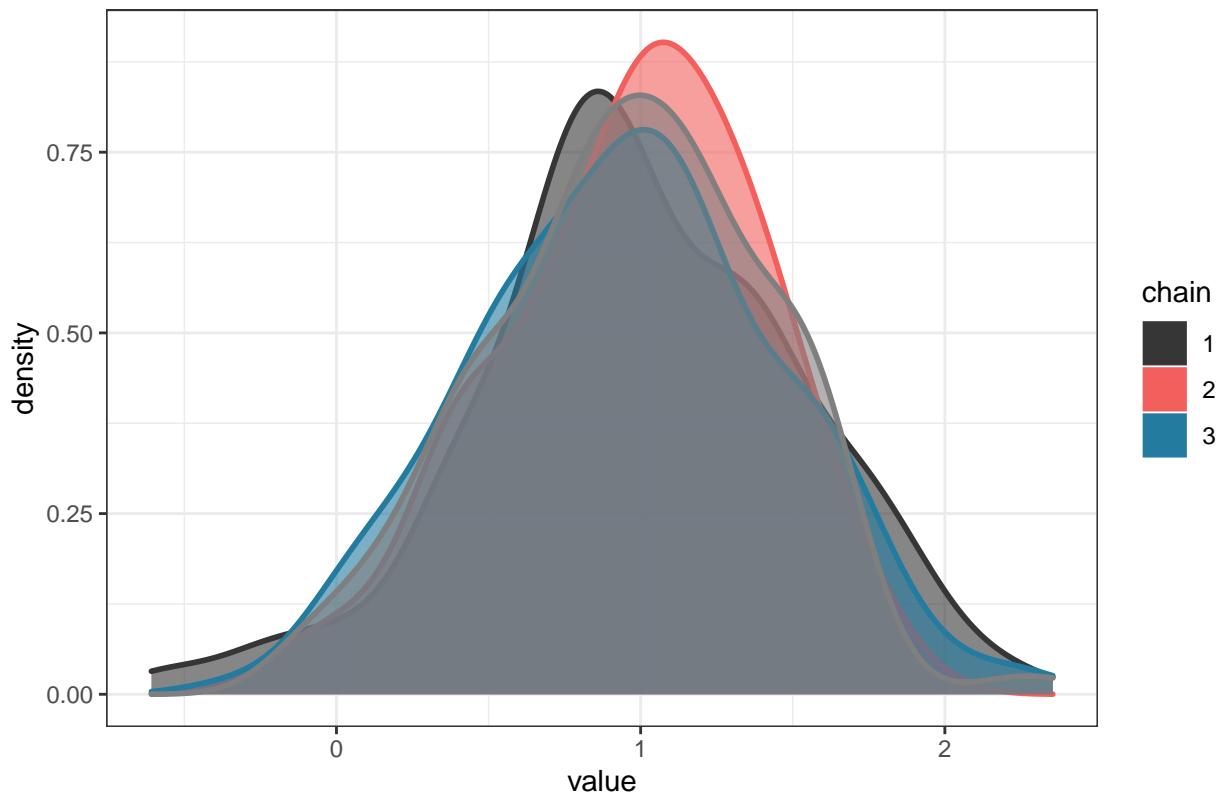
Density plot of bs_gammas_12



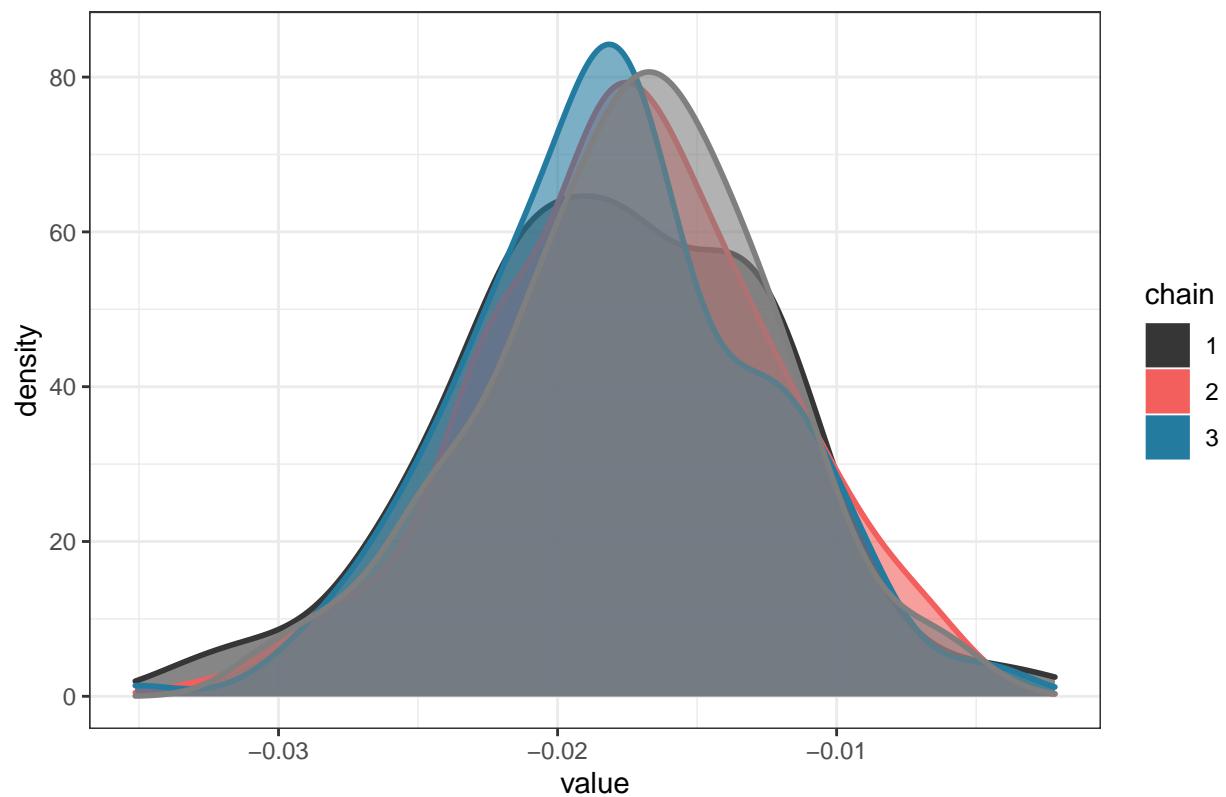
Density plot of tau_bs_gammas



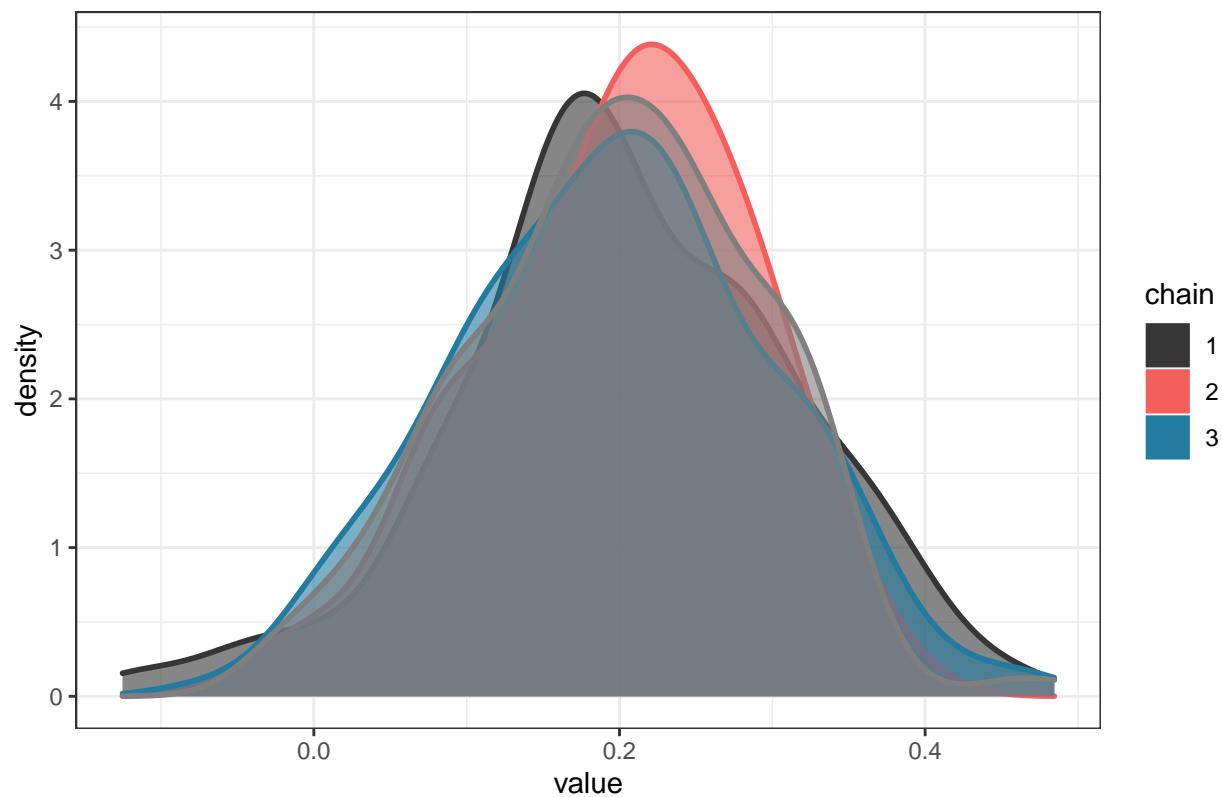
Density plot of LOWC31



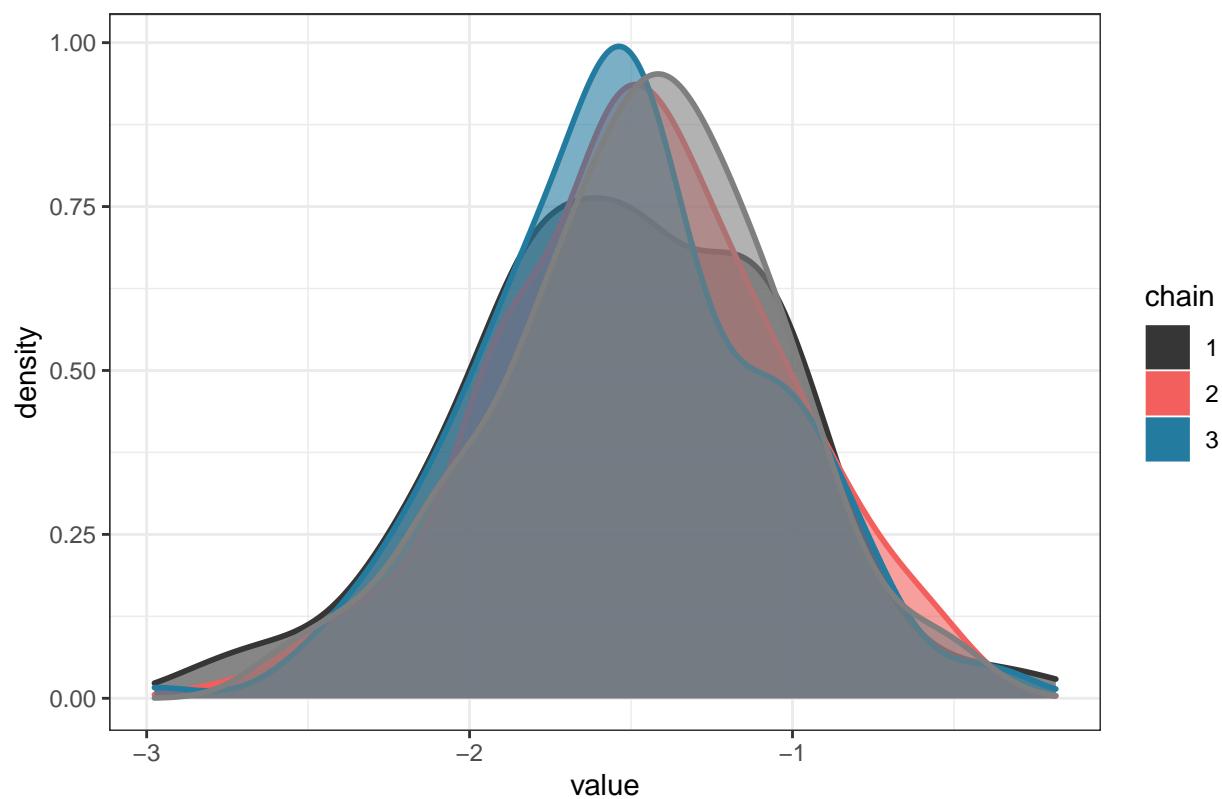
Density plot of value(eGFR)



