mcmccheck

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Simple run without sampling variance

```
a=0.05
b=0.05
p=0
mu=1
svar=0.1
ss=0
epi=1
replicates=5
ss=0
n=500
m=3
maf=mafsim(m)
X <- XsimLD(n,m,maf,r2=0.8) # different from Xsim
## Loading required package: MASS
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##
       select
cor(X)
             [,1]
                       [,2]
                                  [,3]
## [1,] 1.0000000 0.5644634 0.5835990
## [2,] 0.5644634 1.0000000 0.6207102
## [3,] 0.5835990 0.6207102 1.0000000
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`.
```

h2 = 0.54300 150 200 100 100 50 0 0 1.2 1.1 1.25 8.0 0.9 1.0 0.75 1.00 1.50 Еу

```
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 = 2,
           Smode = 2,
           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)
```

У

```
2000 - 1600 - 1200 - 1000 2000 3000 iterations

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

pnap<-scorplot(s,x$shat)
pnap
```

\$psel





