

mcmc-ladder

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Let's sample from a normal distribution centered at 0 with sd = 1.

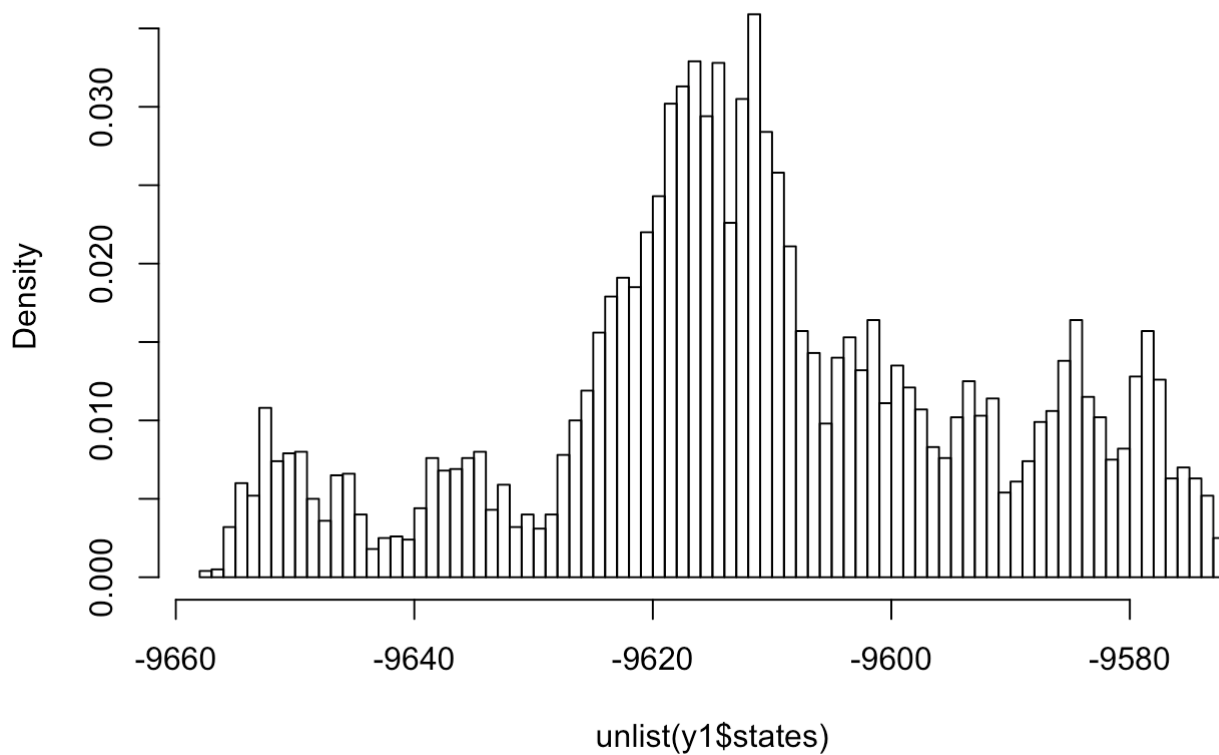
```
niters <- 10000
s0 <- rnorm(1, sd = 10000)

normdensity <- function(x){
  return(dnorm(x,0,1,log=TRUE))
}

sym_proposal_dis <- function(){
  return(rnorm(1, mean = 0, sd = 1))
}

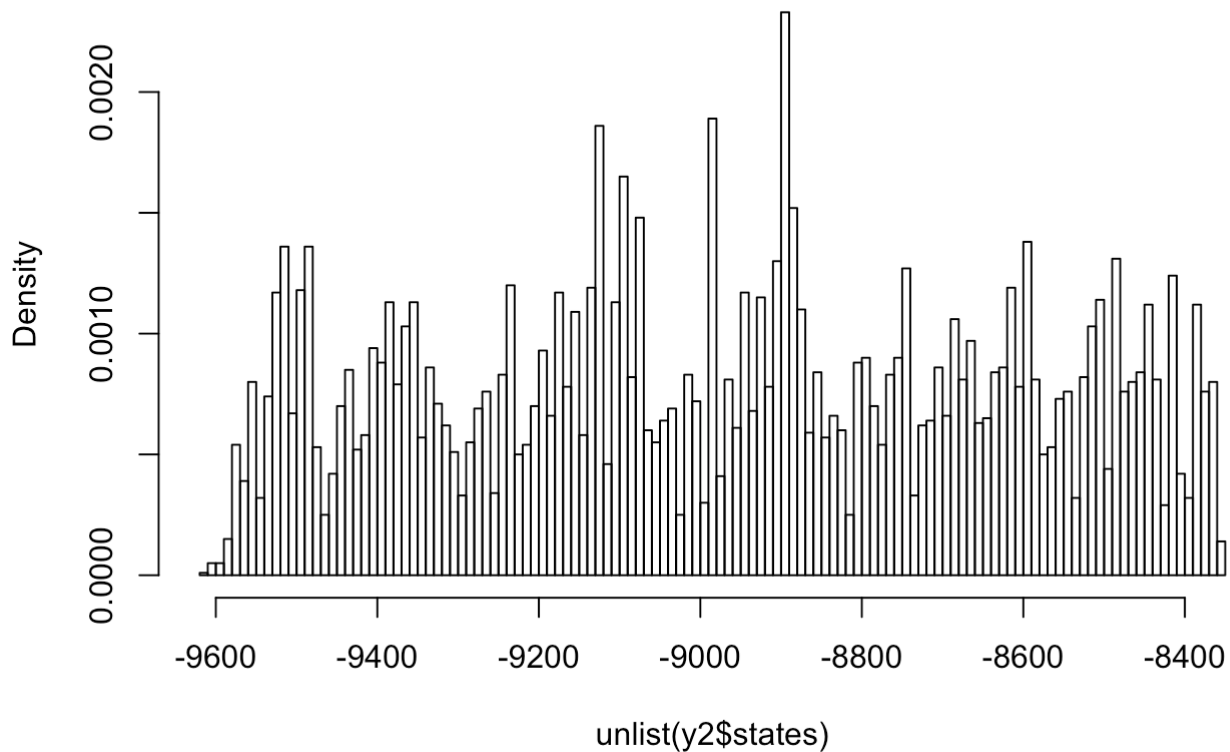
y1 <- run_mcmc(niters, 1000000, prev.chain = list(states=vector(),temp=0), s0, pi = norm
density, sym_proposal_dis)
hist(unlist(y1$states),prob=TRUE, 100)
```