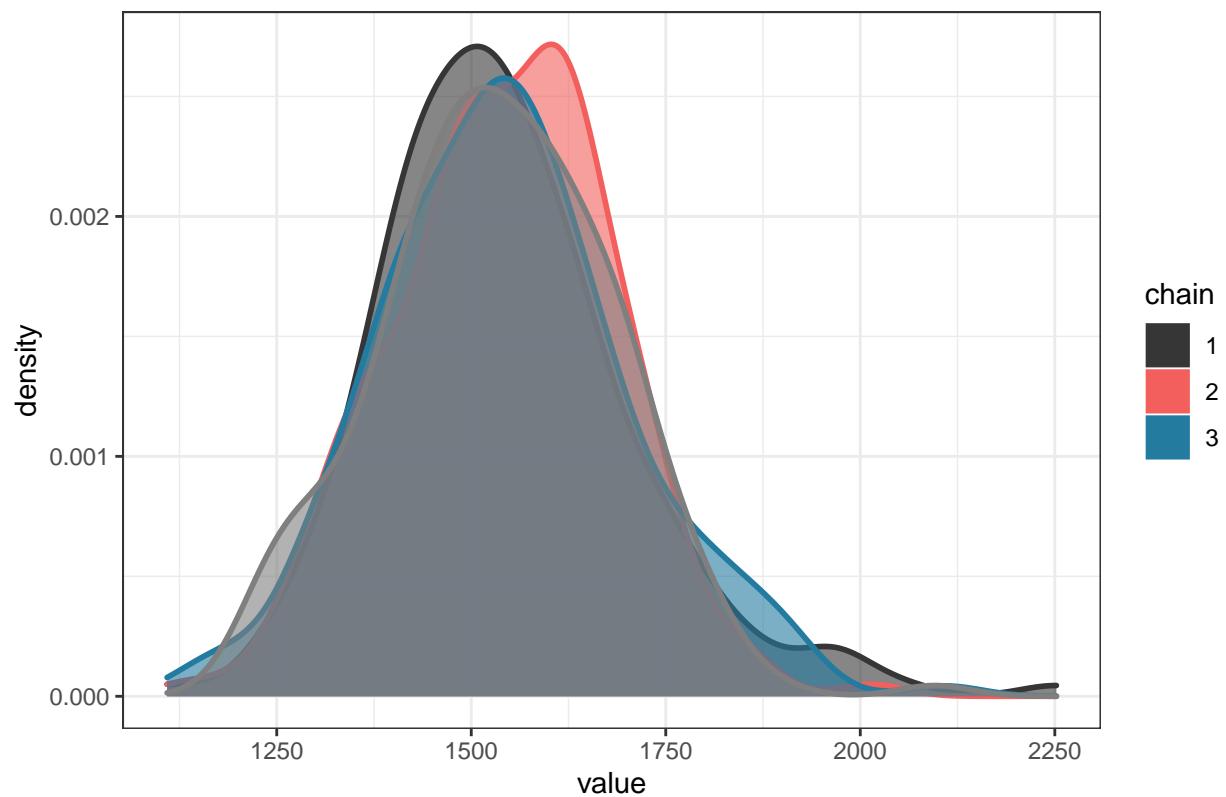
Density plot of



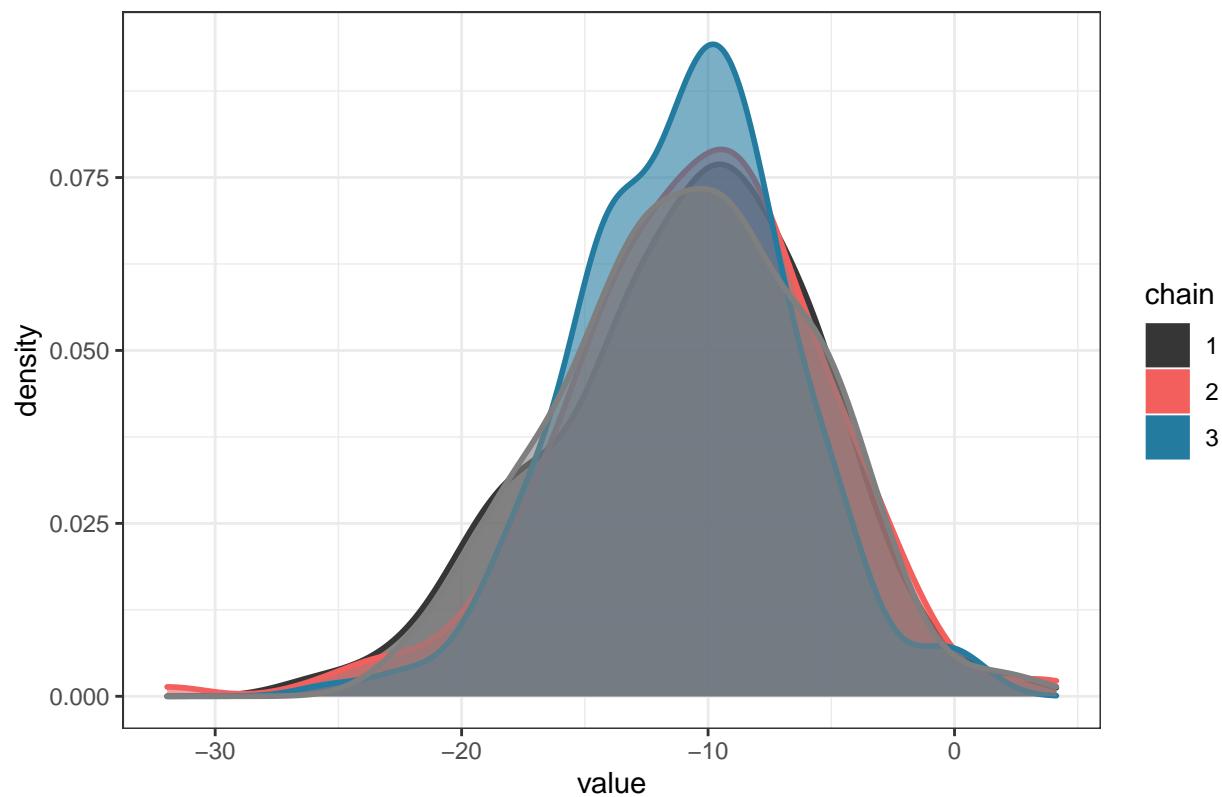
Density plot of .1



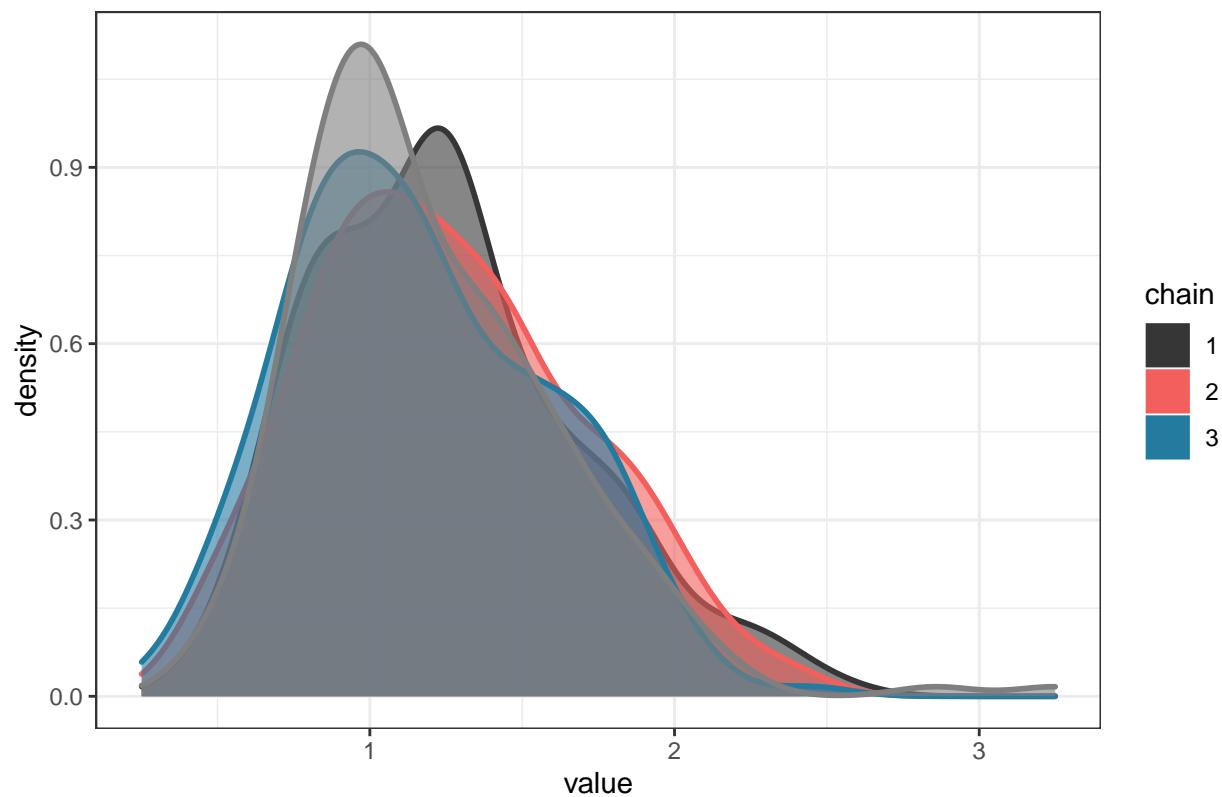
Density plot of $D[1, 1]$



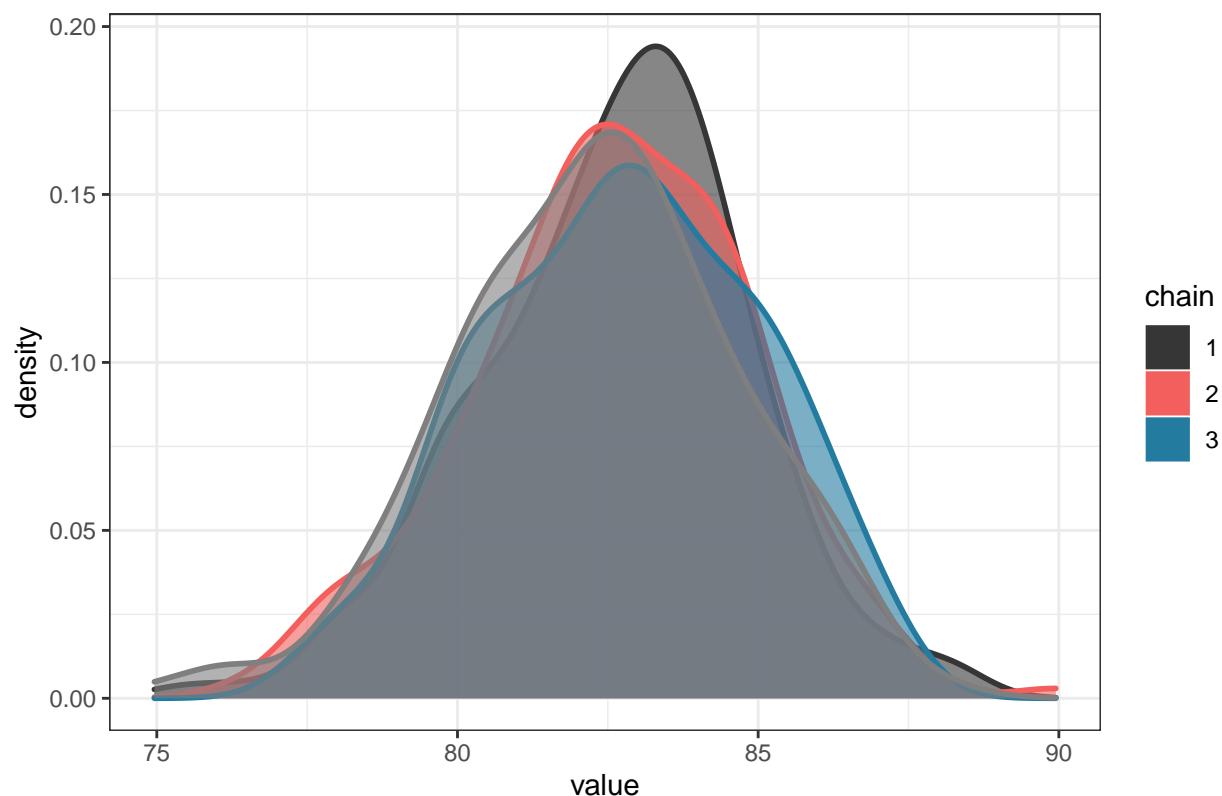
Density plot of $D[2, 1]$



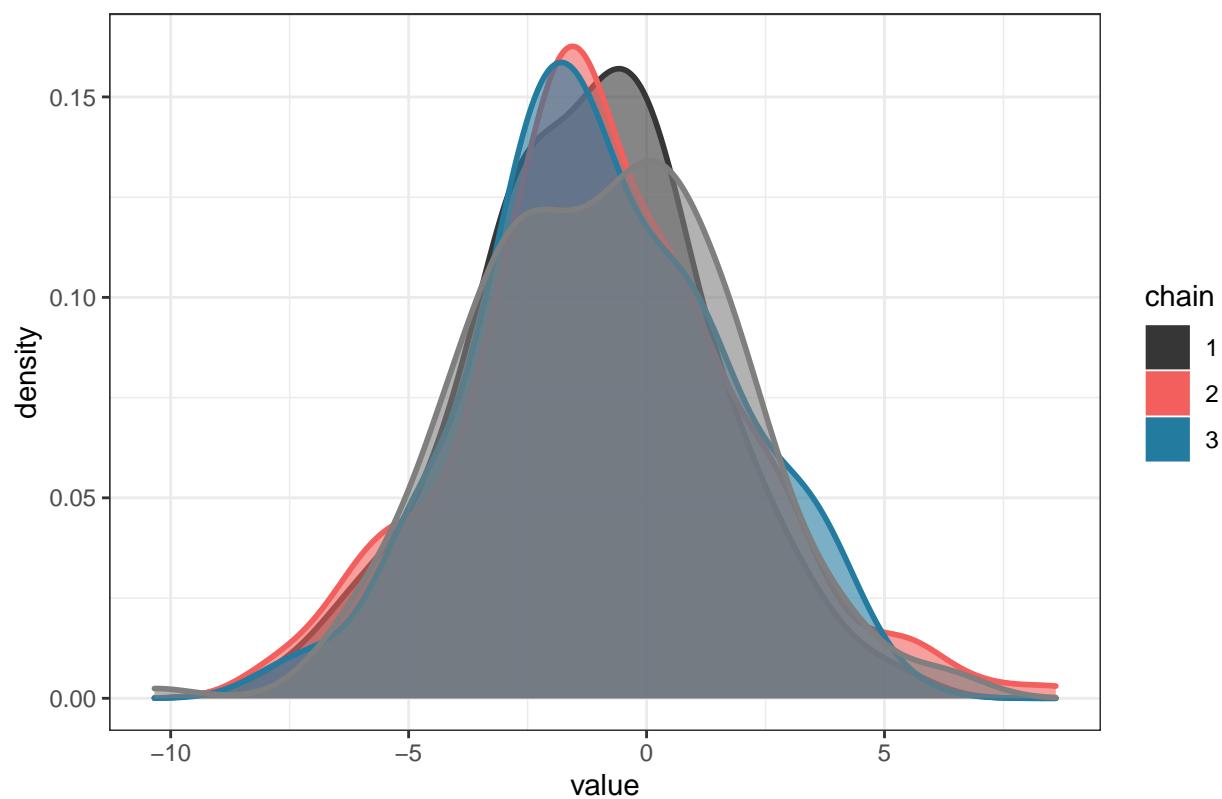
Density plot of $D[2, 2]$



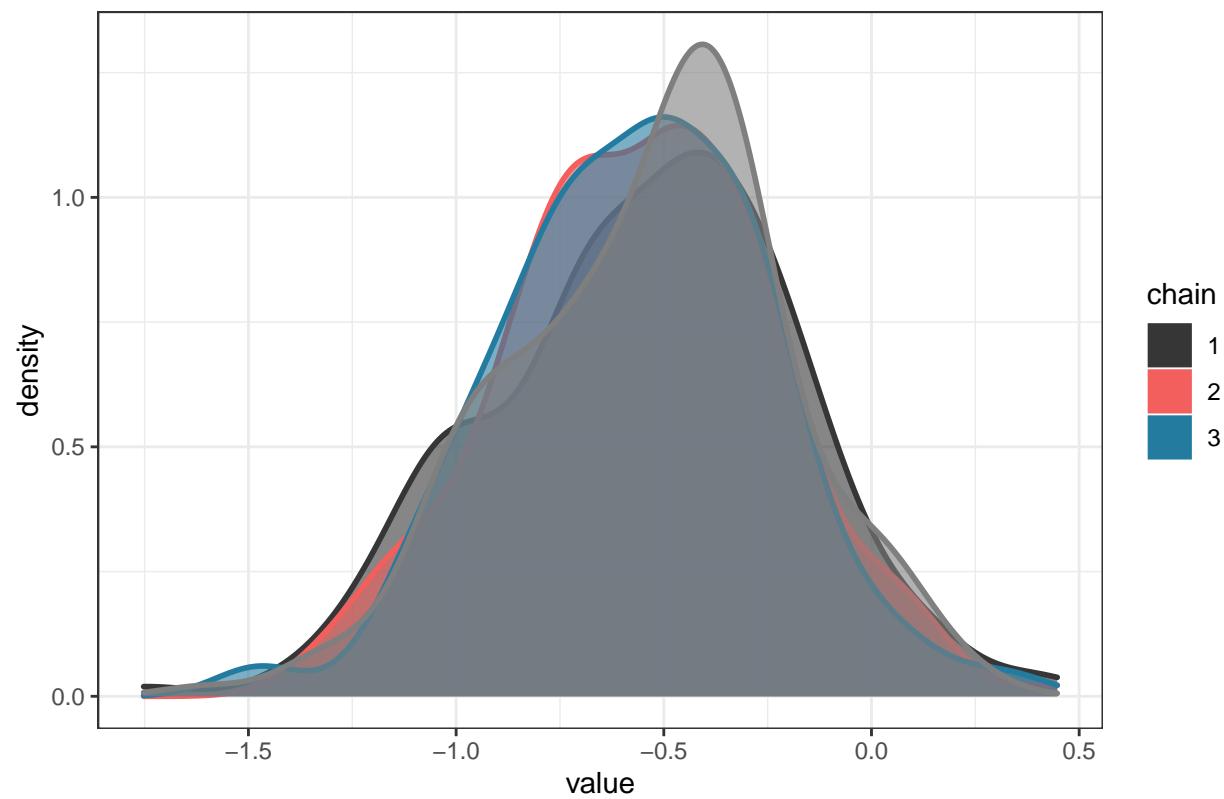
Density plot of (Intercept)



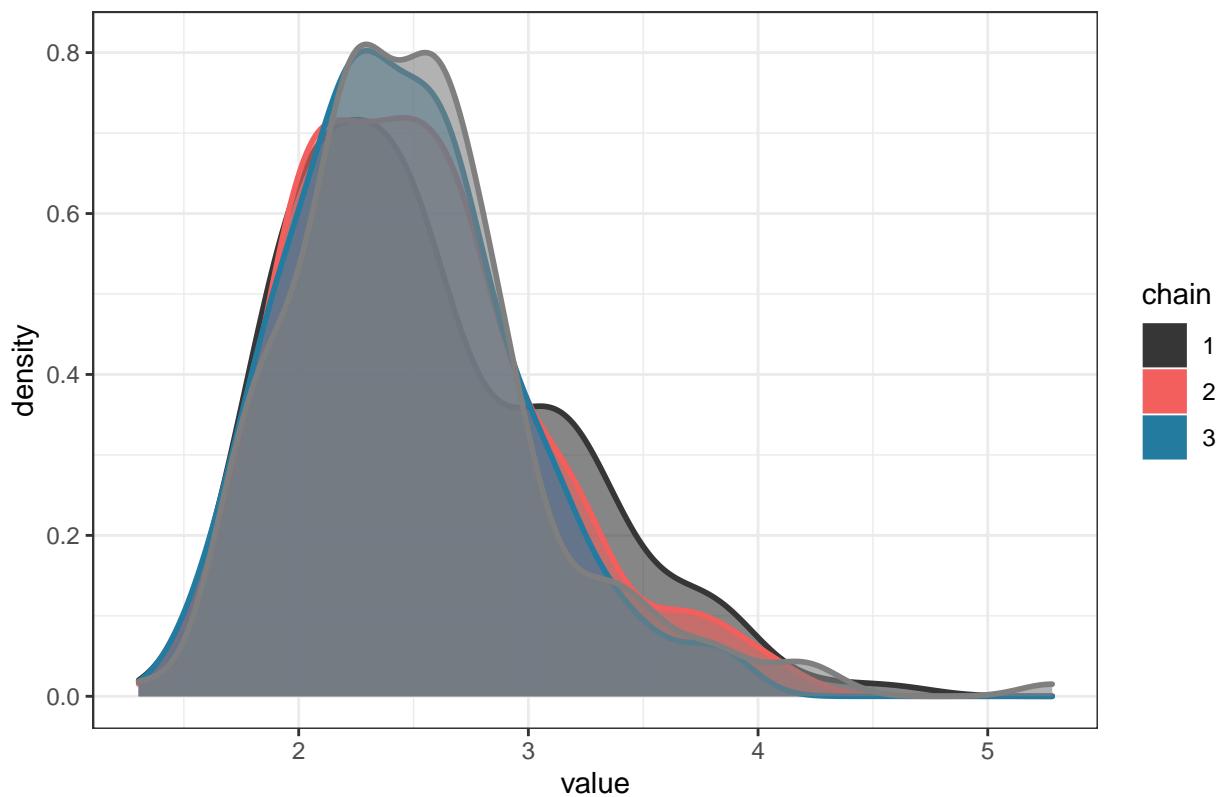
Density plot of LOWC31.1



Density plot of time

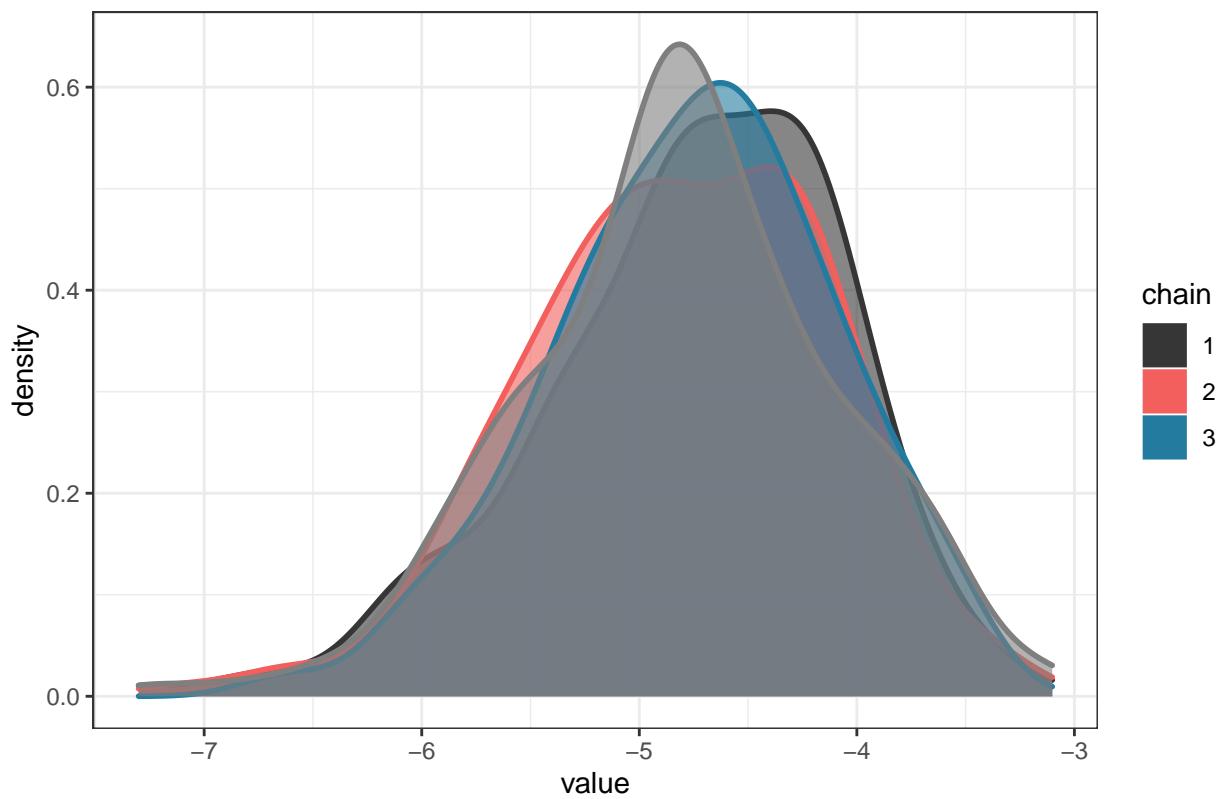


Density plot of sigmas_1

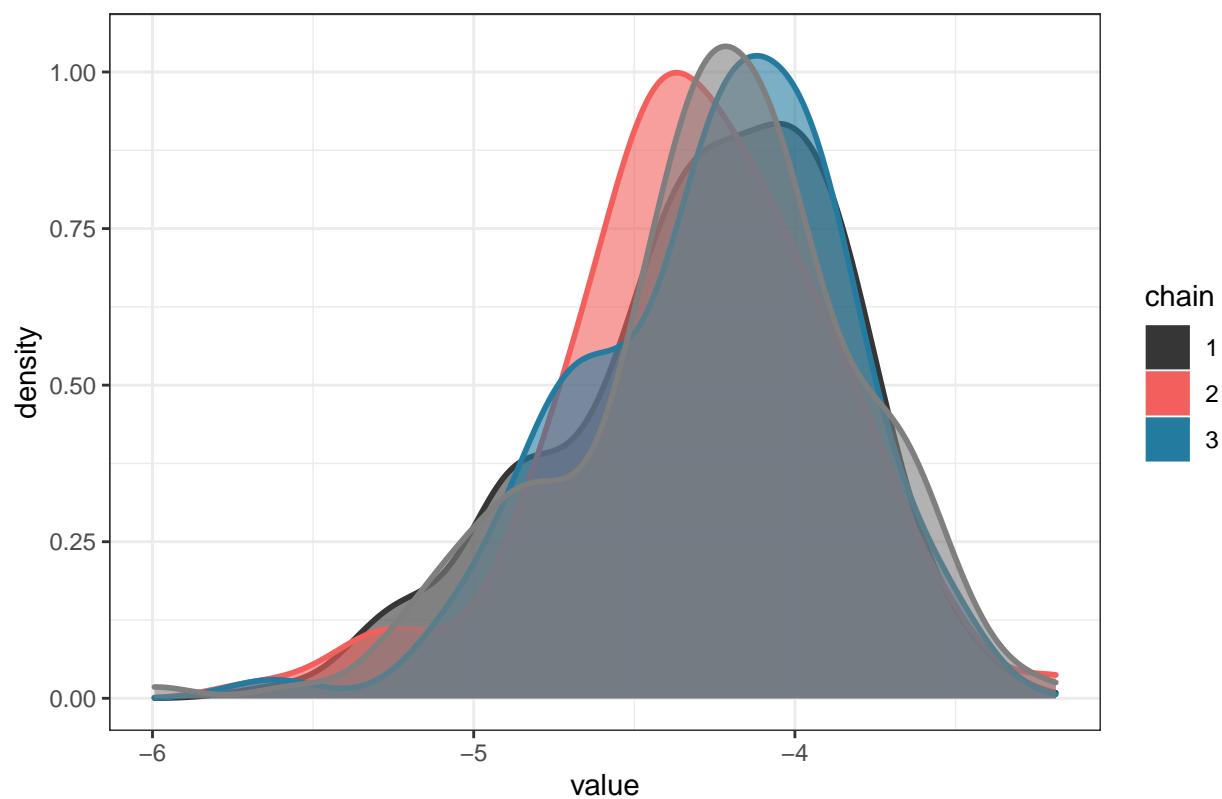


```
densCplt1 <- ggdensityplot(jointCFit1)
```

