

mcmccheck

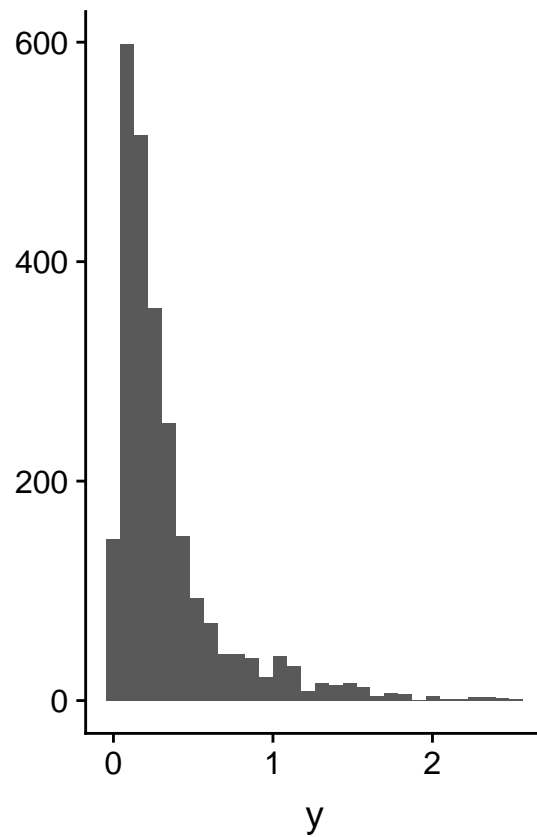
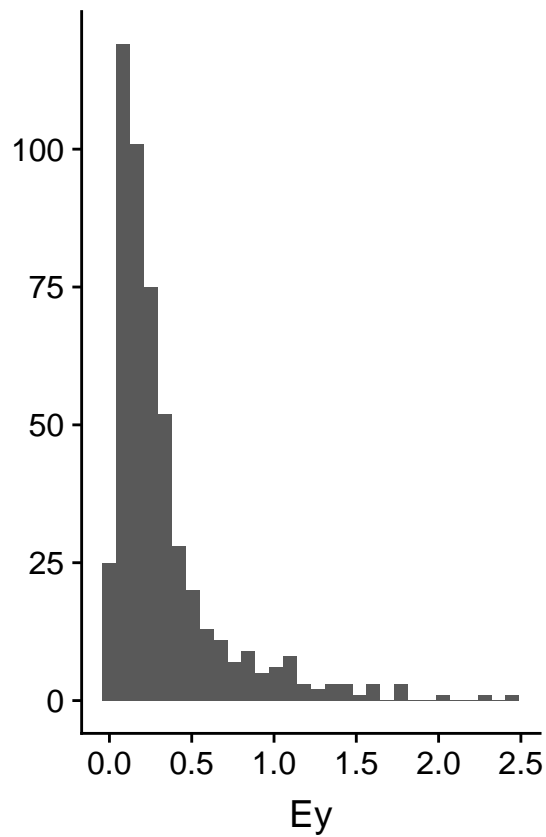
Moi Exposito-Alonso