Histogram of unlist(y1\$states)



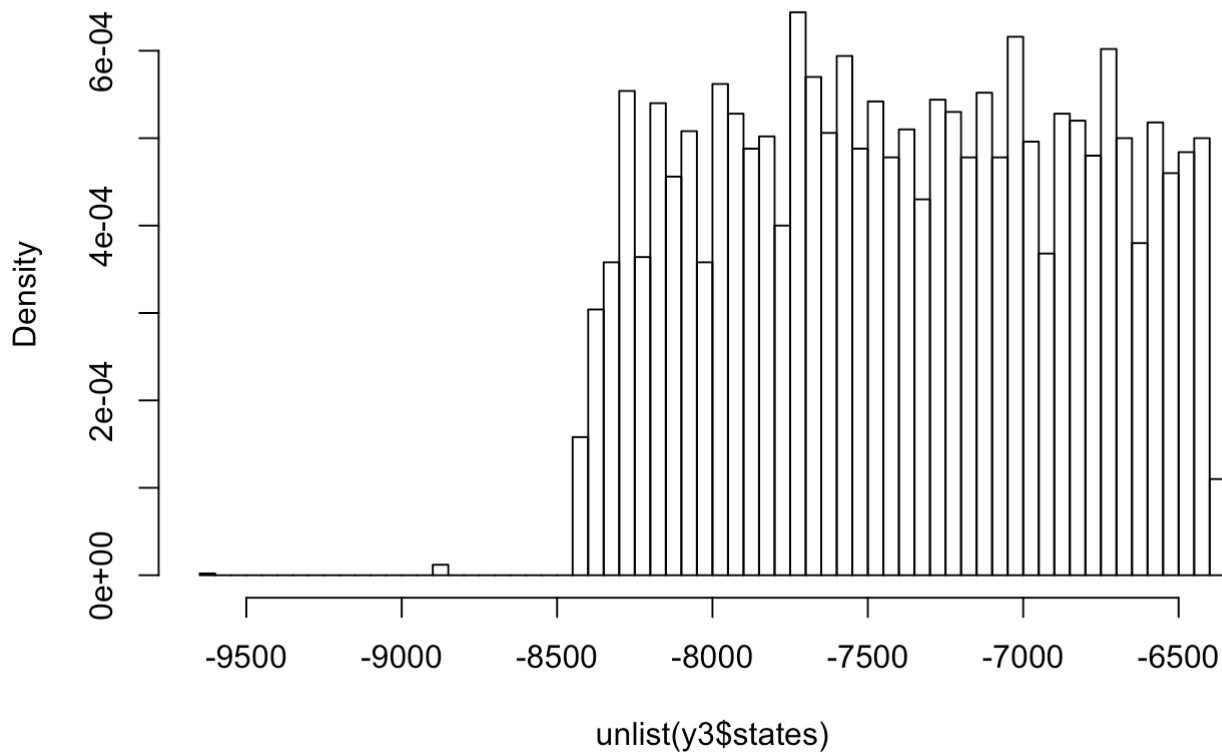
```
#sym_proposal_dis <- function(){  
# return(rnorm(1, 0, sd = 10000))  
#}  
  
y2 <- run_mcmc(niters, 10000, prev.chain = y1, s0, pi = normdensity, sym_proposal_dis)  
hist(unlist(y2$states),prob=TRUE, 100)
```