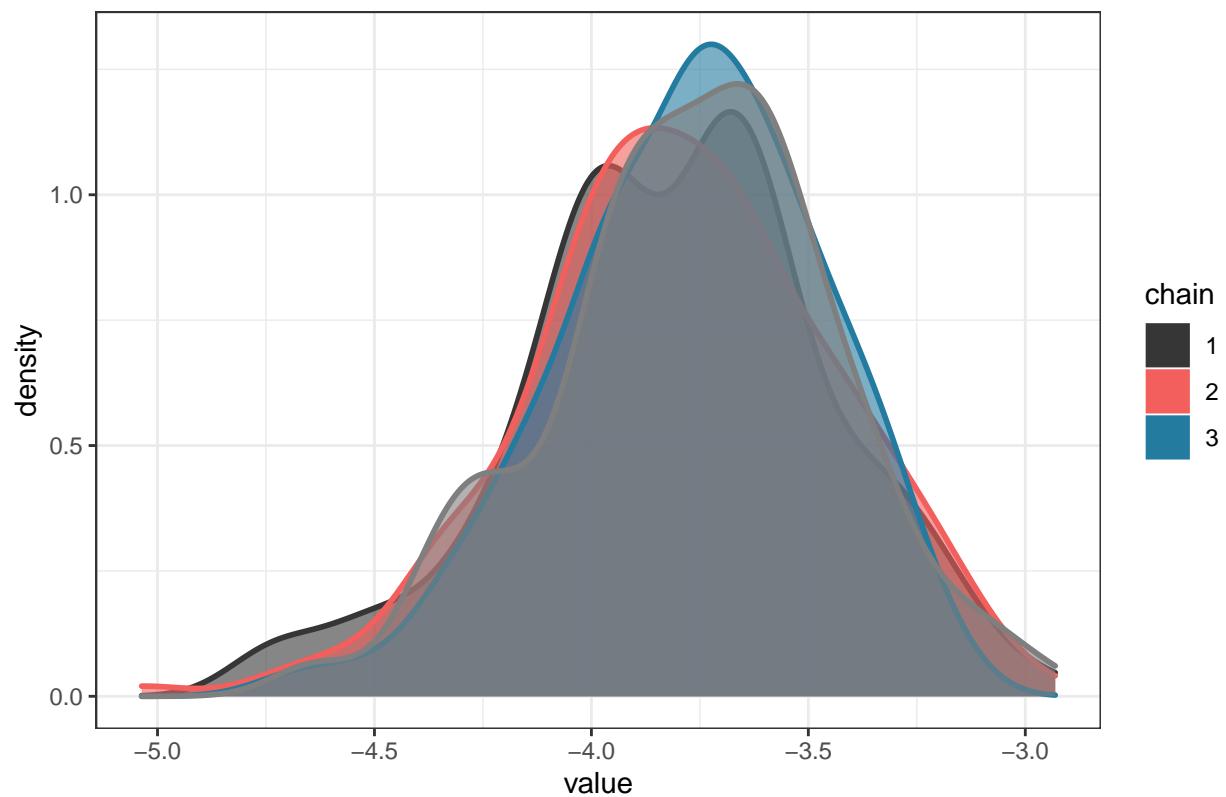
Density plot of bs_gammas_1



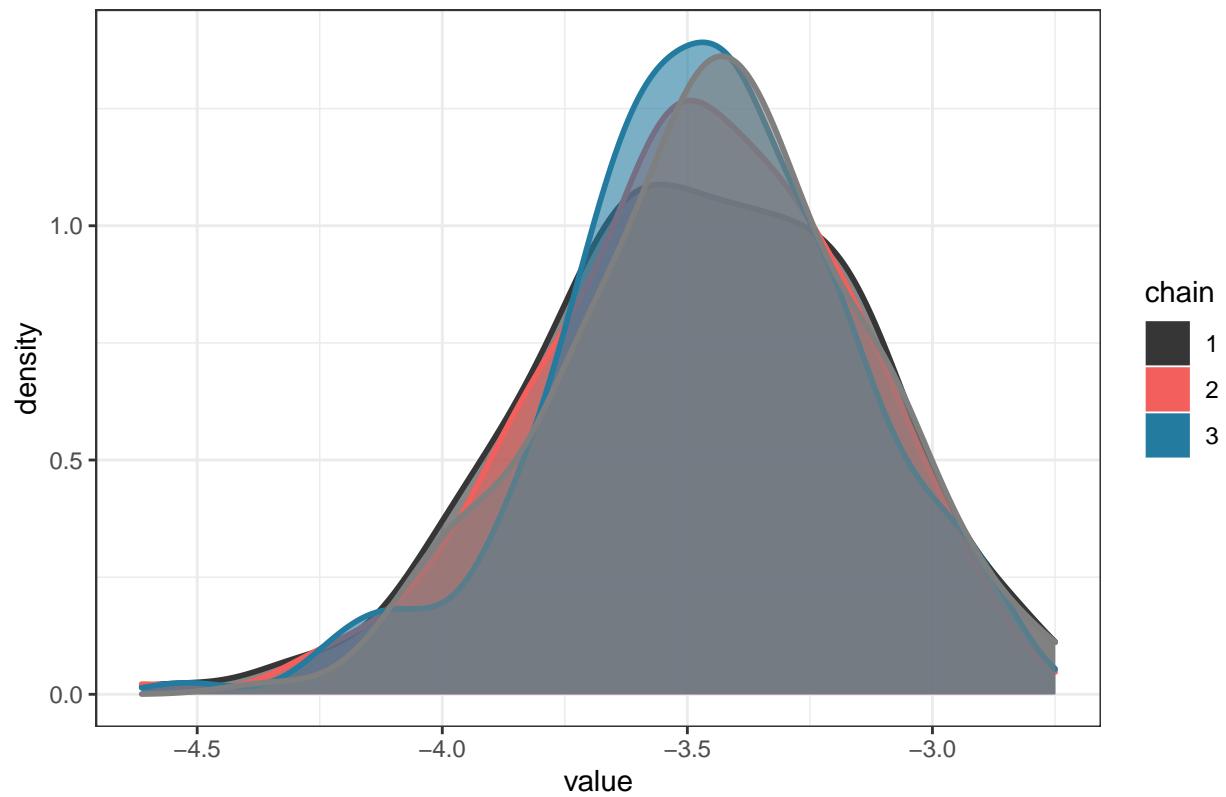
Density plot of bs_gammas_2



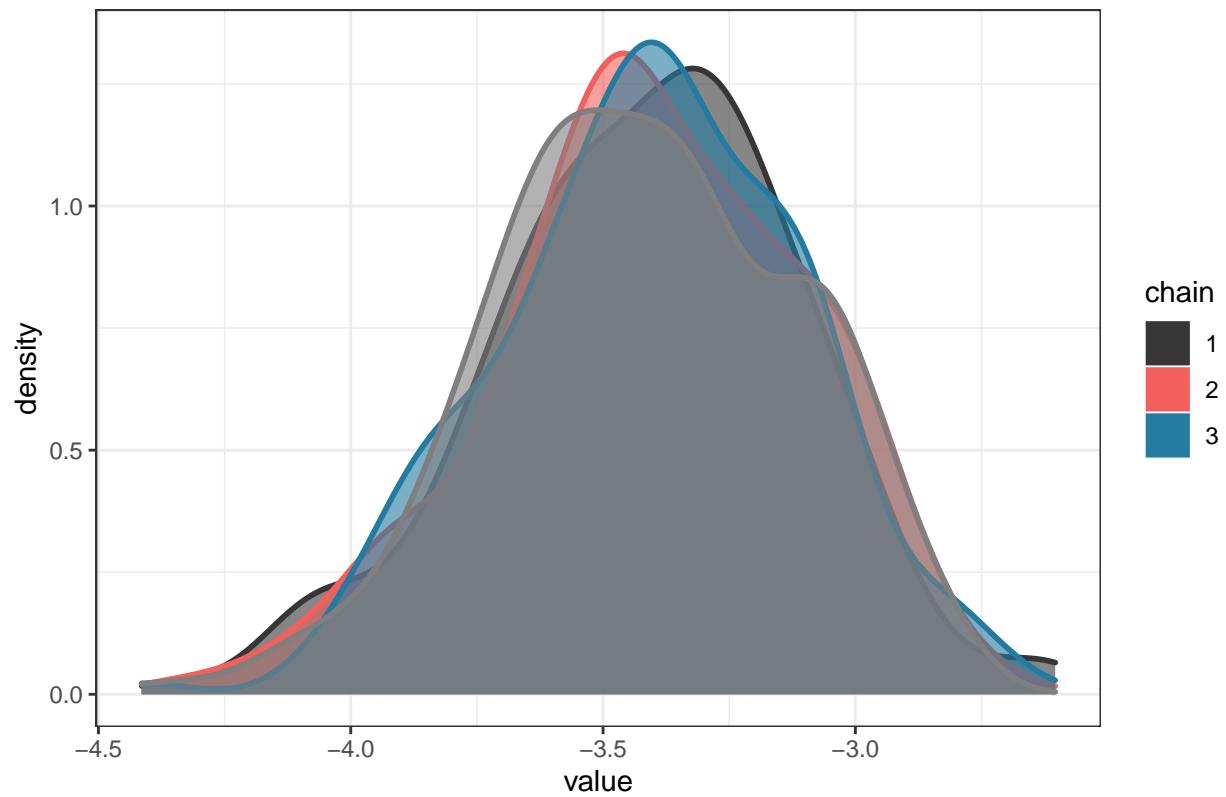
Density plot of bs_gammas_3



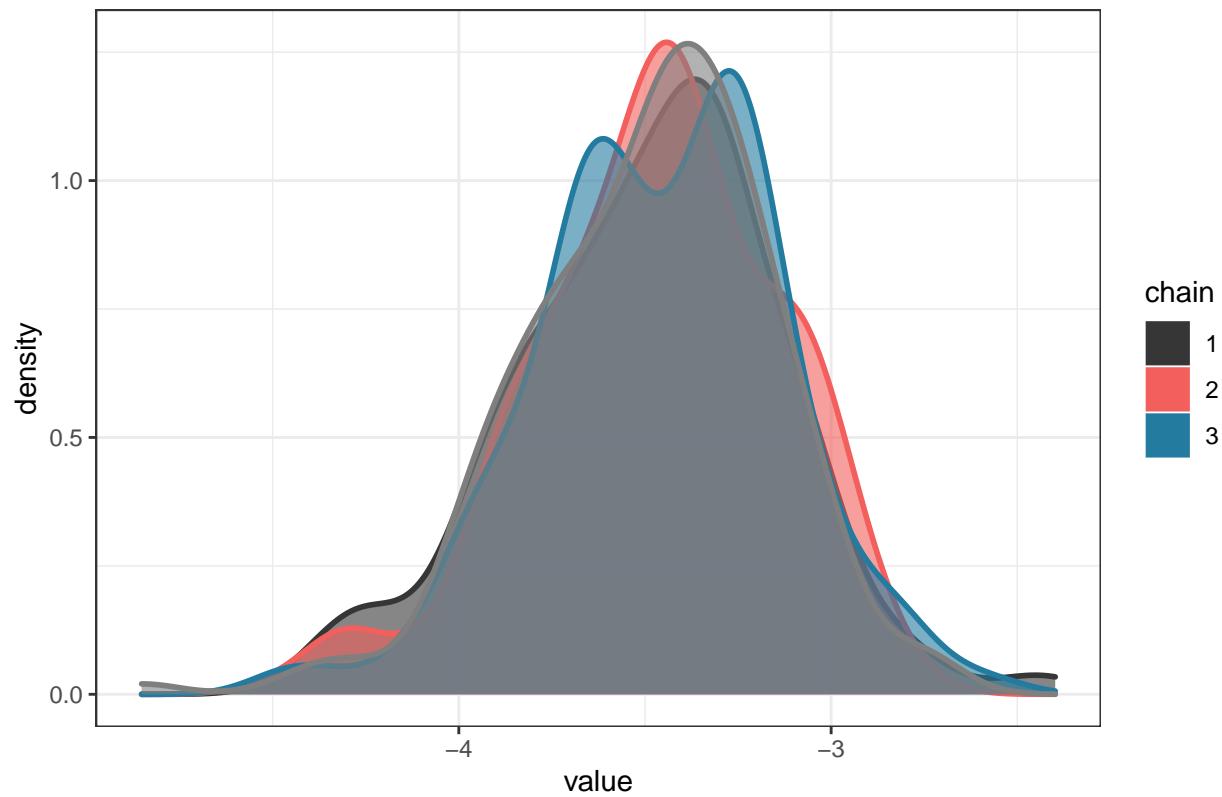
Density plot of bs_gammas_4



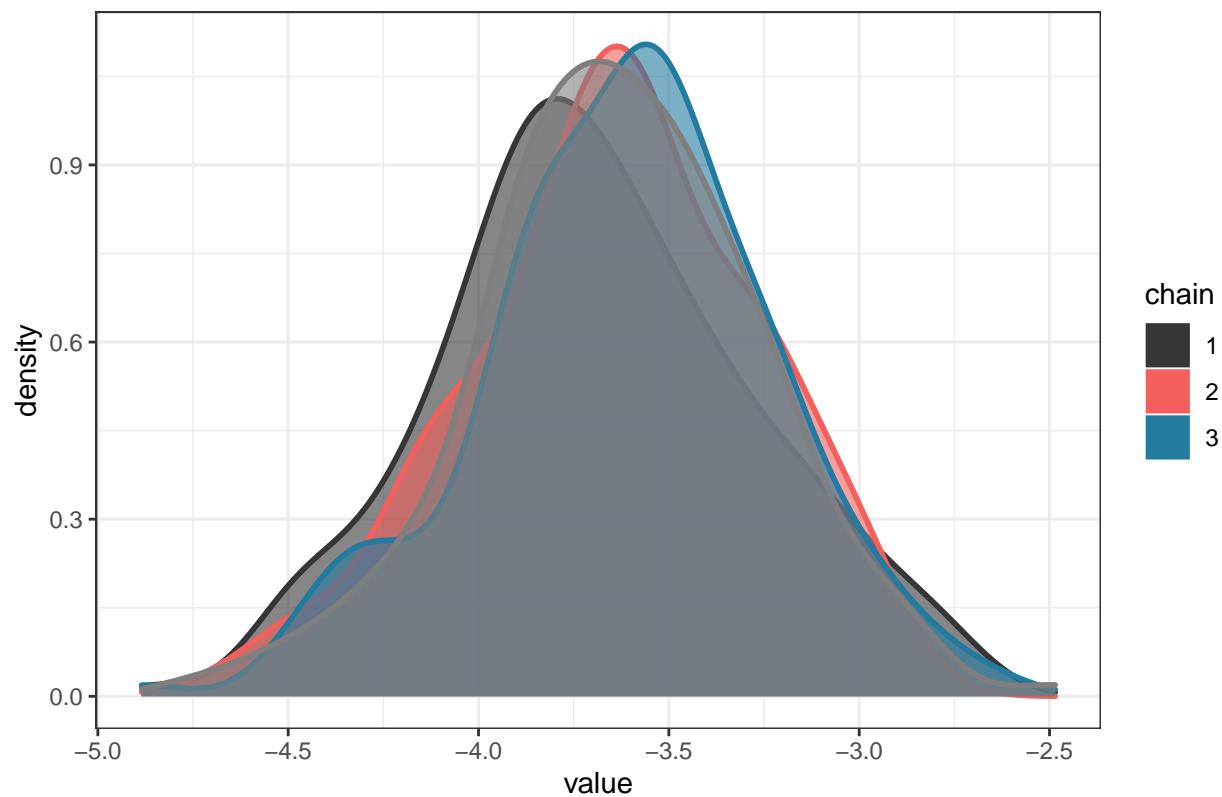
Density plot of bs_gammas_5



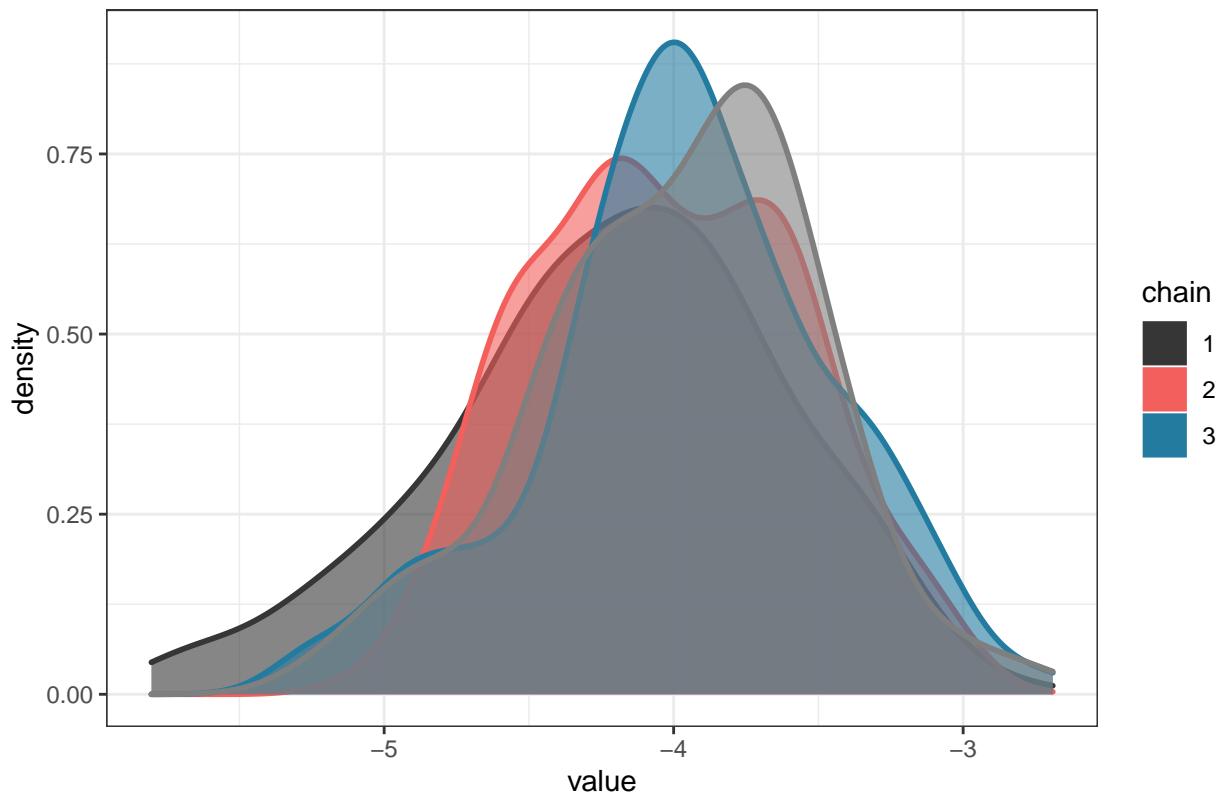
Density plot of bs_gammas_6



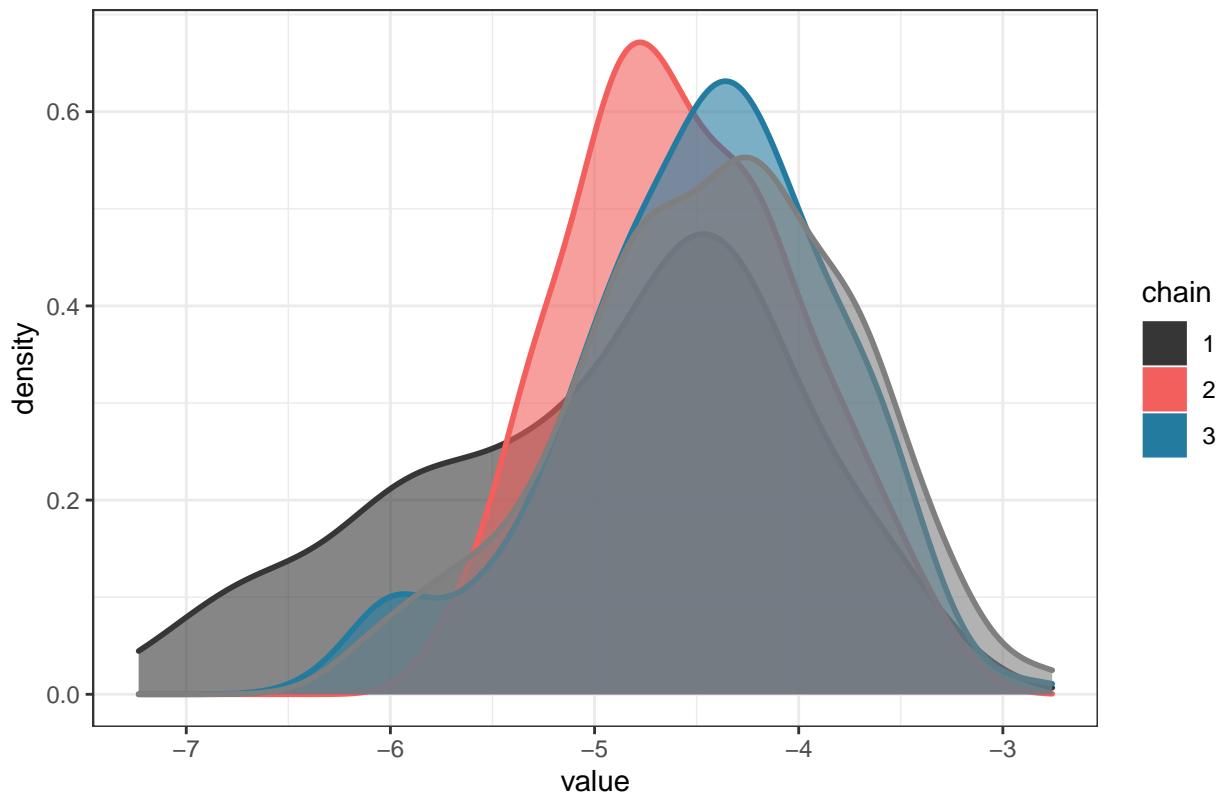
Density plot of bs_gammas_7



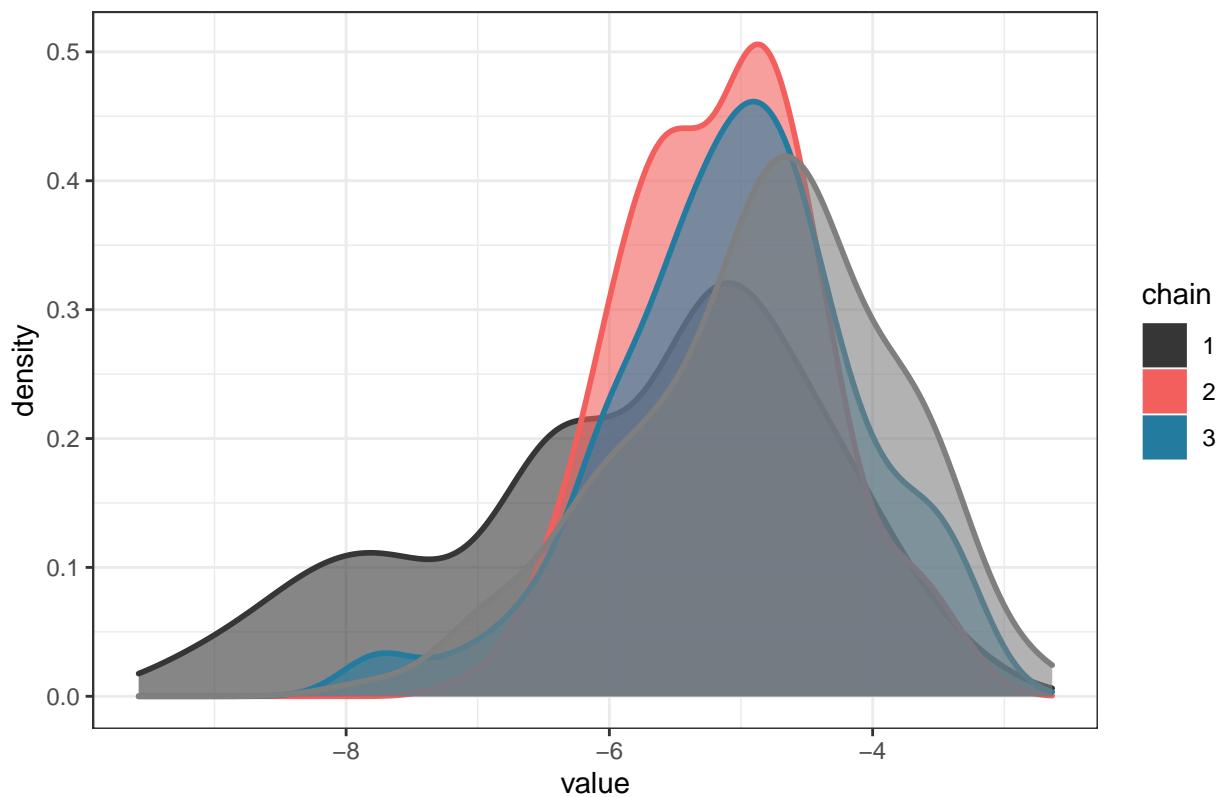
