mcmccheck

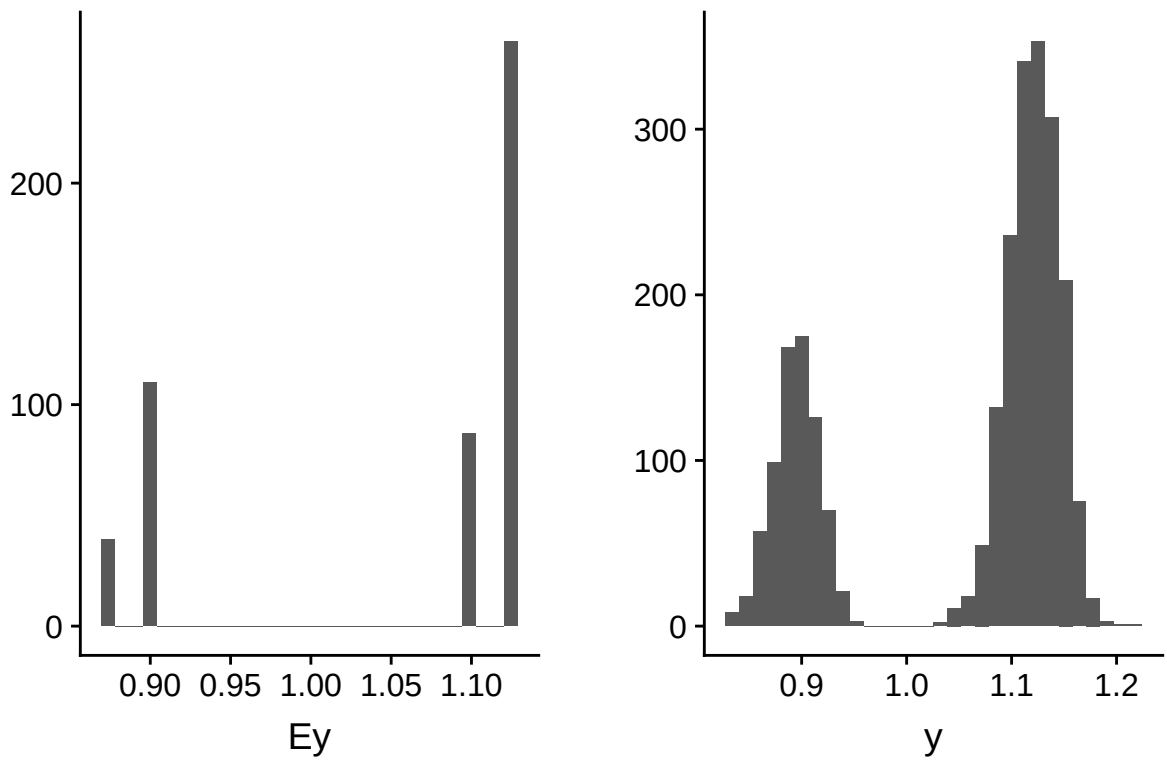
Moi Exposito-Alonso

2019-04-04

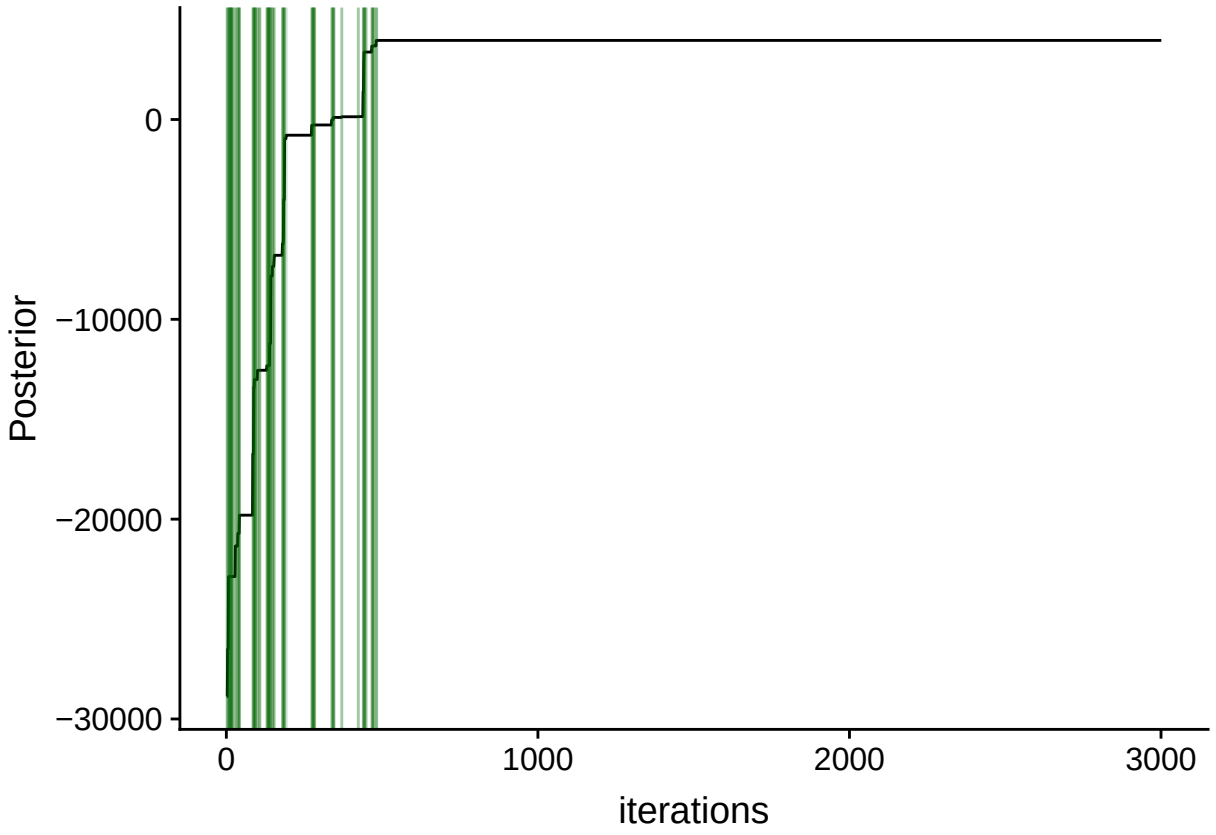
Simple run without sampling variance

```
a=0.01
b=0.01
p=0
mu=1
svar=0.1
ss=0
epi=1
replicates=5
ss=0
n=500
m=3
maf=mafsim(m)
X <- Xsim(n,m,maf)
s= ssim(m,svar)
Ey=wsim(X,s,mode=2)
y=sampleW(Ey,a,b,p,rep = replicates)
h=sort(rep.int(1:n,replicates))

title <- ggdraw() + draw_label(paste("h2= ",format(var(Ey) / var(y),digits=2)),fontface = 'bold')
plot_grid(title,
          plot_grid(qplot(Ey),qplot(y)),
          ncol = 1, rel_heights = c(0.1, 1)
         )
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
x<-napMCMC(y,h,X,m=1:m,n=1:n,rnorm(m,0,0.1),
           test=F,
           verbose=F,
           iterations=1000 * m,
           FITmode = 2,
           PRImode = 1,
           Smode = 1 ,
           bmin=b,bmax=b,
           amin=b,amax=a,
           pmin=p,pmax=p,
           svarmin=svar,svarmax=svar,
