

# mcmccheck

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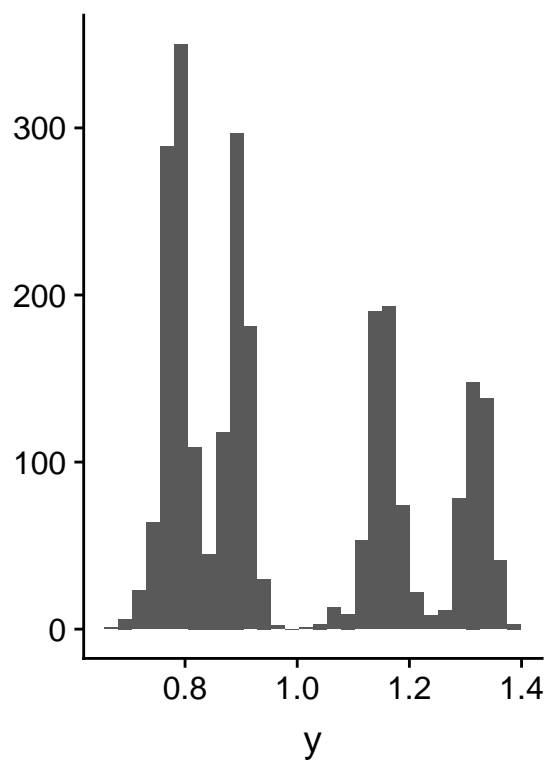
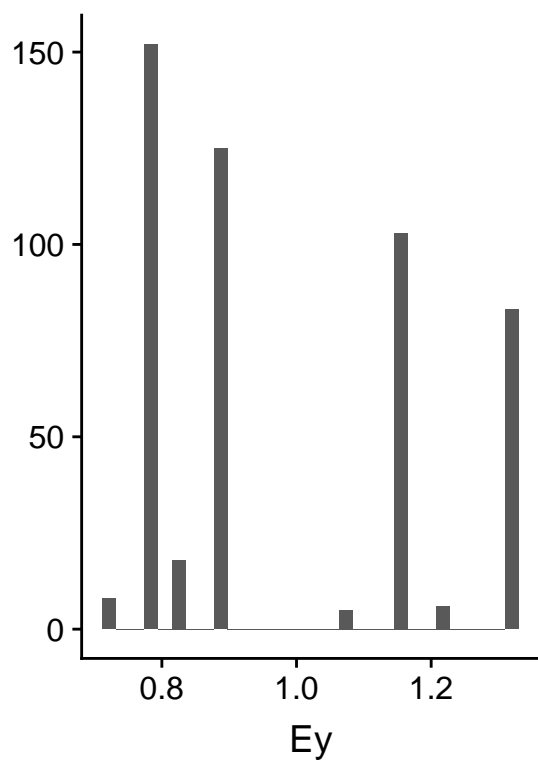
## Simple run without sampling variance

```
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)
)

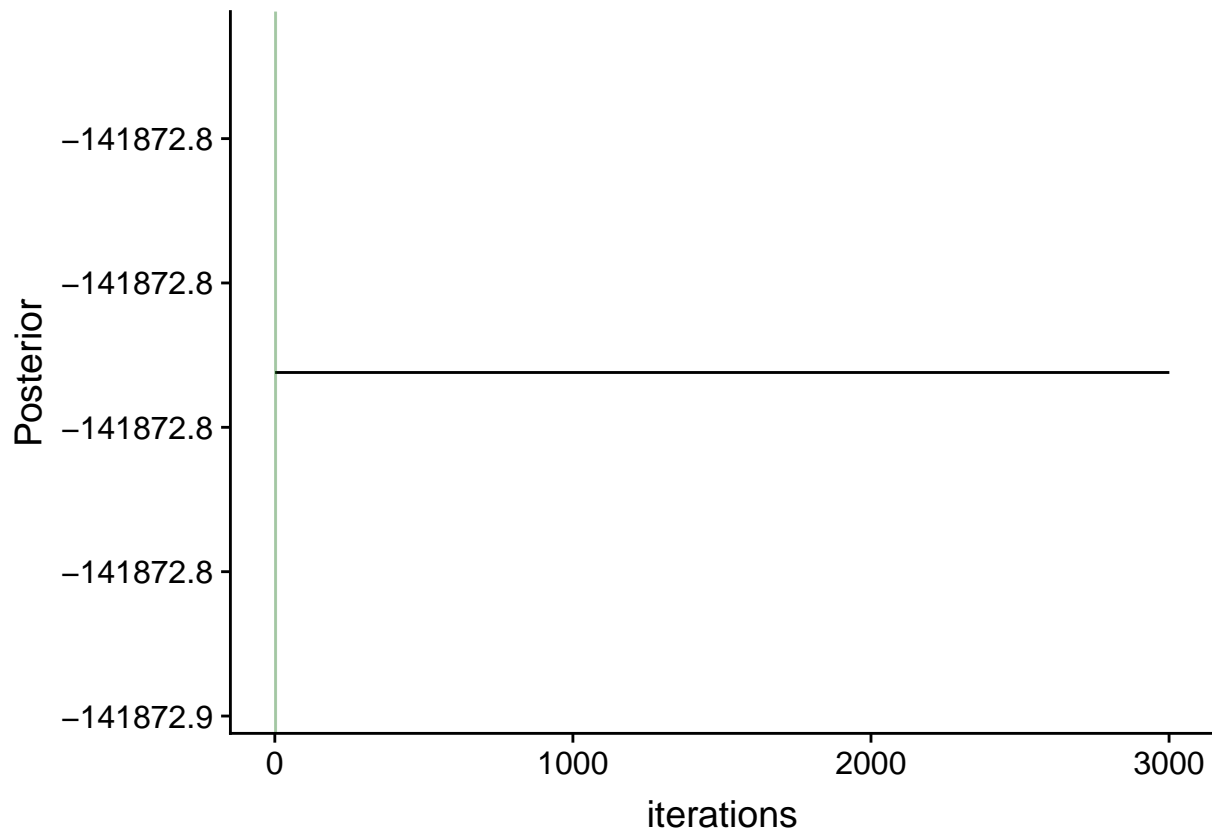
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

**h2= 0.99**



```
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)
```



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

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

inap<-indplot(y,h,x$w)
igwa<-indplot(y,h,X %*% BMridge(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)
```