Density plot of bs_gammas_8



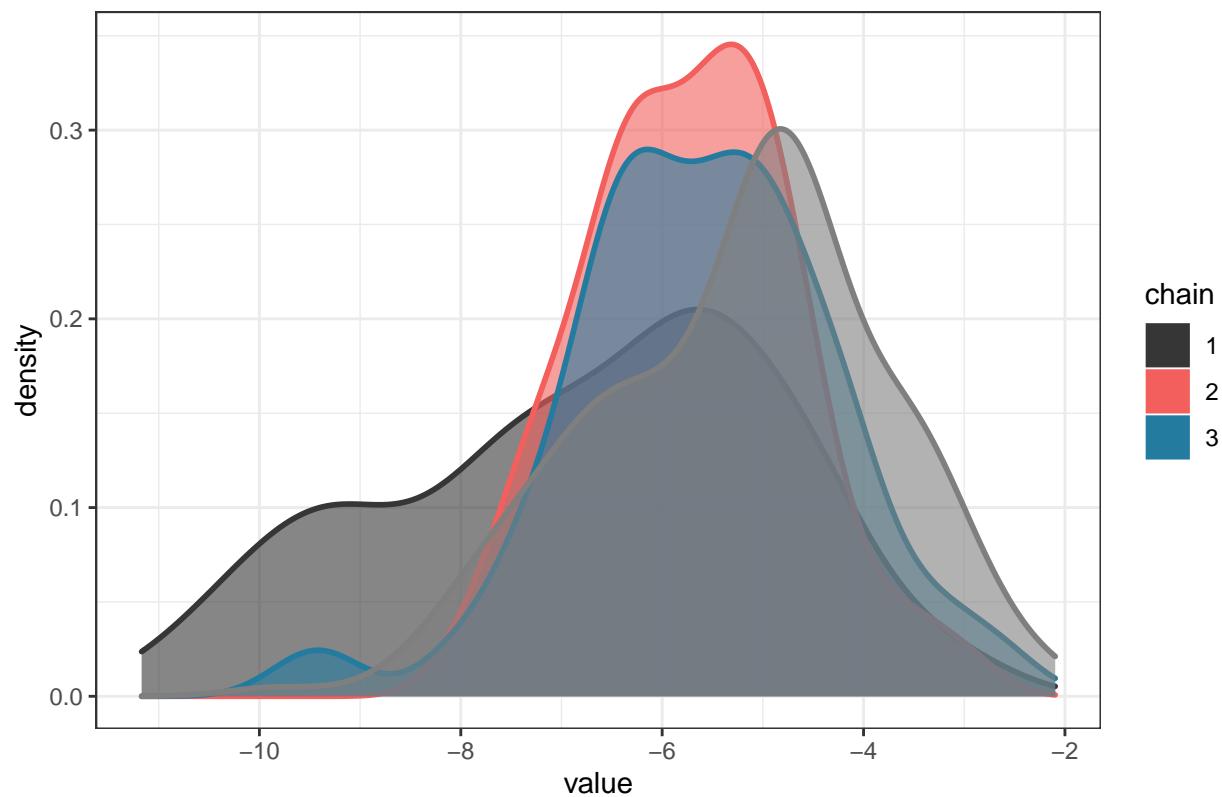
Density plot of bs_gammas_9



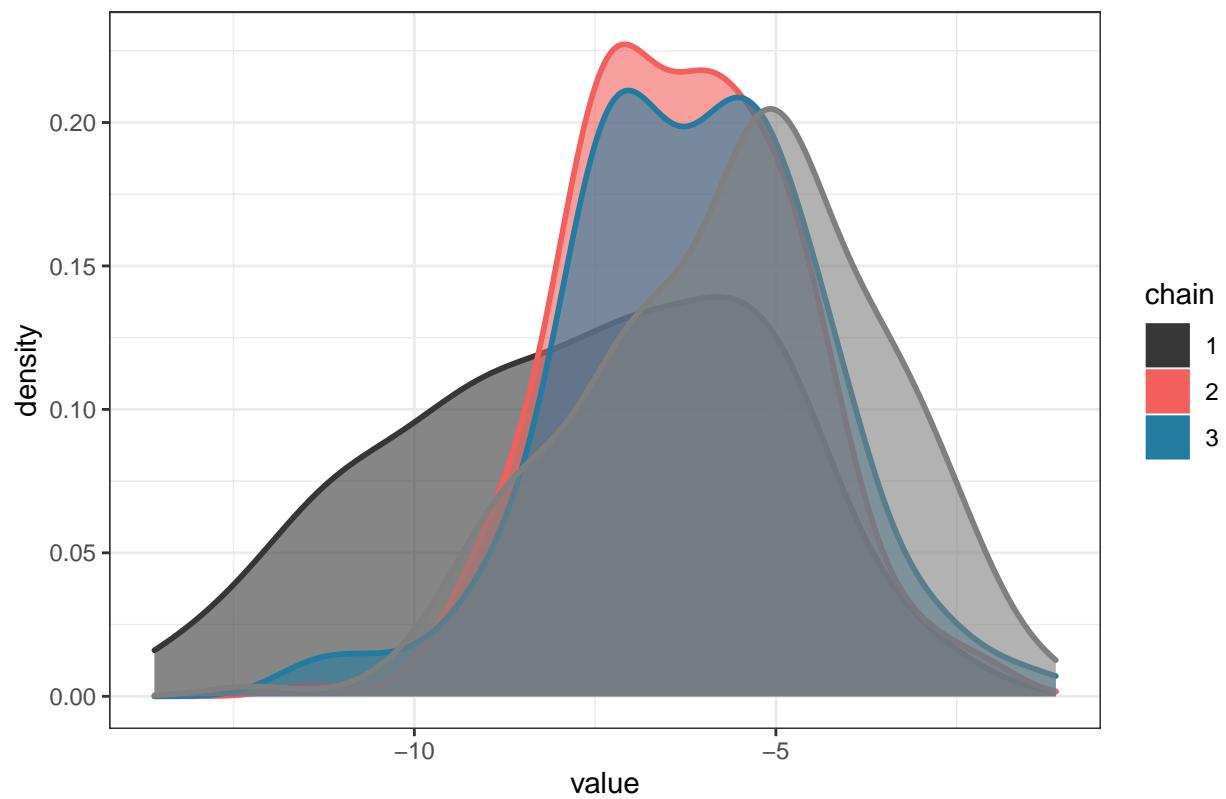
Density plot of bs_gammas_10



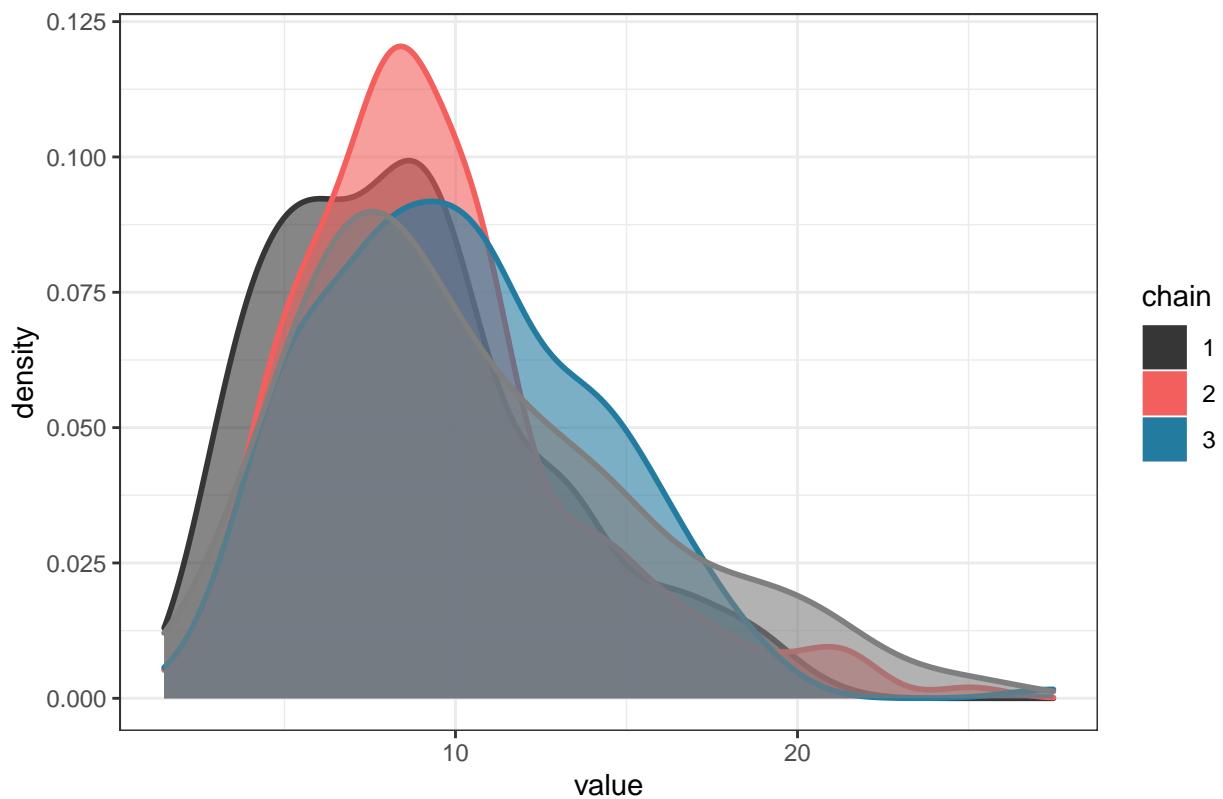
Density plot of bs_gammas_11



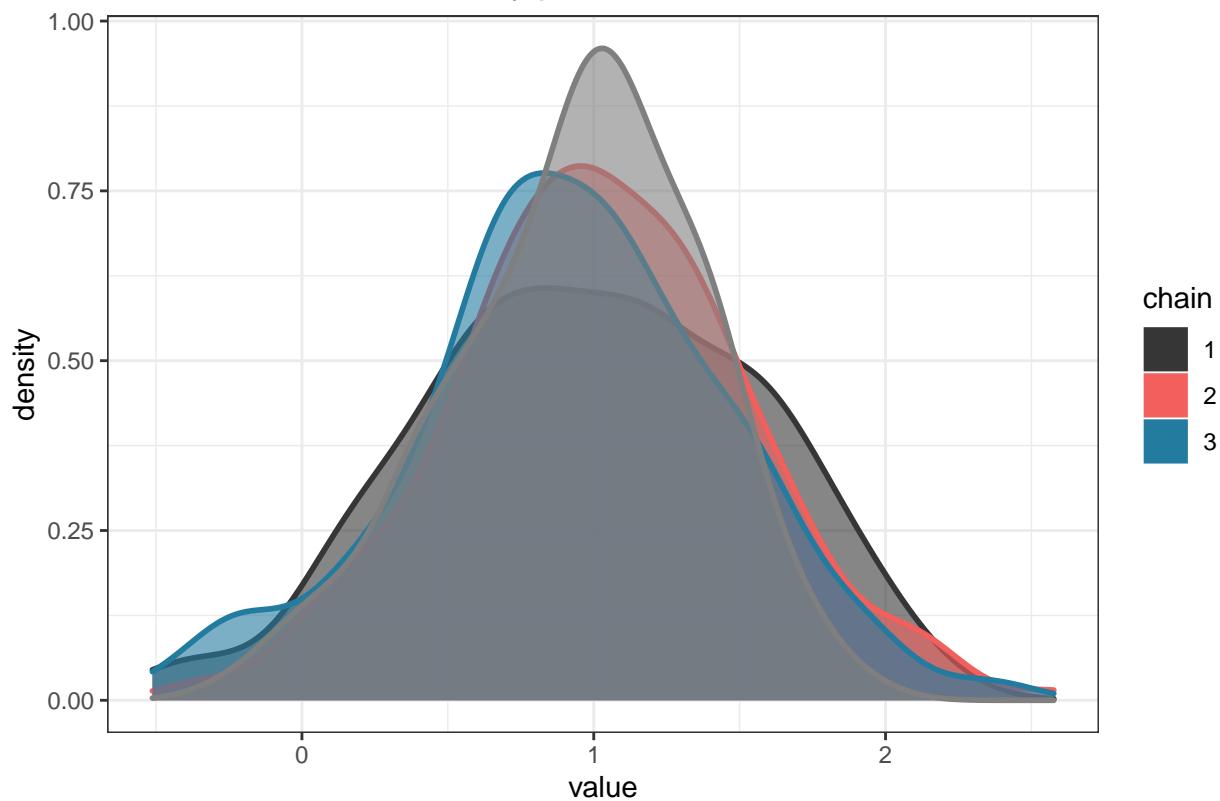
Density plot of bs_gammas_12



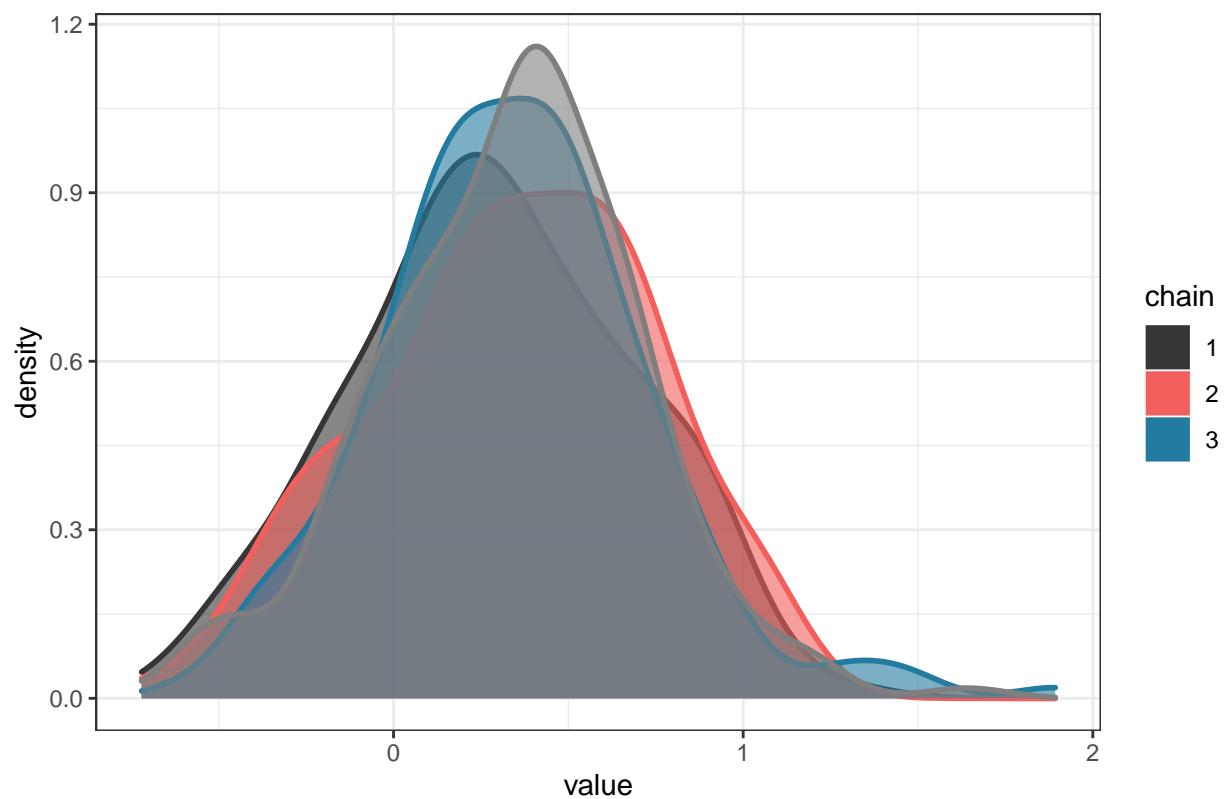
Density plot of tau_bs_gammas



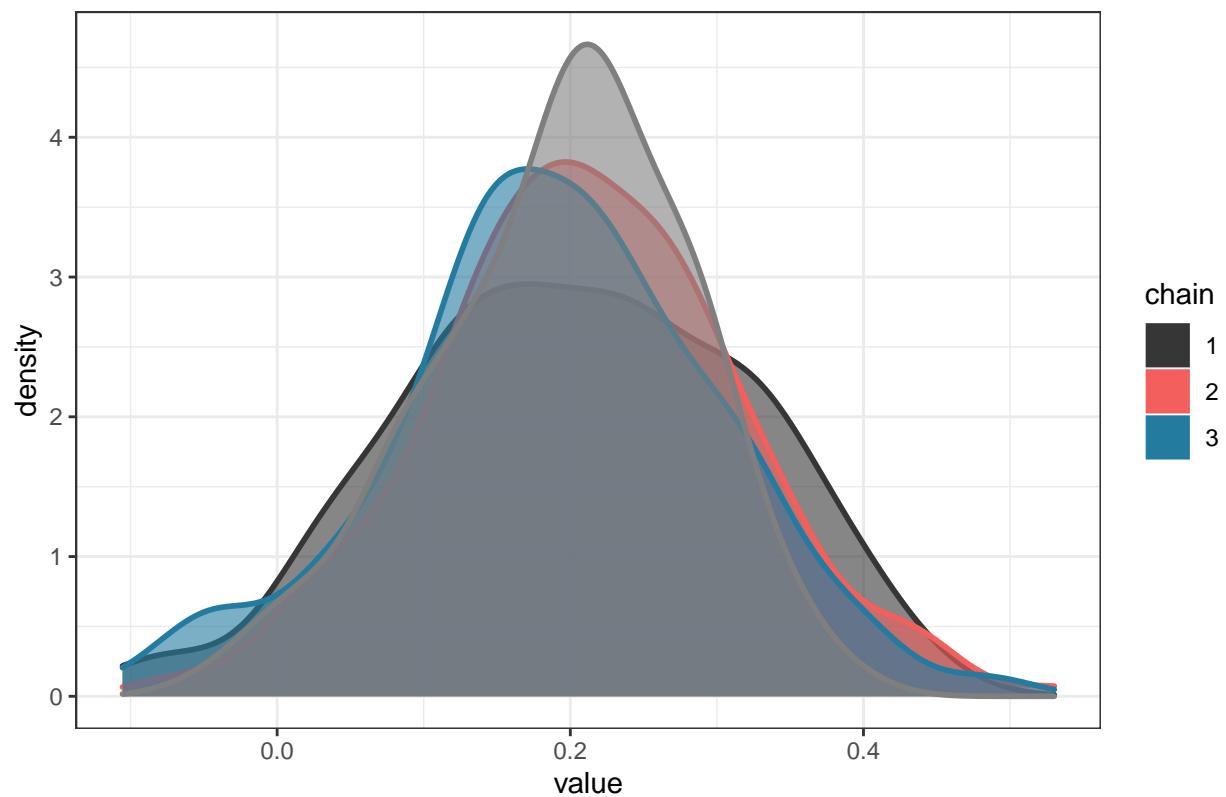
Density plot of LOWC31



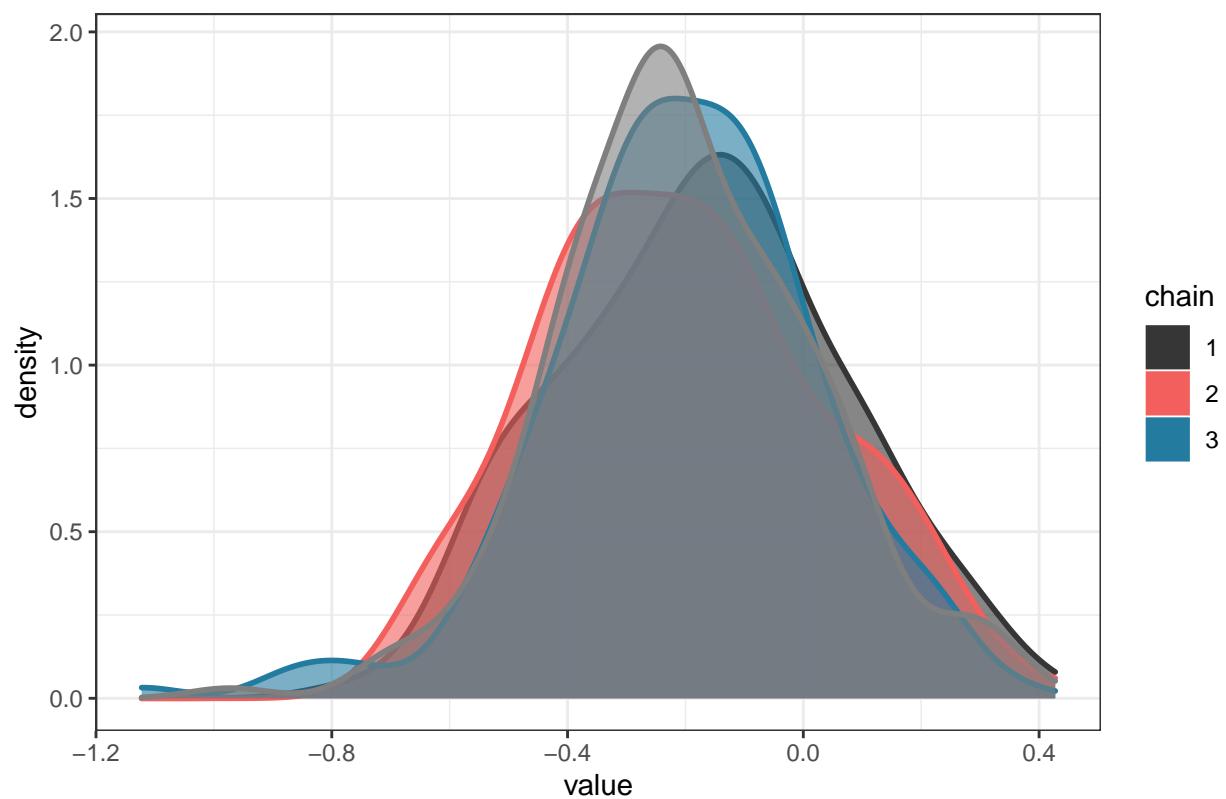
Density plot of slope(eGFR)