           ssmin=ss,ssmax=ss,
           mumin=mu,mumax=mu)

posteriorplot(x)
```




```
# LIKELIHOOD(y,h,wC(X,x$shat,3),b,a,p,mu,epi,verbose = TRUE)
# LIKELIHOOD(y,h,BMmgwa(X,My(y,h)),b,a,p,mu,epi,verbose = TRUE)
```

```
pnap<-scorplot(s,x$shat)
pgwa<-scorplot(s,BMmgwa(X,My(y,h)))
pfinal<-plot_grid(
          pnap$psel,
          pgwa$psel,
          labels=c("NAP","mGWA")
          )
# print(pfinal)


inap<-indplot(y,h,x$w)
igwa<-indplot(y,h,X %*% BMmgwa(X,My(y,h))+mu)
pfin2<-plot_grid(
          inap,
          igwa,
          labels=c("NAP","mGWA")
          )
```

```
## Warning: Removed 1 rows containing missing values (geom_hline).
## Warning: Removed 1 rows containing missing values (geom_vline).
## Warning: Removed 1 rows containing missing values (geom_hline).
## Warning: Removed 1 rows containing missing values (geom_vline).
```

```
# print(pfin2)
p<-plot_grid(pfinal,pfin2,ncol=1)
print(p)
```