Histogram of unlist(y2\$states)



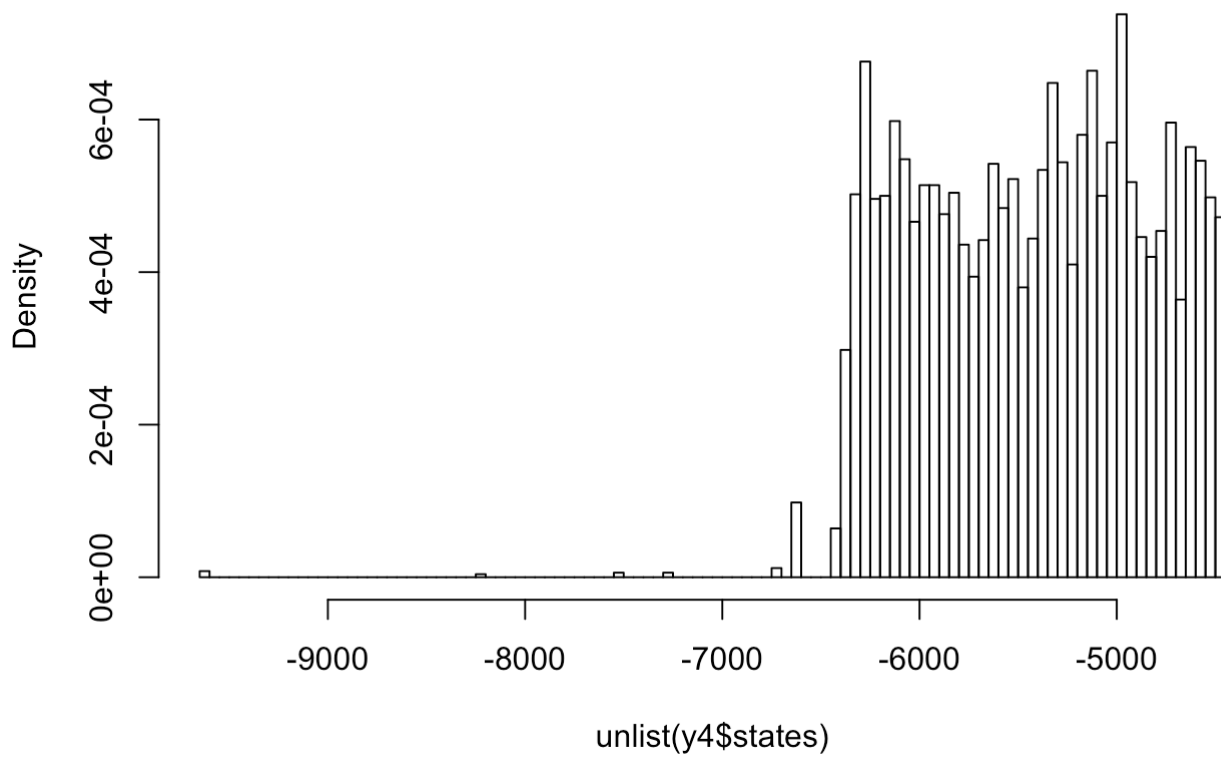
```
#sym_proposal_dis <- function(){  
# return(rnorm(1, 0, sd = 10000))  
#}  
  
y3 <- run_mcmc(niters, 100, prev.chain = y2, s0, pi = normdensity, sym_proposal_dis)  
hist(unlist(y3$states),prob=TRUE, 100)
```

Histogram of unlist(y3\$states)



```
#sym_proposal_dis <- function(){  
# return(rnorm(1, 0, sd = 10000))  
#}  
  
y4 <- run_mcmc(niters, 1, prev.chain = y3, s0, pi = normdensity, sym_proposal_dis)  
hist(unlist(y4$states),prob=TRUE, 100)  
  
x = seq(-100,100,length=1000)  
lines(x,exp(unlist(lapply(x,normdensity))),type="l", col = "red")
```

Histogram of unlist(y4\$states)



```
plot(c(y1$log1, y2$log1, y3$log1, y4$log1))
```