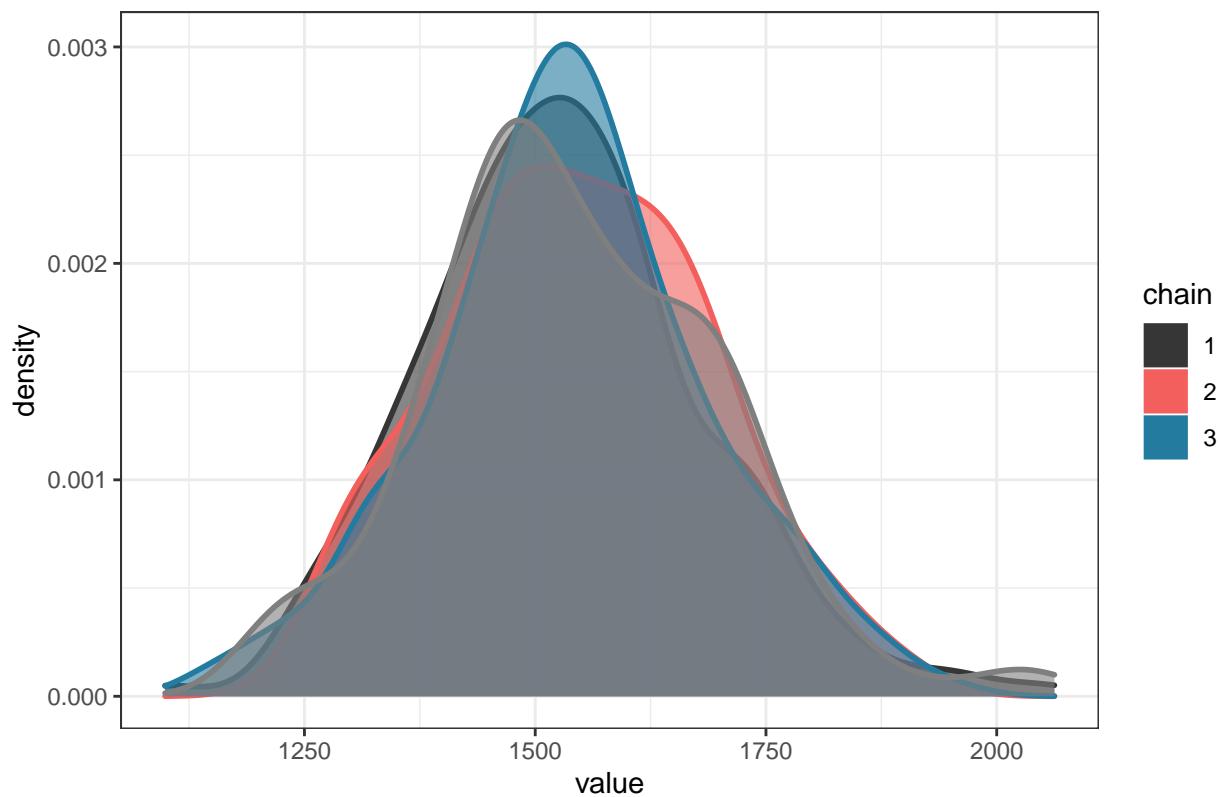
Density plot of



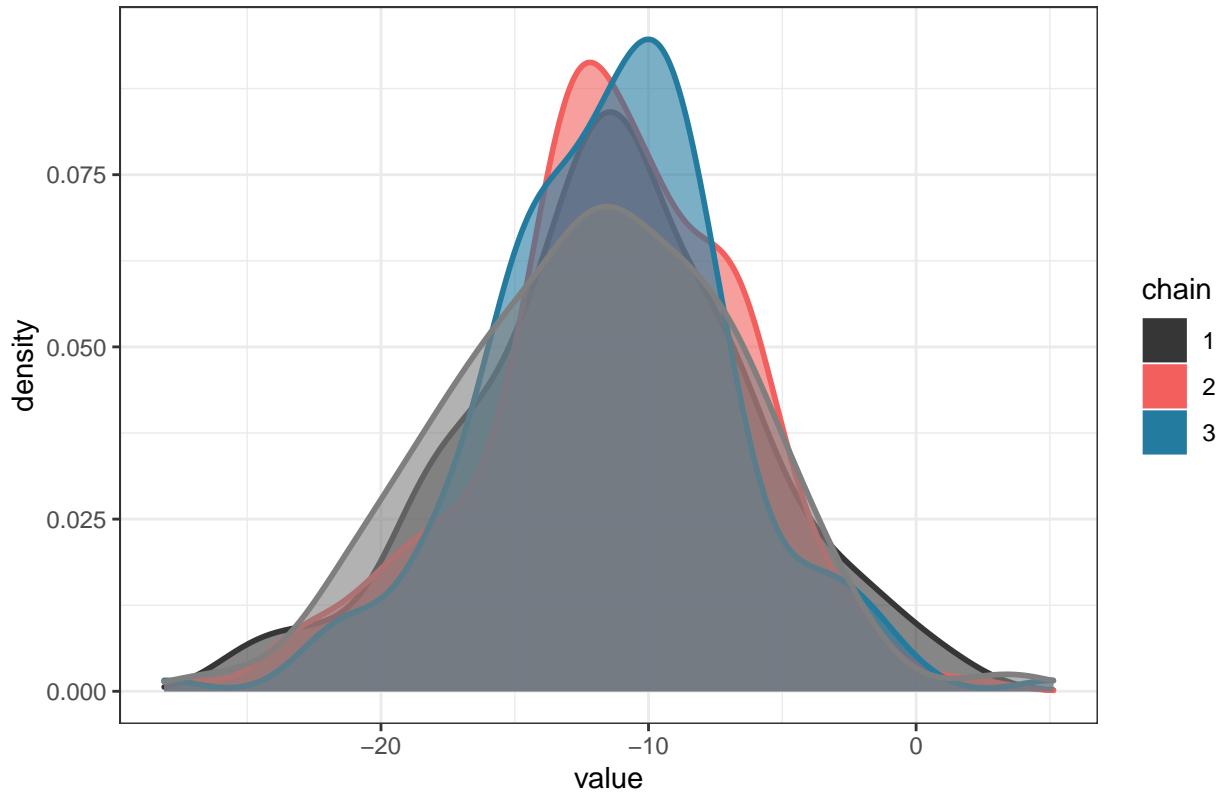
Density plot of .1



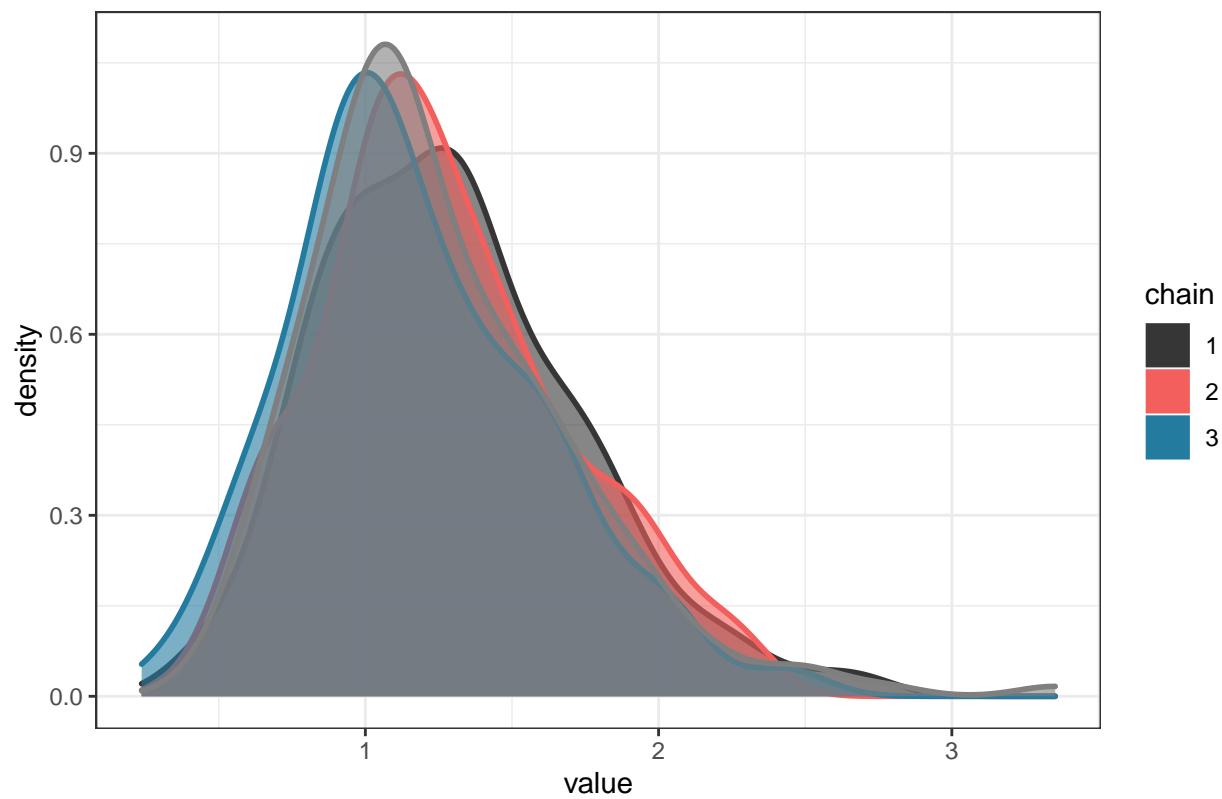
Density plot of $D[1, 1]$



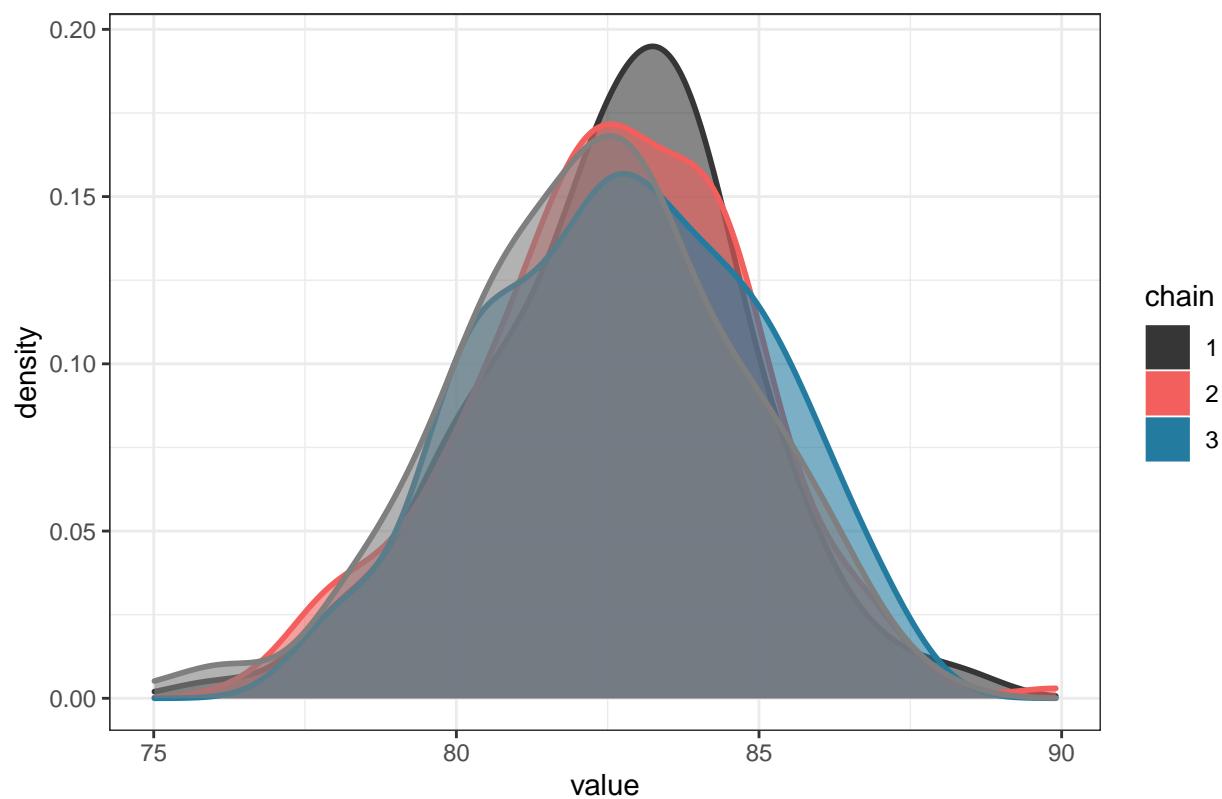
Density plot of $D[2, 1]$



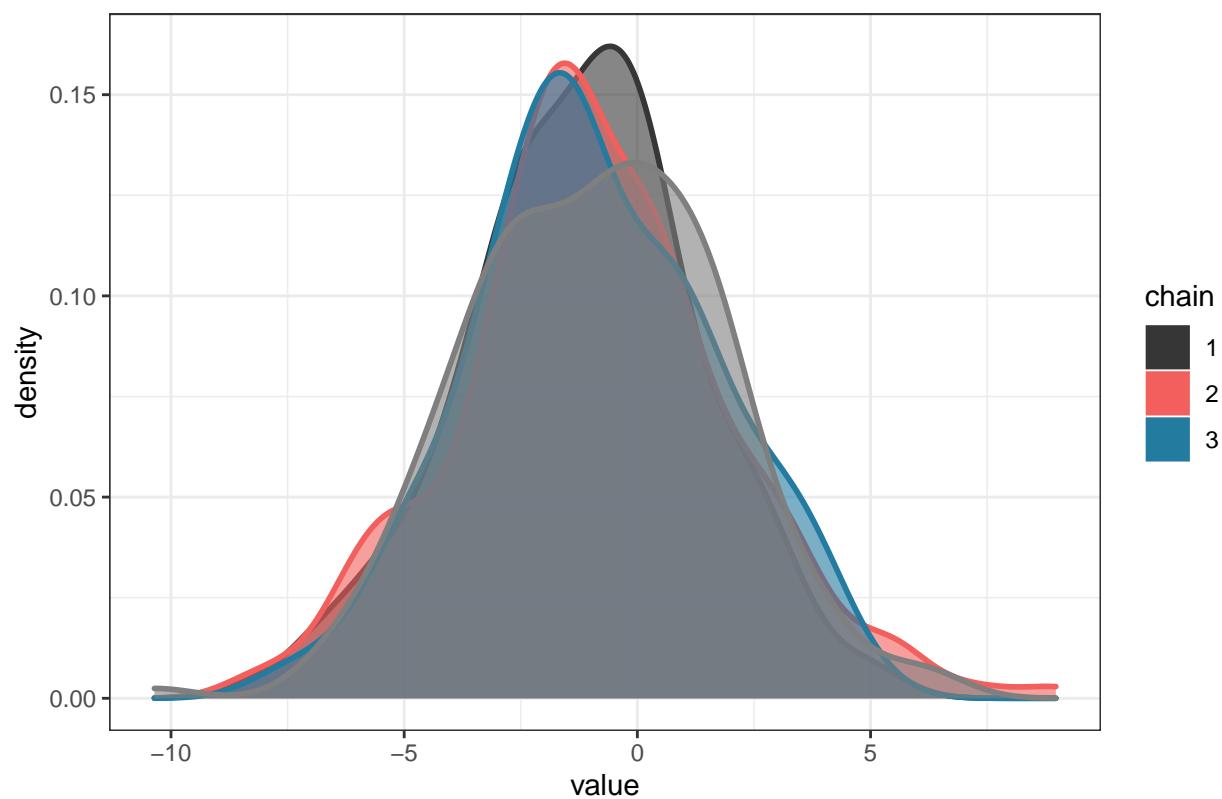
Density plot of $D[2, 2]$



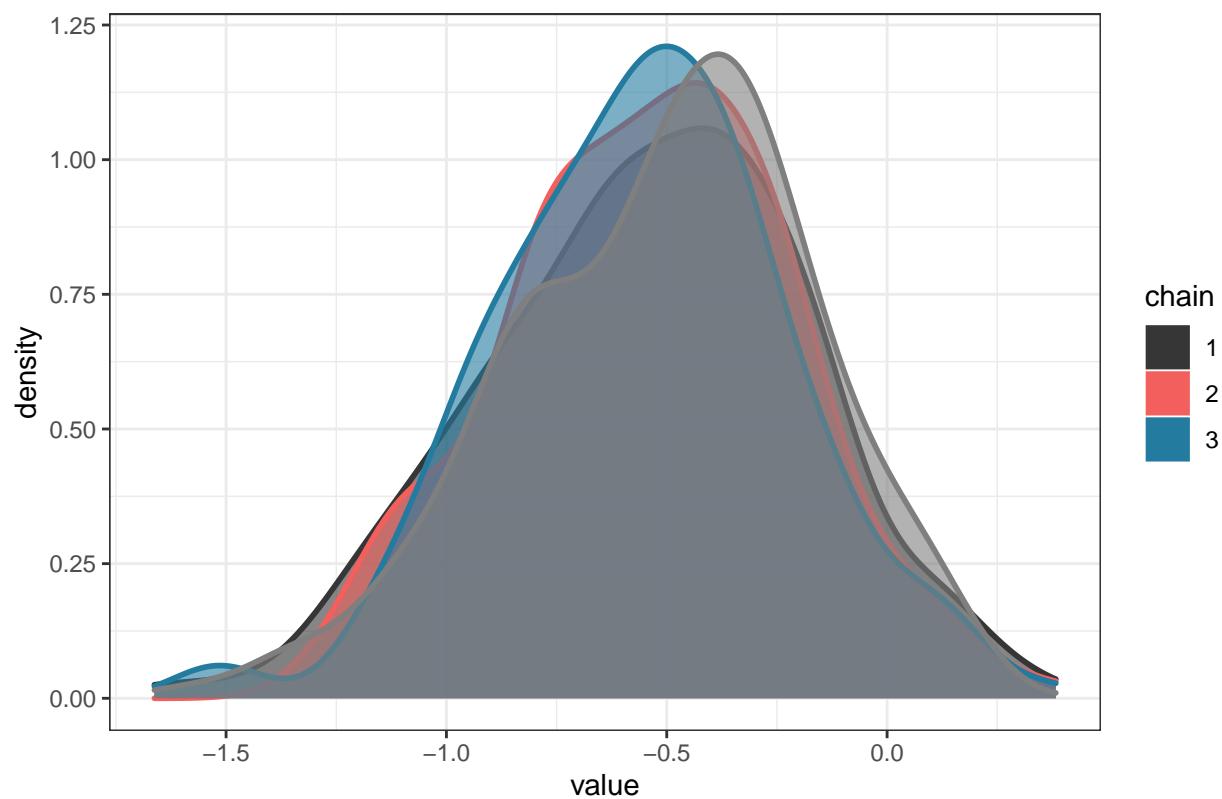
Density plot of (Intercept)



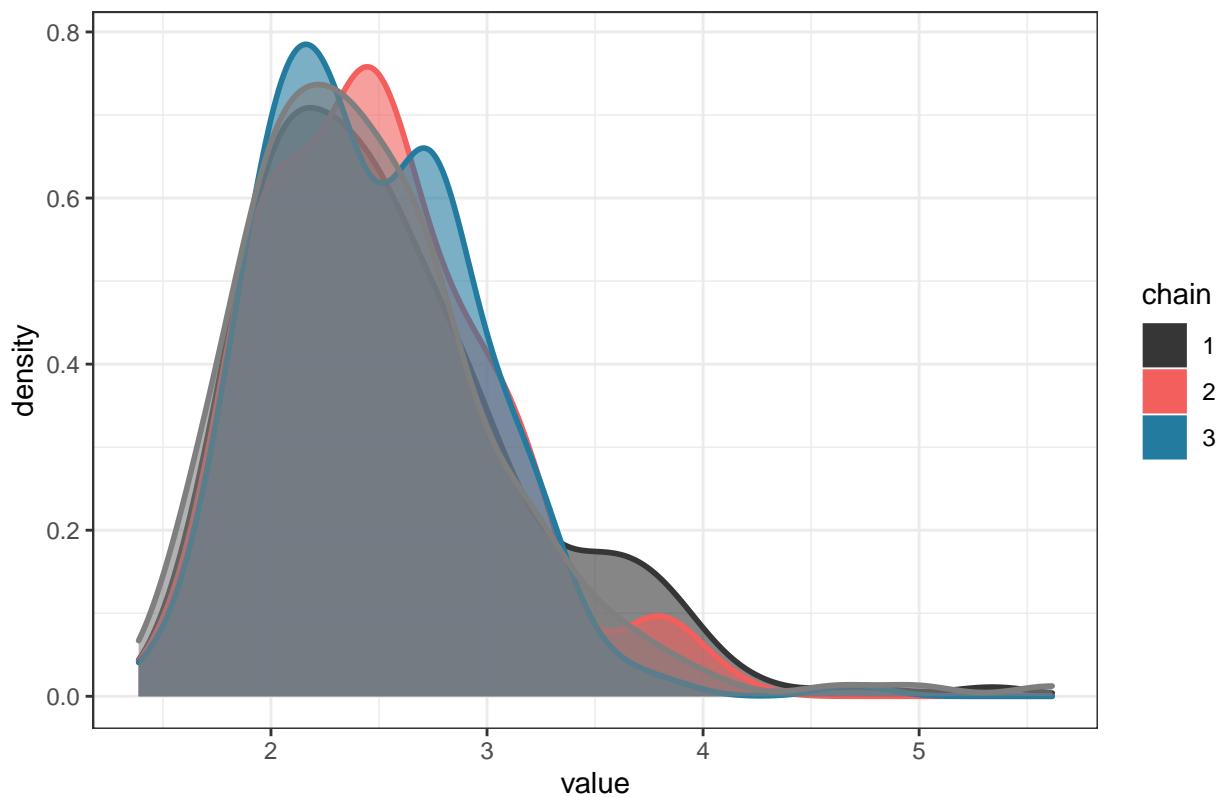
Density plot of LOWC31.1



Density plot of time

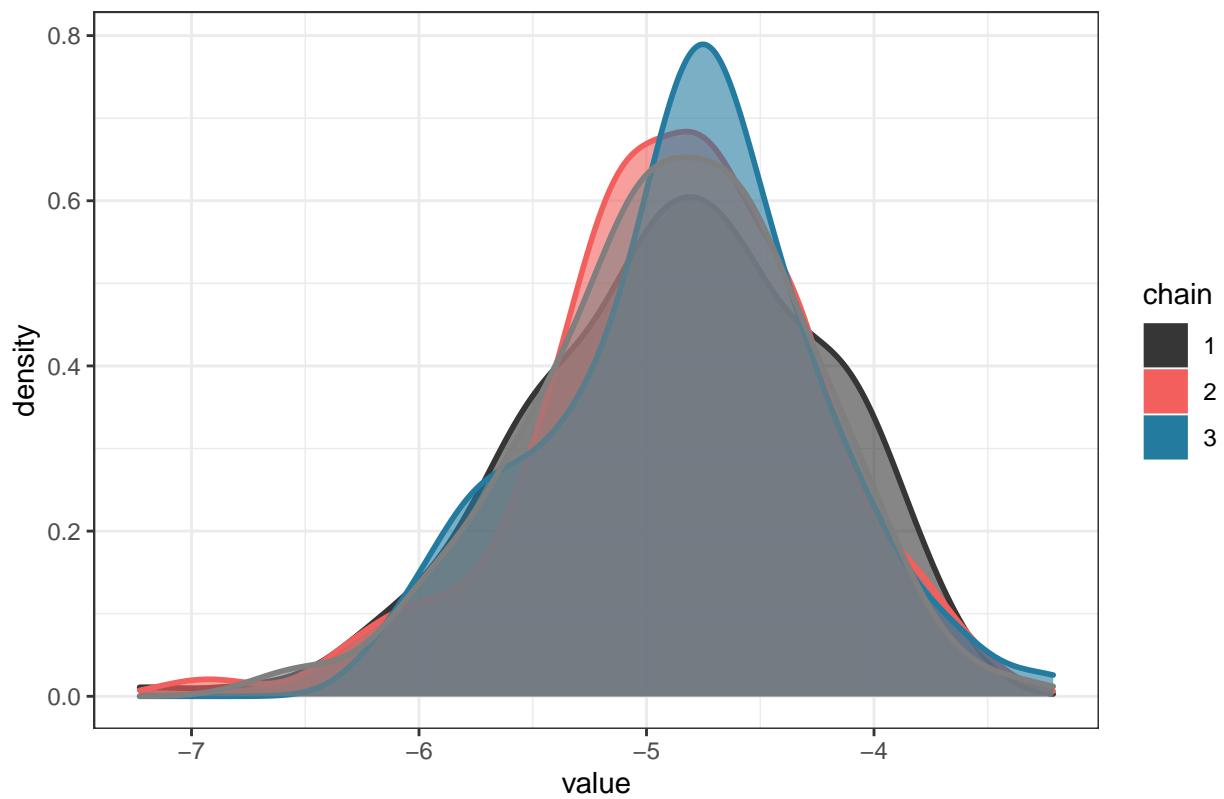


Density plot of sigmas_1

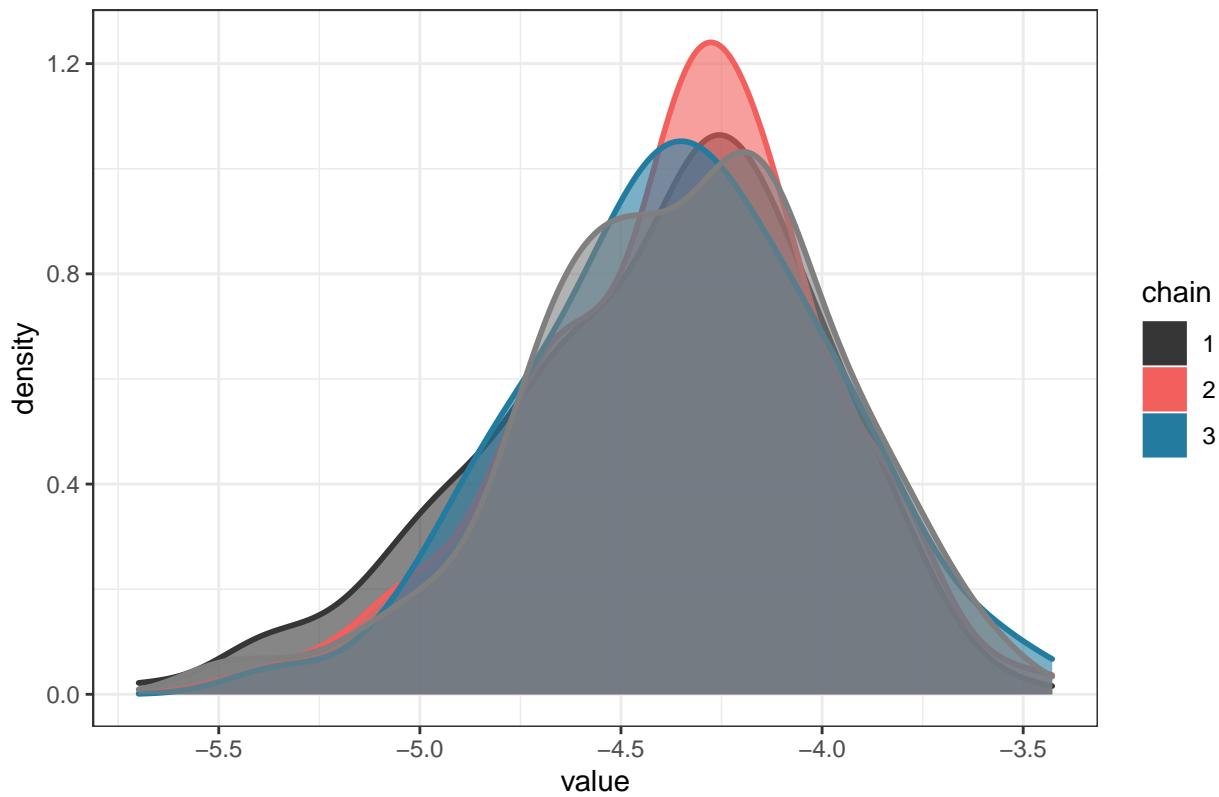


```
densCplt2 <- ggdensityplot(jointCFit2)
```

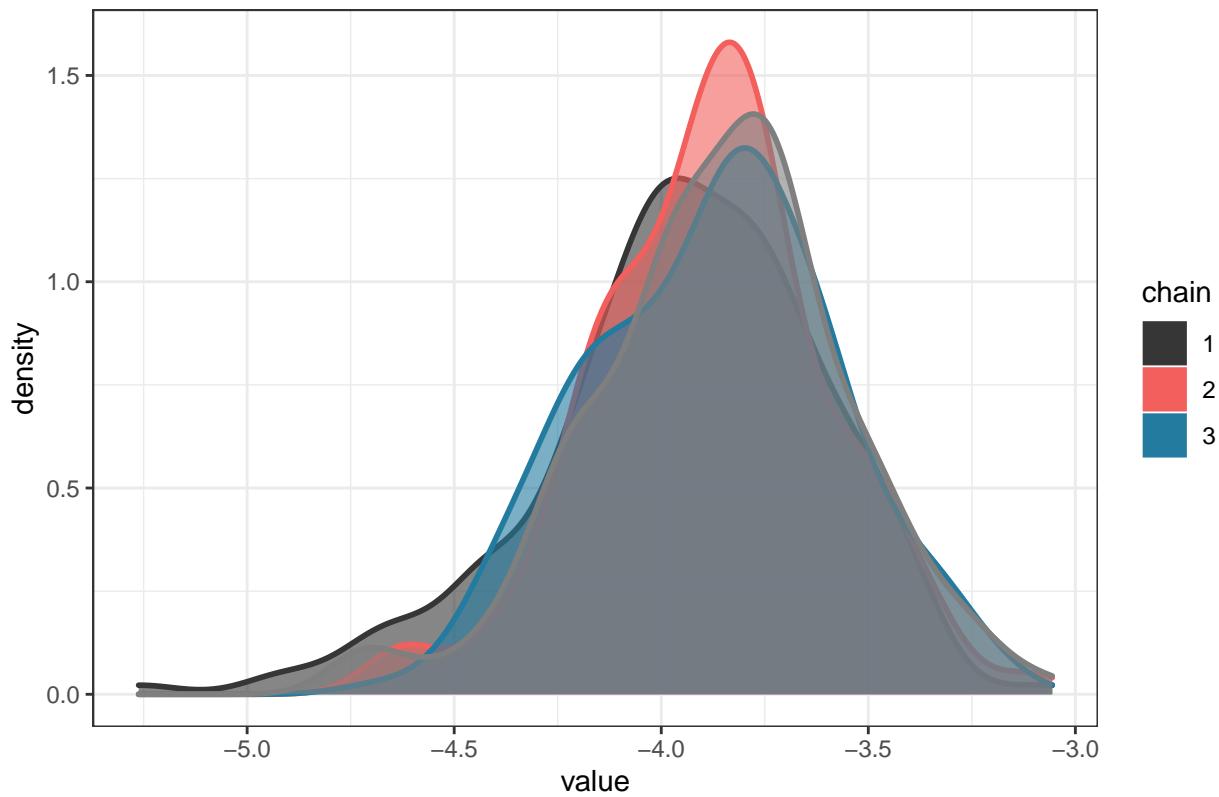
Density plot of bs_gammas_1



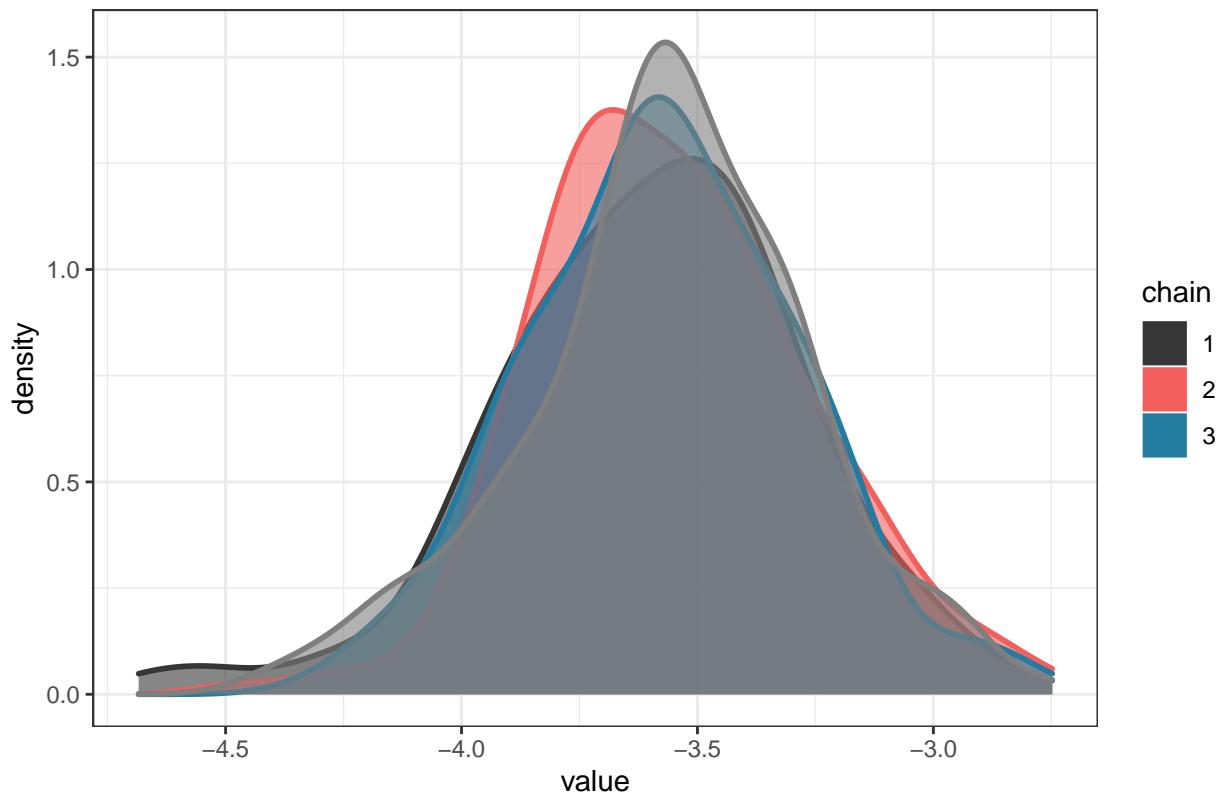
Density plot of bs_gammas_2



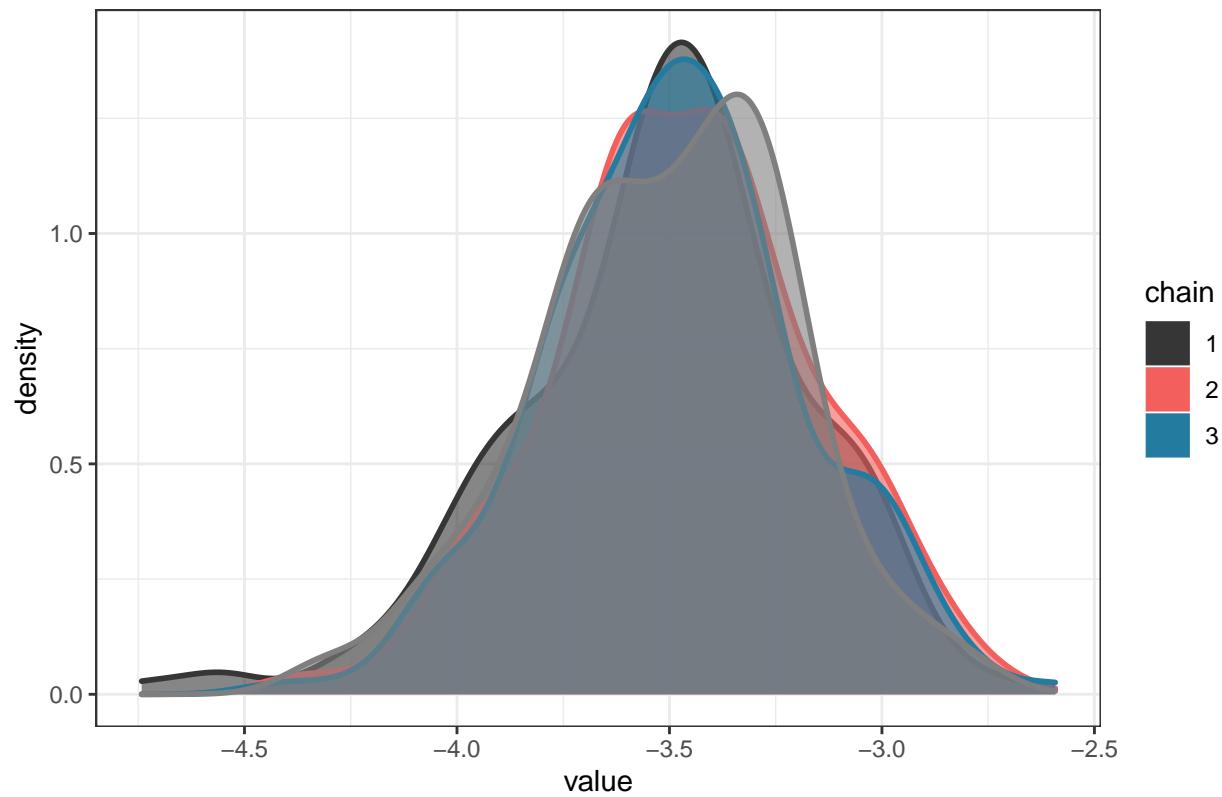
Density plot of bs_gammas_3



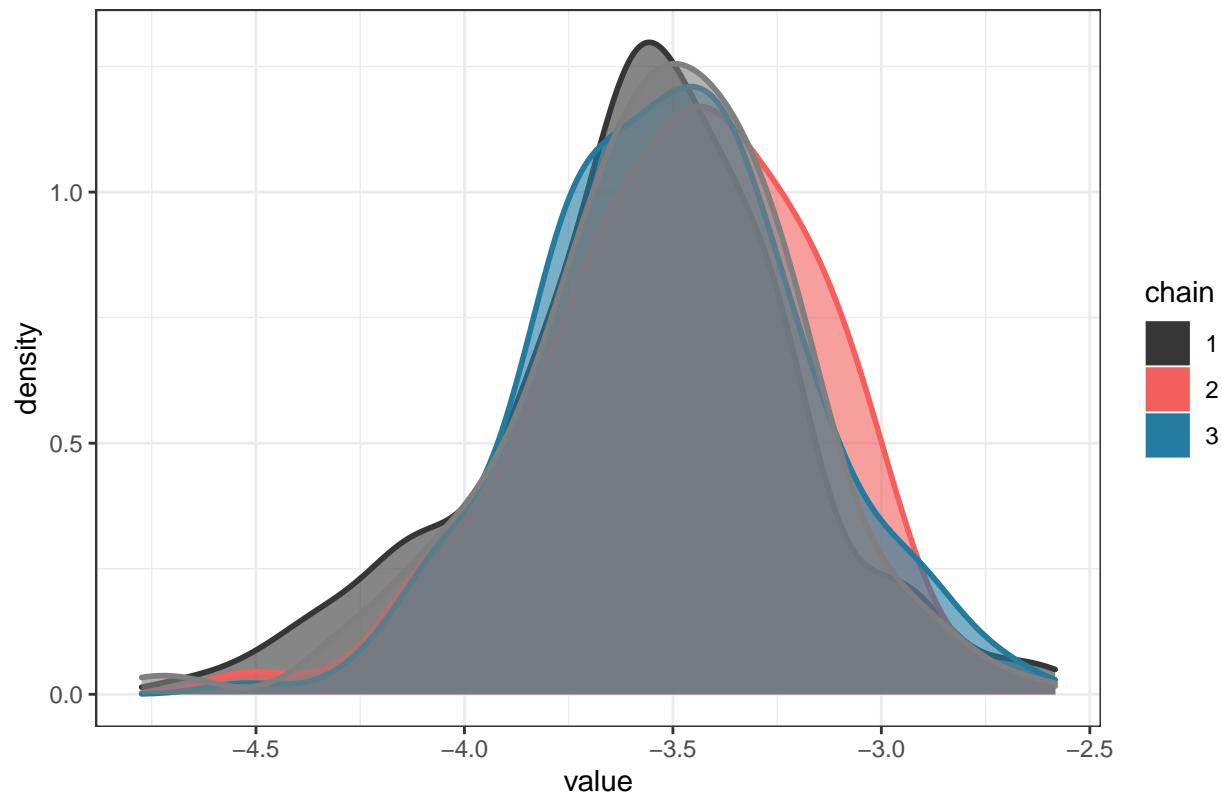
Density plot of bs_gammas_4



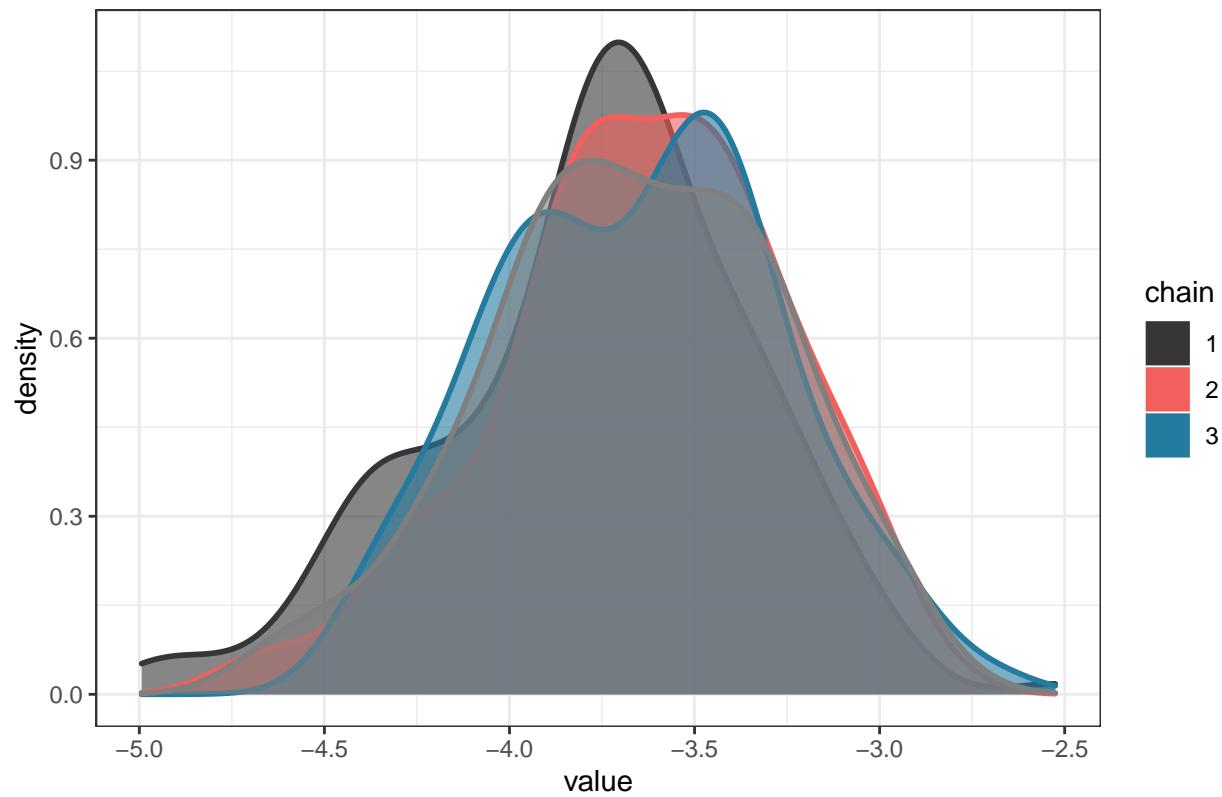
Density plot of bs_gammas_5



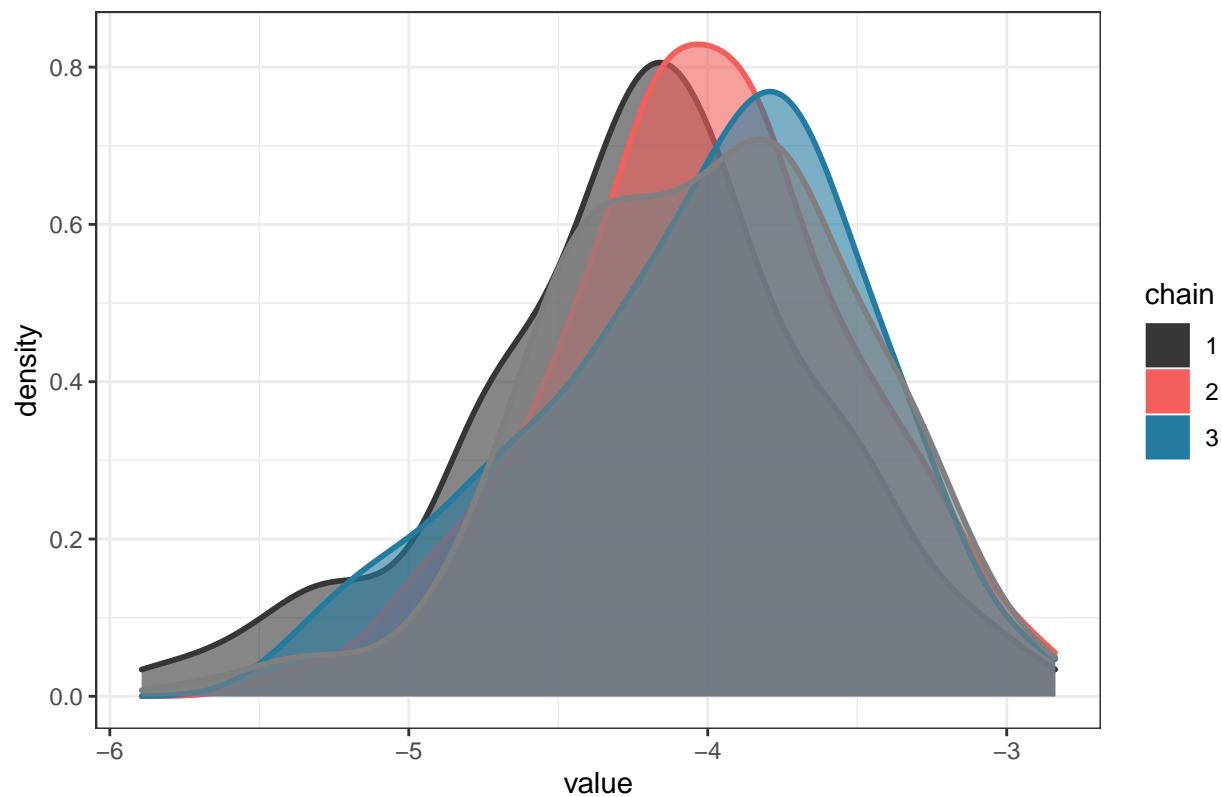
Density plot of bs_gammas_6



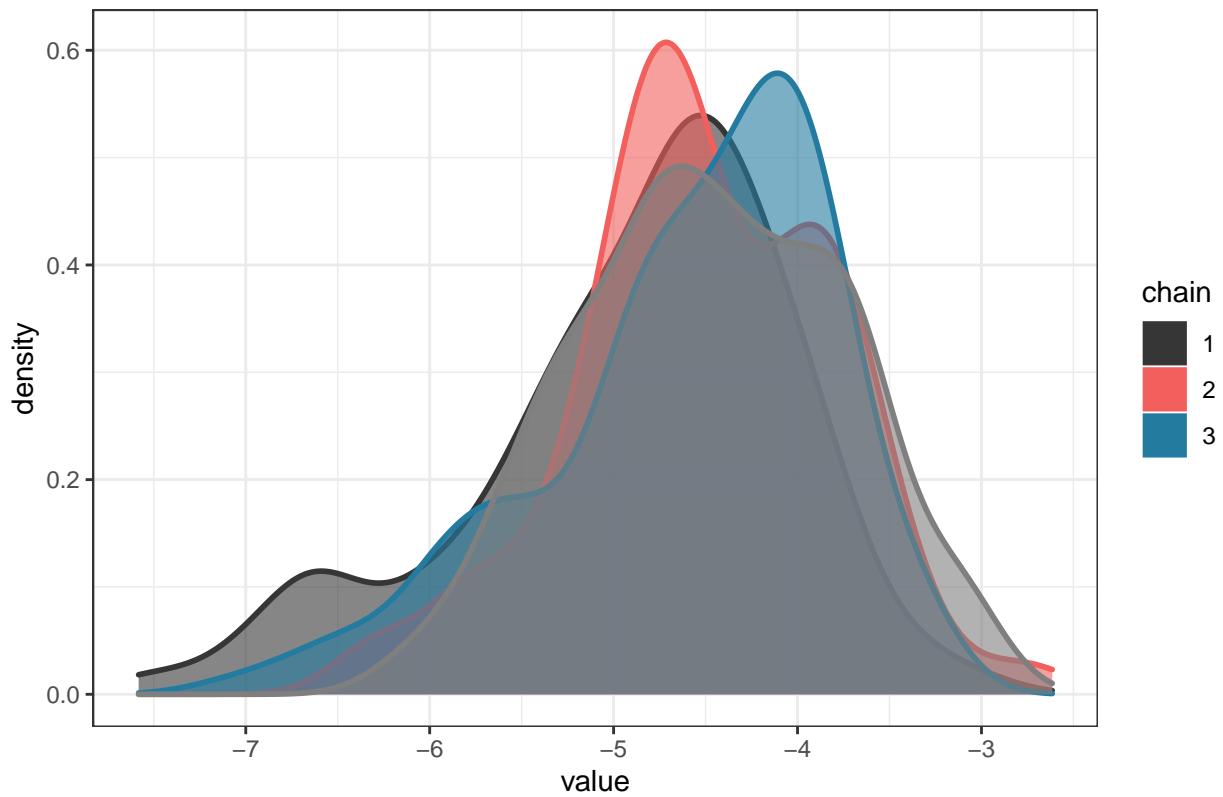
Density plot of bs_gammas_7



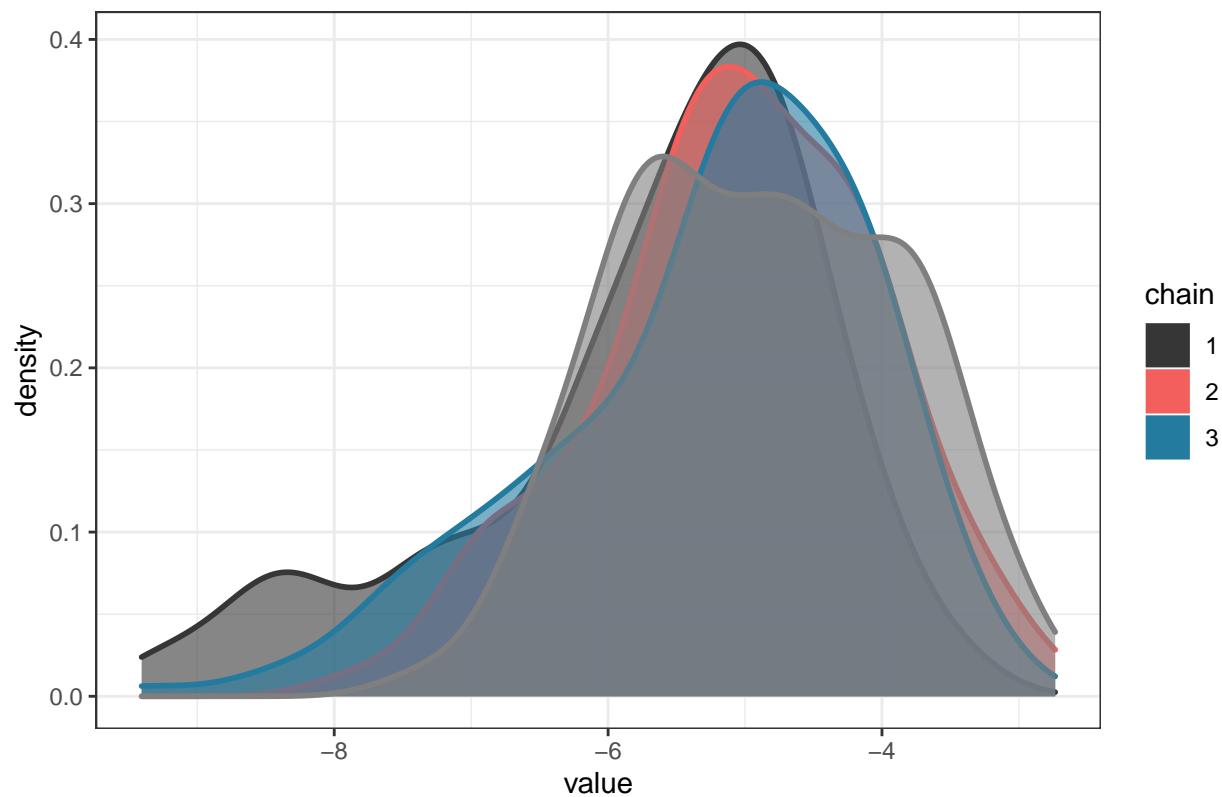
Density plot of bs_gammas_8



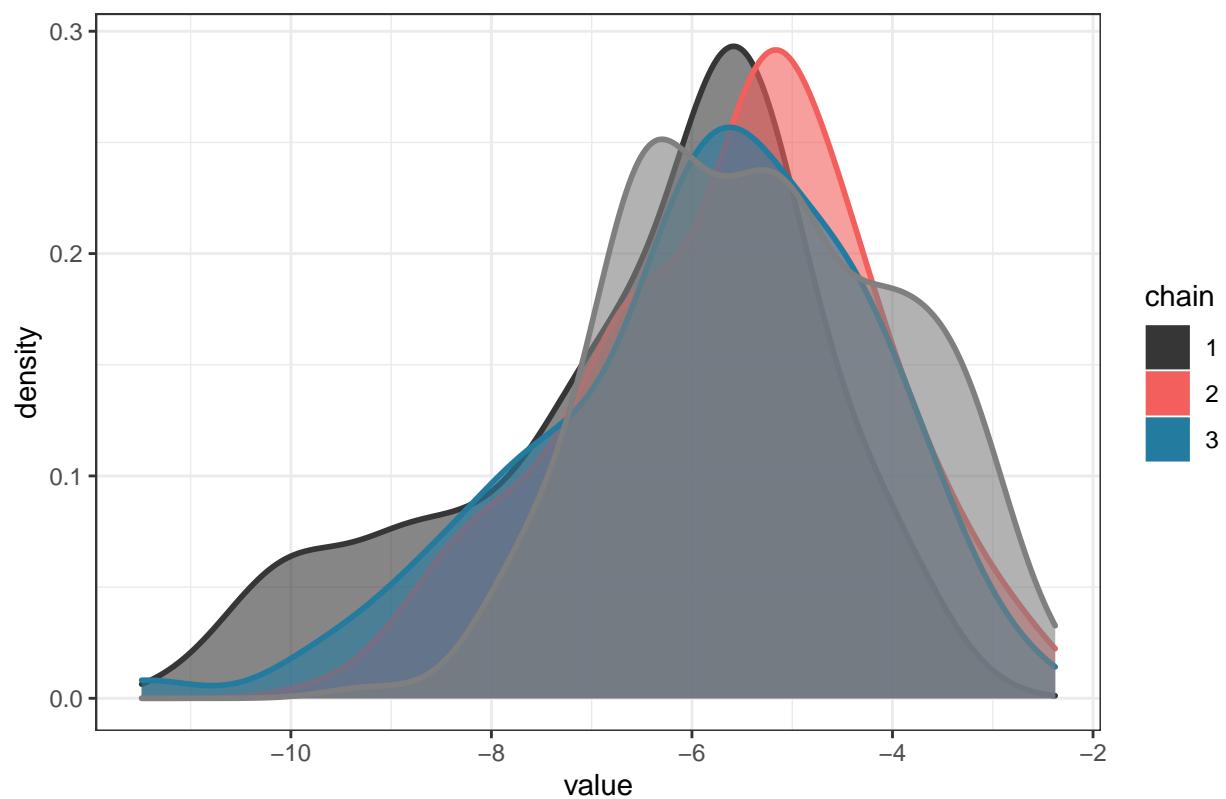
Density plot of bs_gammas_9



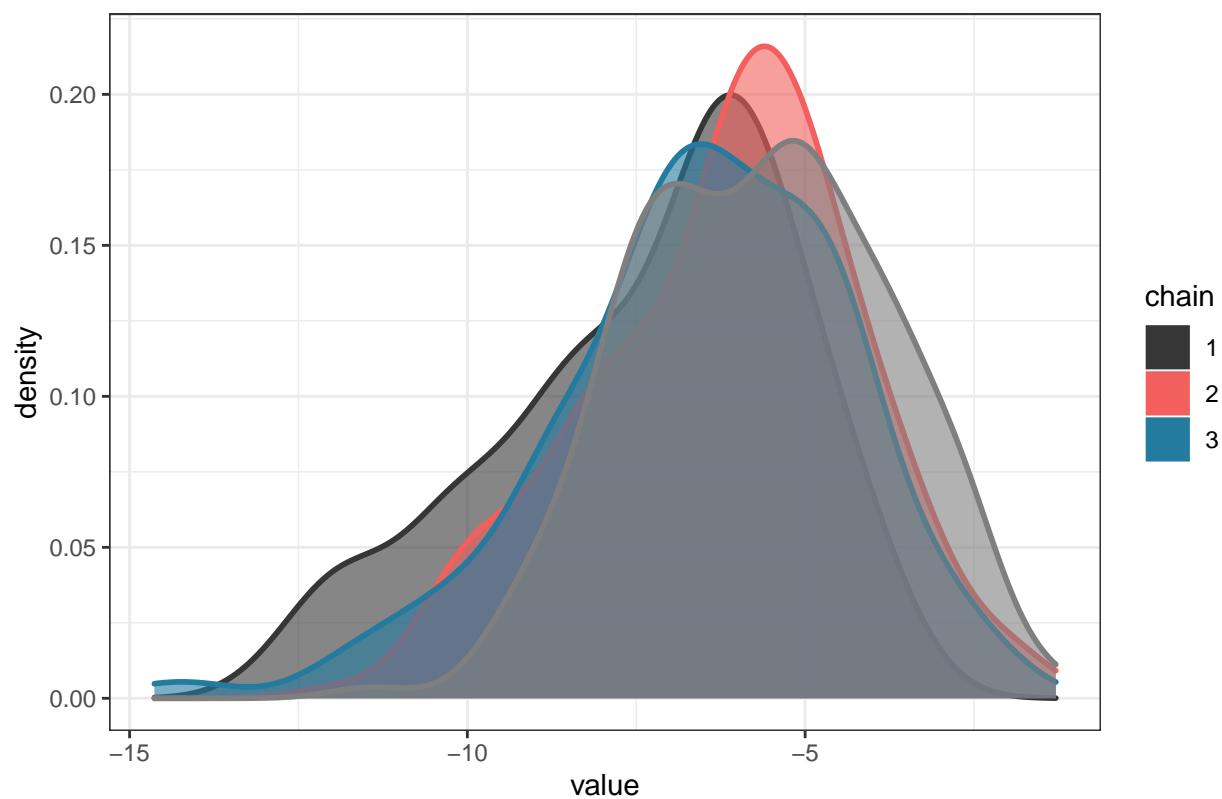
Density plot of bs_gammas_10



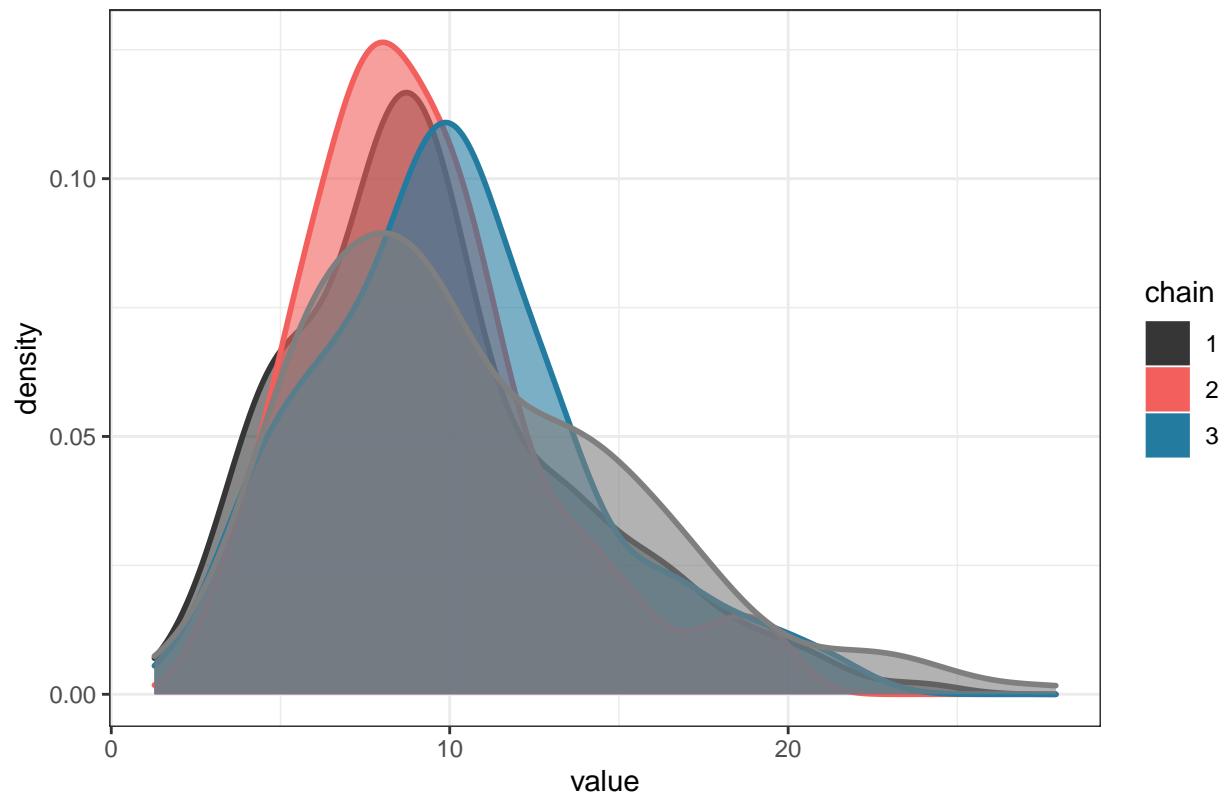
Density plot of bs_gammas_11



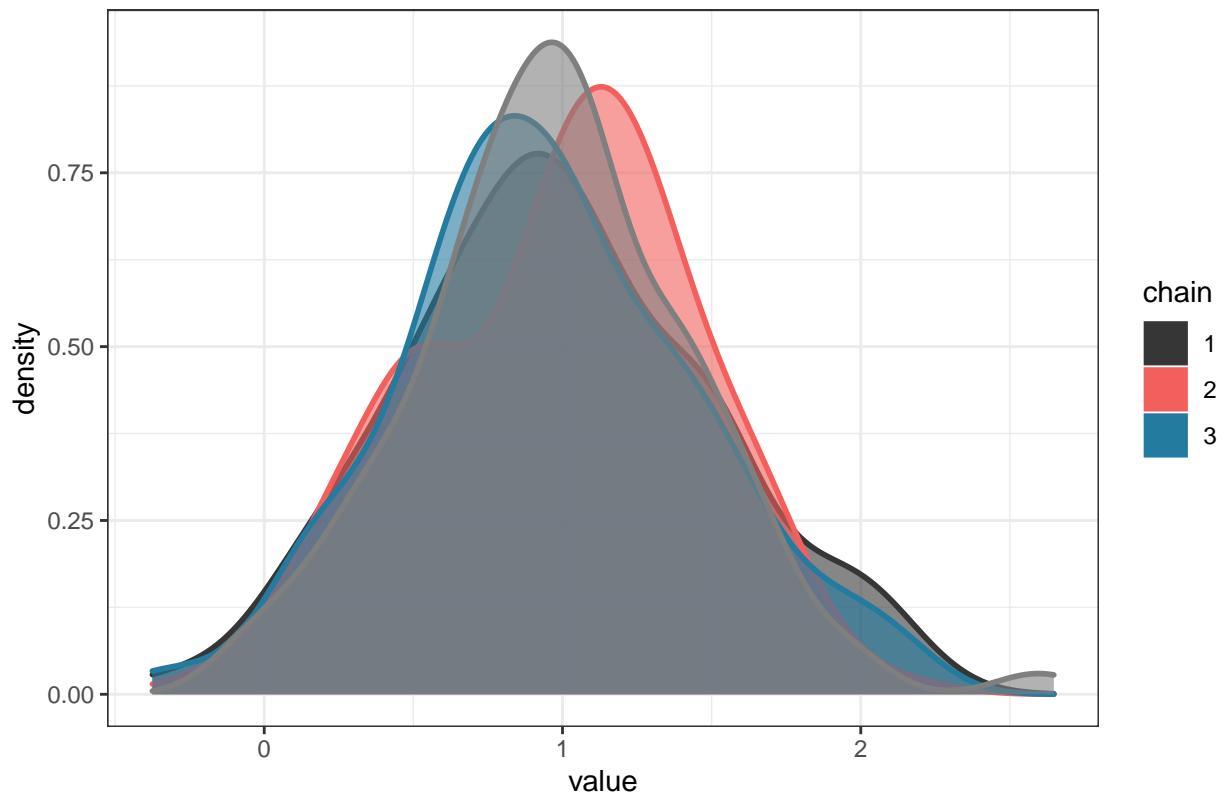
Density plot of bs_gammas_12



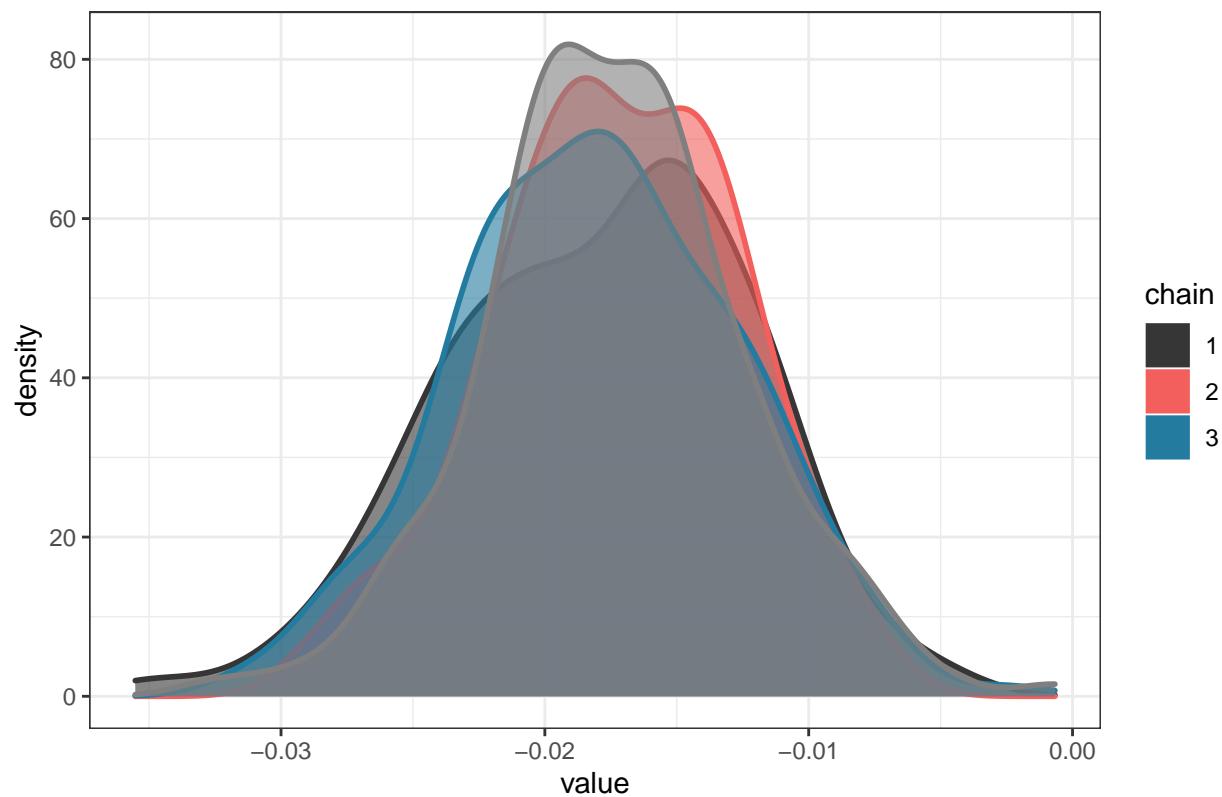
Density plot of tau_bs_gammas



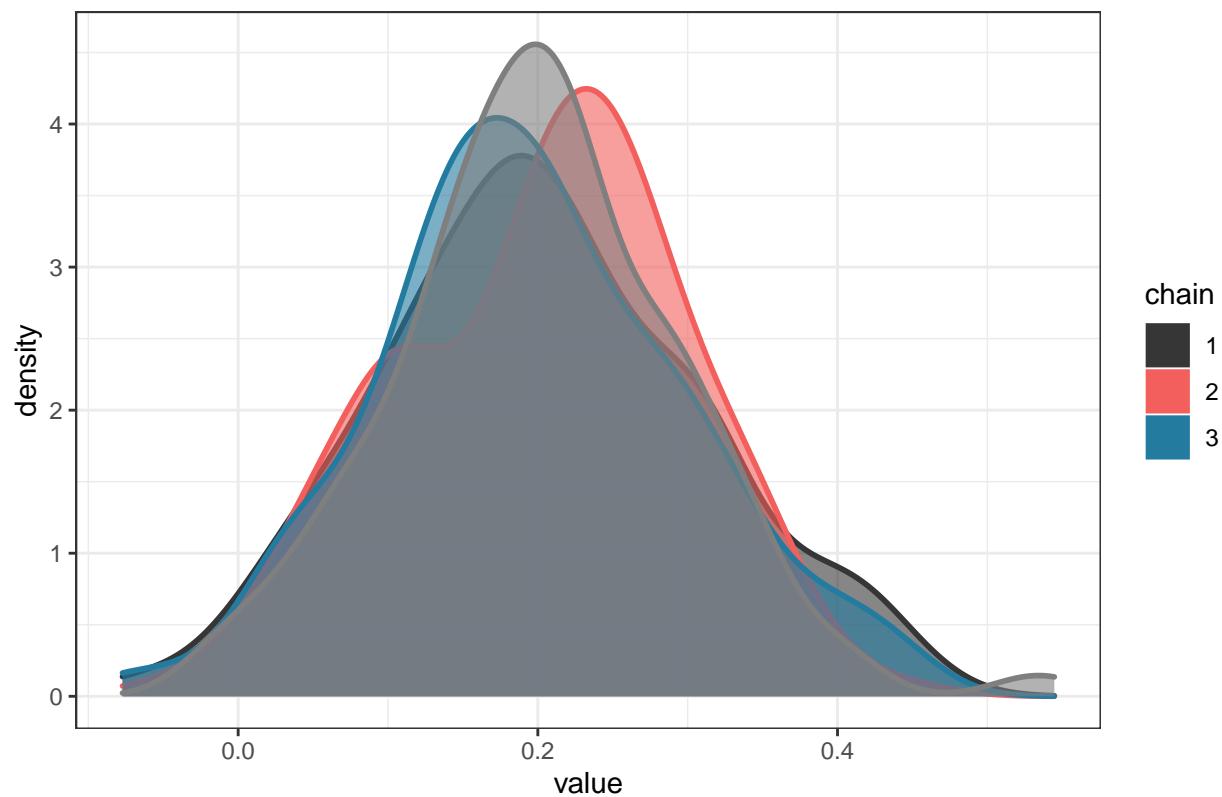
Density plot of LOWC31



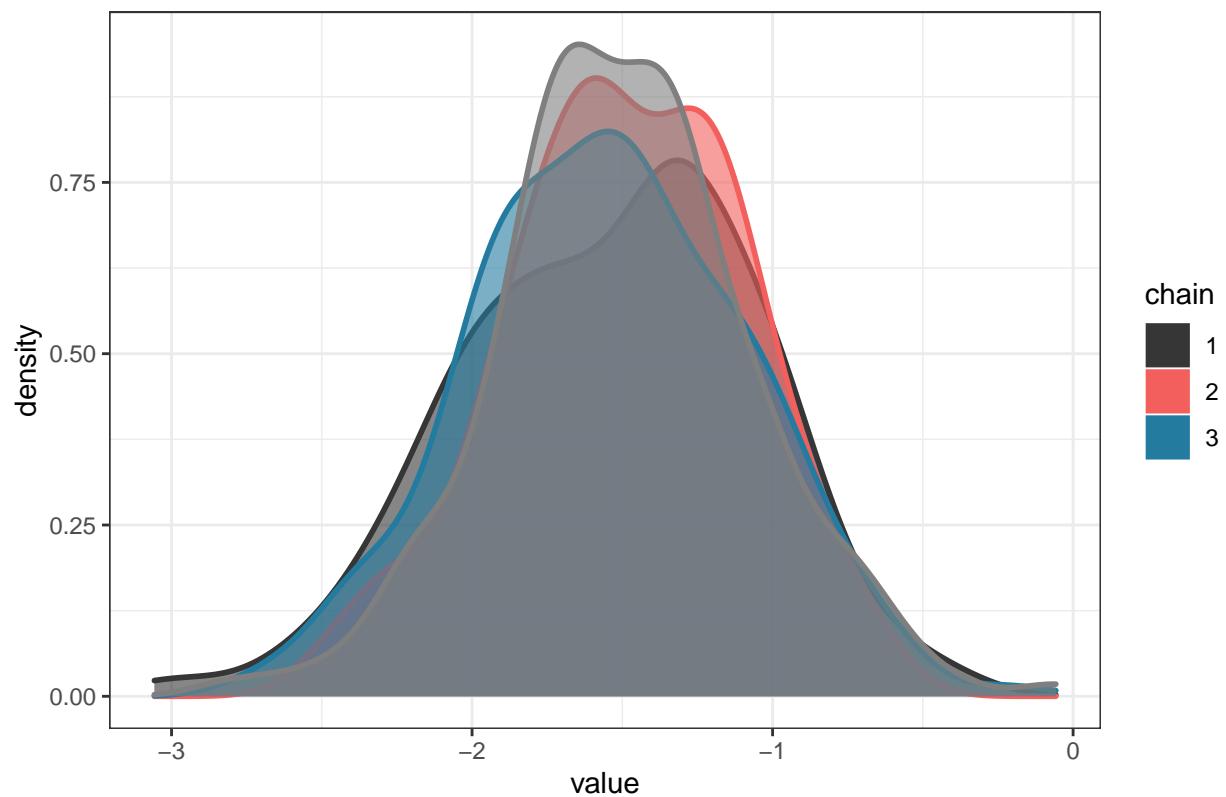
Density plot of area(eGFR)



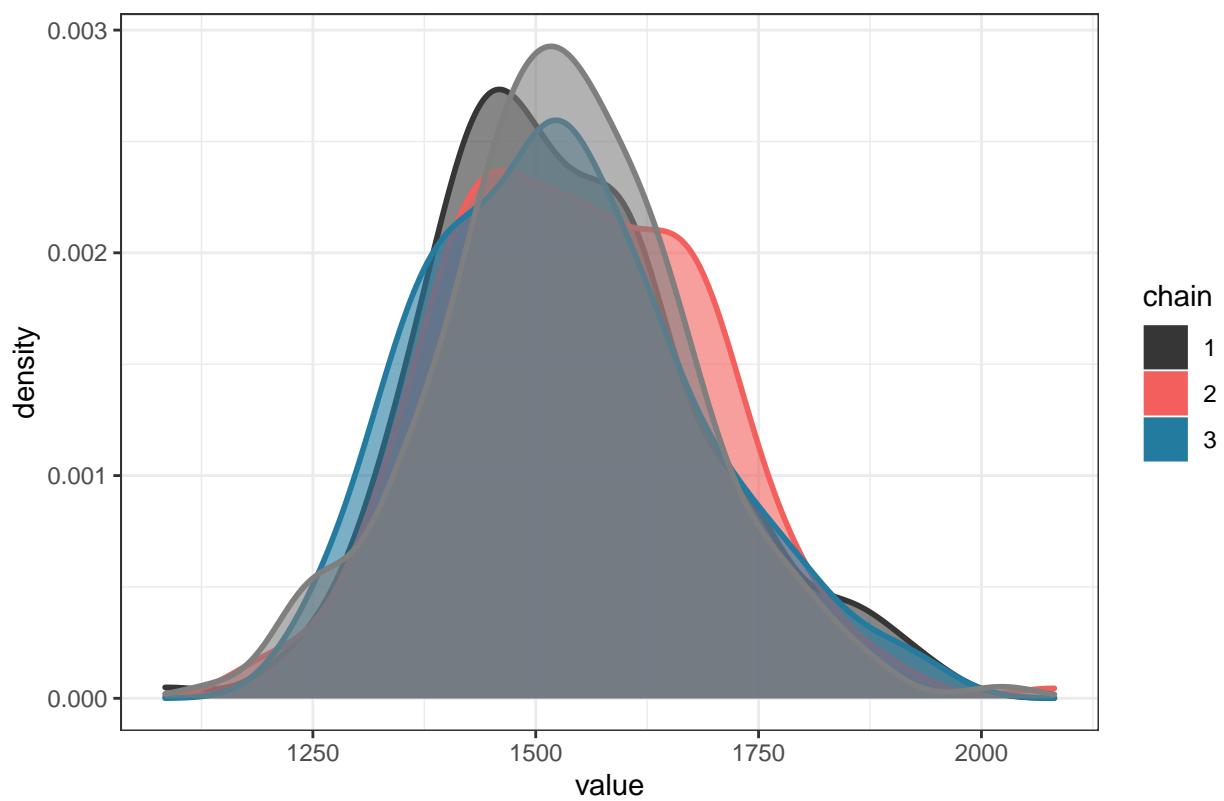
Density plot of



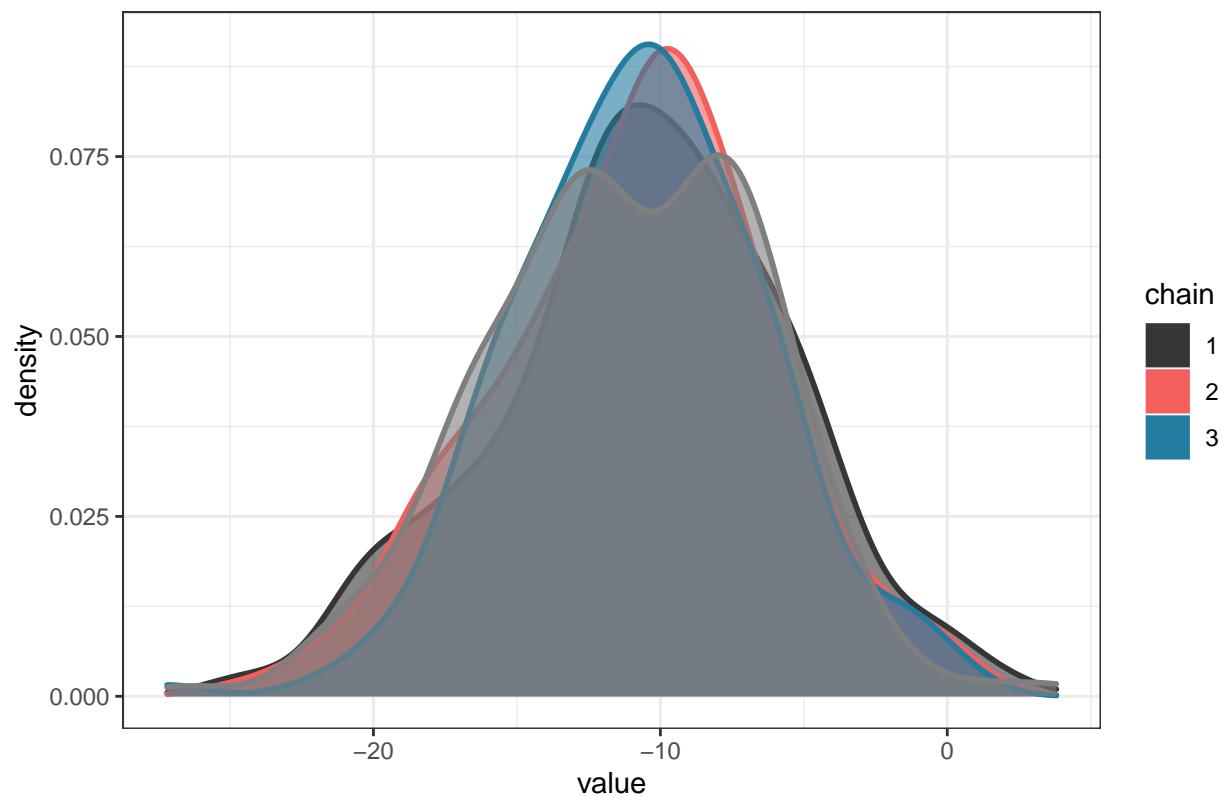
Density plot of .1



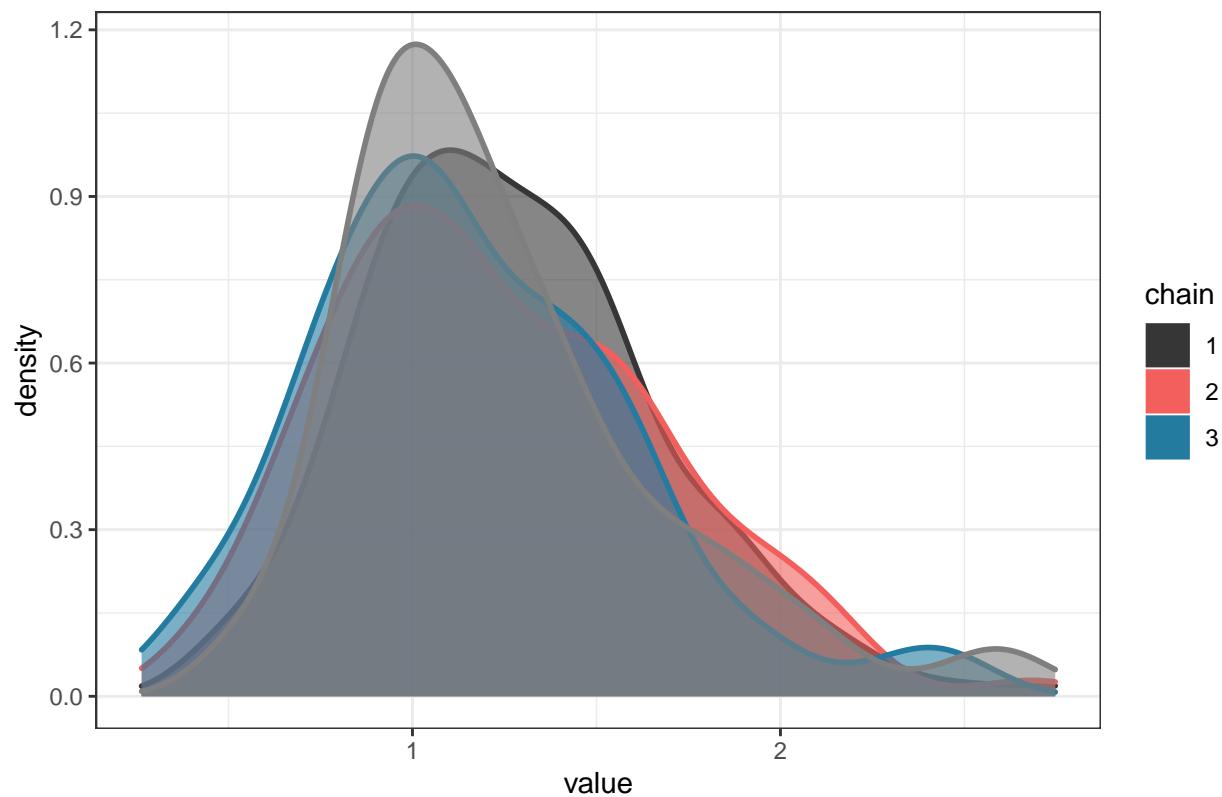
Density plot of $D[1, 1]$



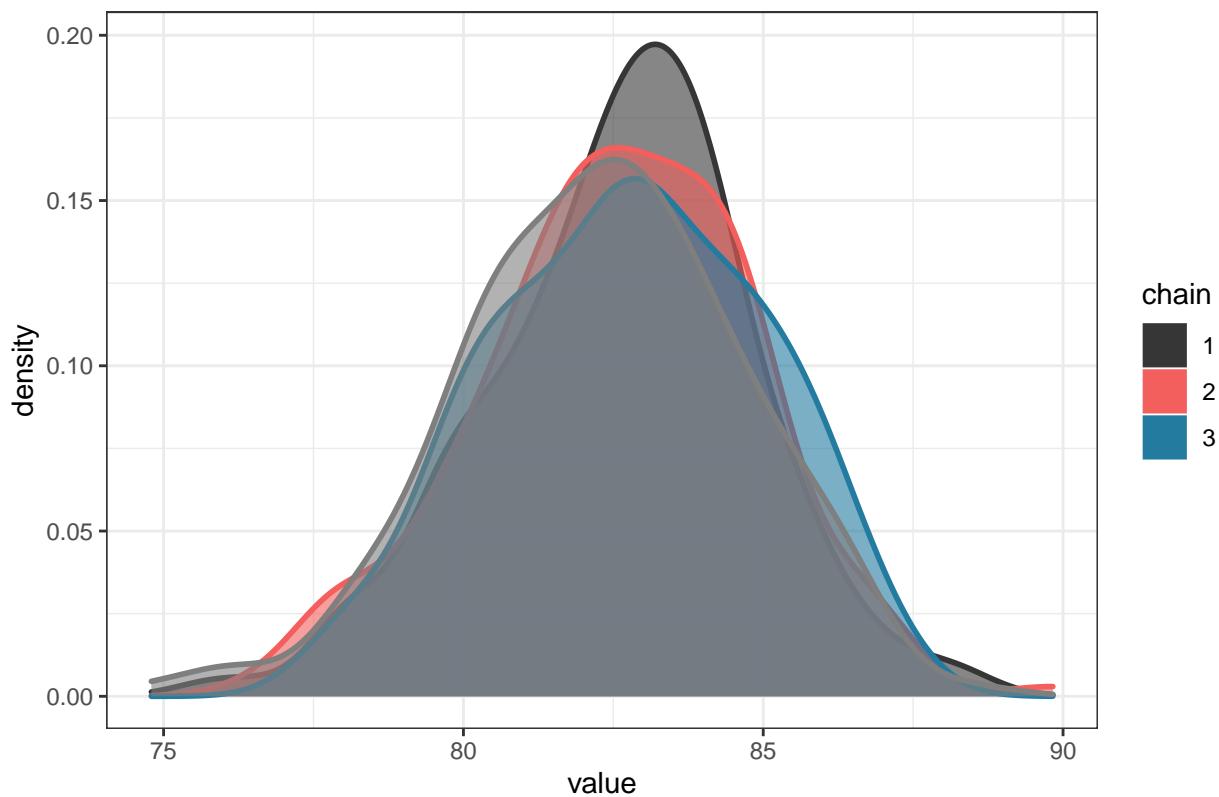
Density plot of $D[2, 1]$



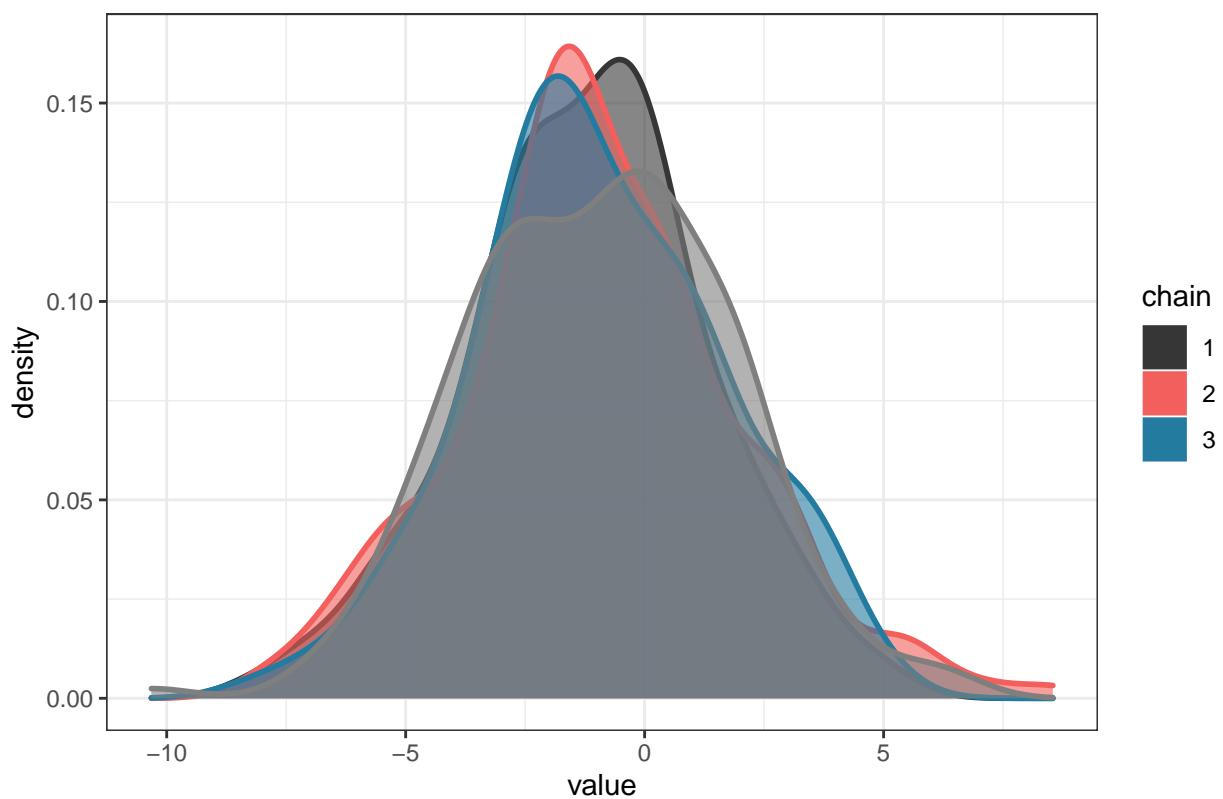
Density plot of $D[2, 2]$



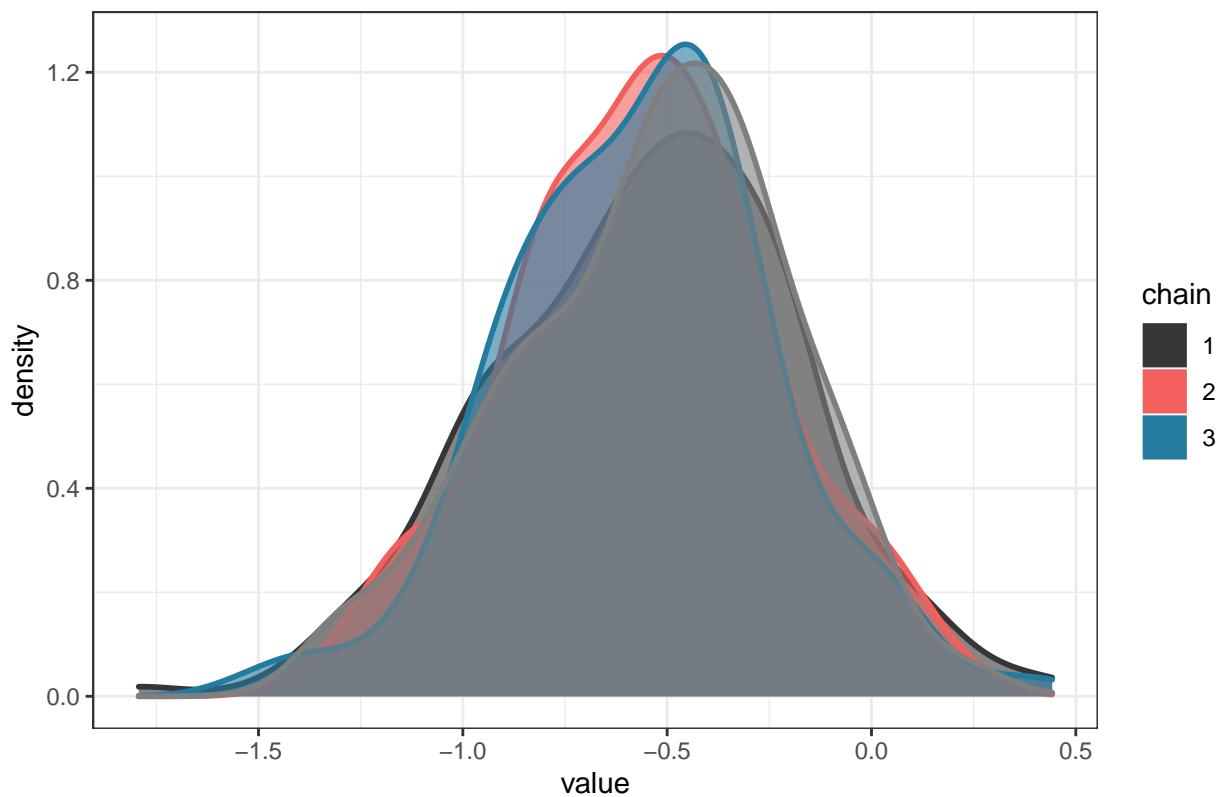
Density plot of (Intercept)

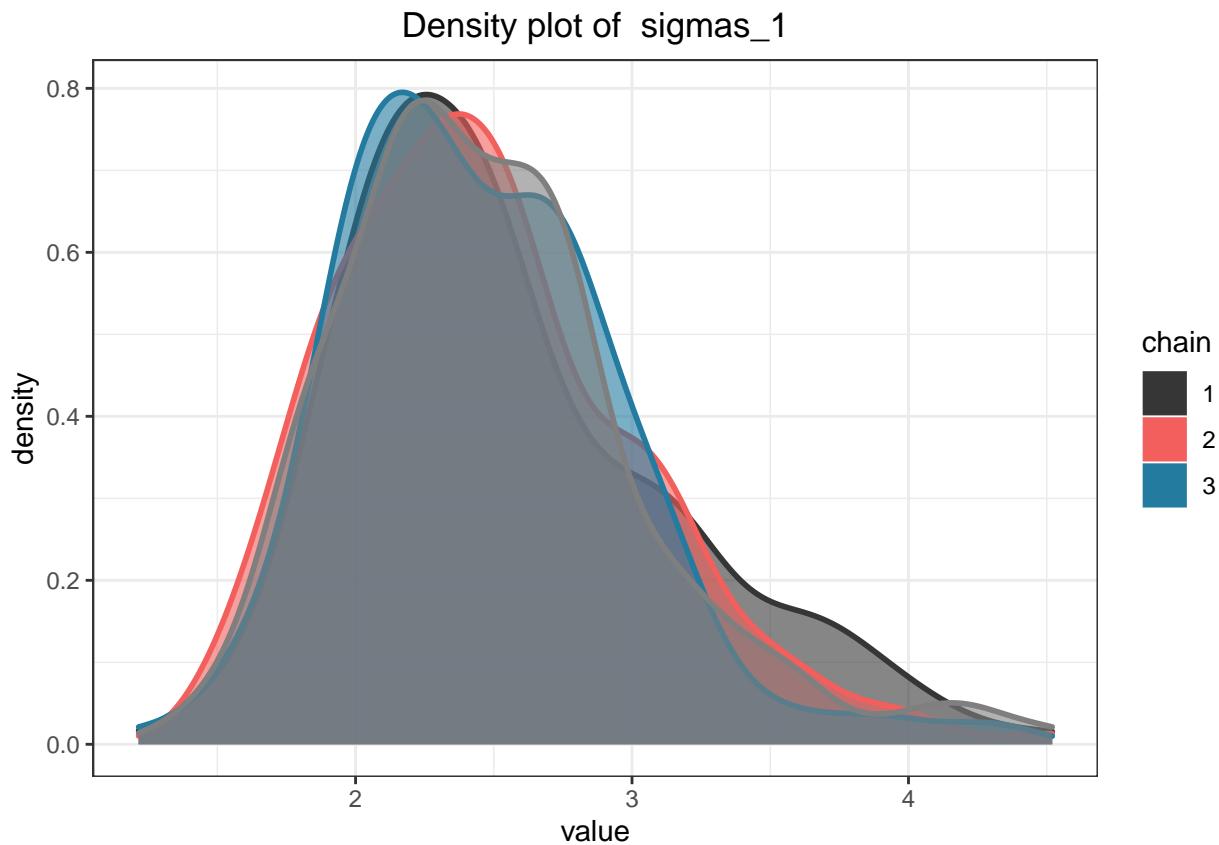


Density plot of LOWC31.1



Density plot of time





```
densCplt
```

```
## NULL
```

```
densCplt1
```

```
## NULL
```

```
densCplt2
```

```
## NULL
```

Save analyses

```
name <- paste("C:/Documenti/Manenti/LES/JOHNS HOPKINS/jm_analysis_sle_lowc3", format(as.Date(Sys.Date()))
save.image(name)
```