2019-04-04

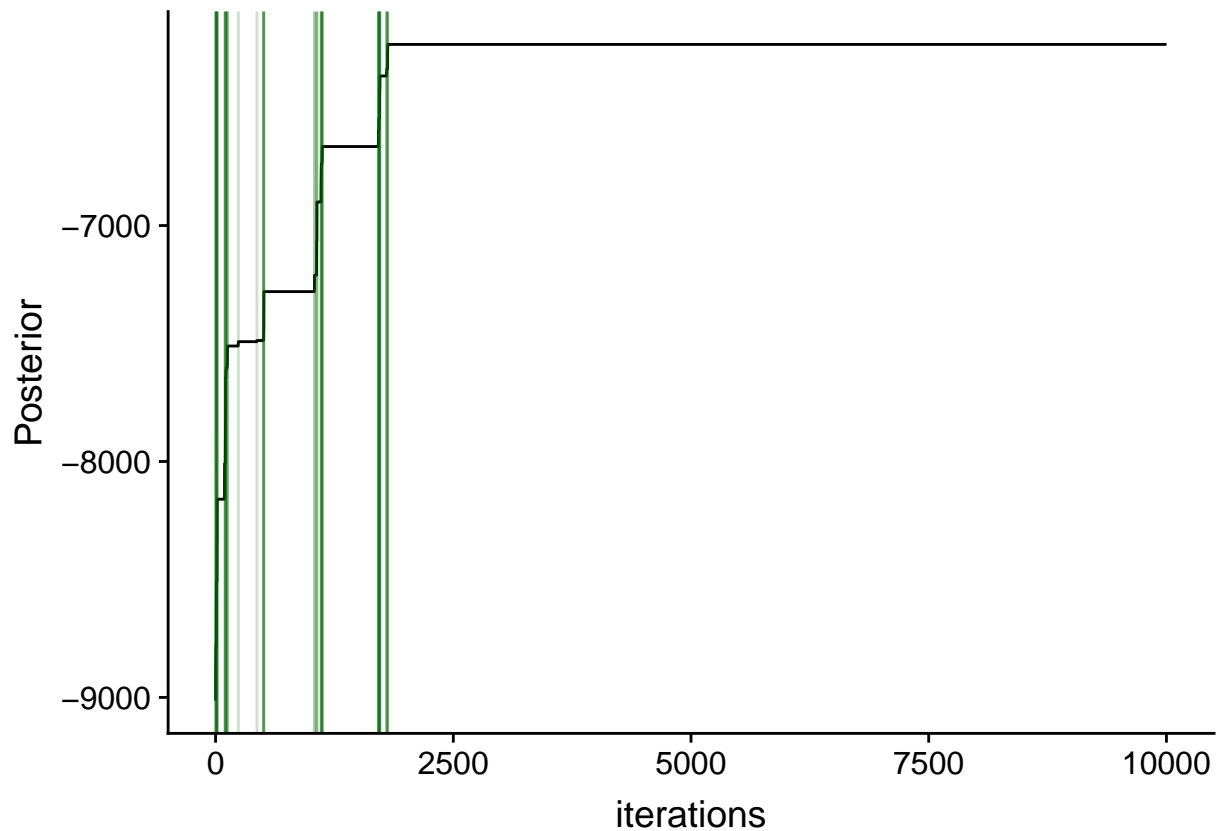
Simple run without sampling variance

```
a=0.01
b=0.01
p=0
mu=1
svar=0.1
ss=0
epi=1
replicates=5
ss=0
n=500
m=100
maf=mafsim(m)
X <- Xsim(n,m,maf)
s= ssim(m,svar)
Ey=wsim(X,s,mode=2,epi = 1,mu = mu)
y=sampleW(Ey,a,b,p,rep = replicates)
h=sort(rep.int(1:n,replicates))
plot_grid(qplot(Ey),qplot(y))

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



```
x<-napMCMC(y,h,X,m=1:m,n=1:n,rnorm(m,0,0.1),
  test=F,
  verbose=F,
  iterations=100 * m,
  FITmode = 2,
  PRImode = 1,
  Smode = 1,
  mumin=mu,mumax=mu)
# bmin=b,bmax=b,
# amin=b,amax=a,
# pmin=p,pmax=p,
# svarmin=svar,svarmax=svar,
# ssmin=ss,ssmax=ss,
posteriorplot(x)
```



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

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

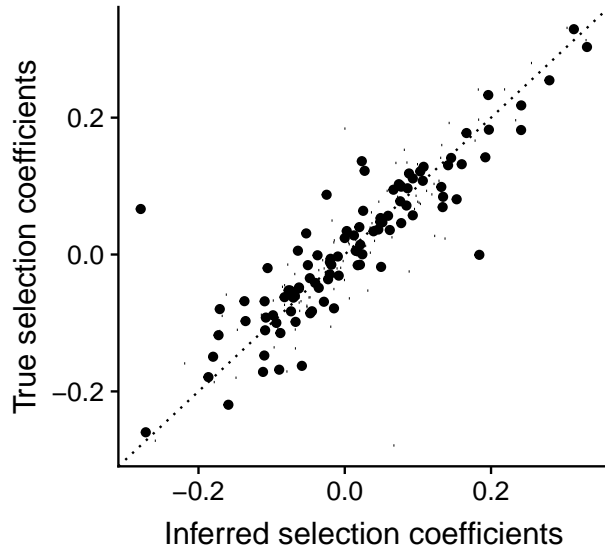
```
# print(pfin2)
```

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

```
print(p)
```

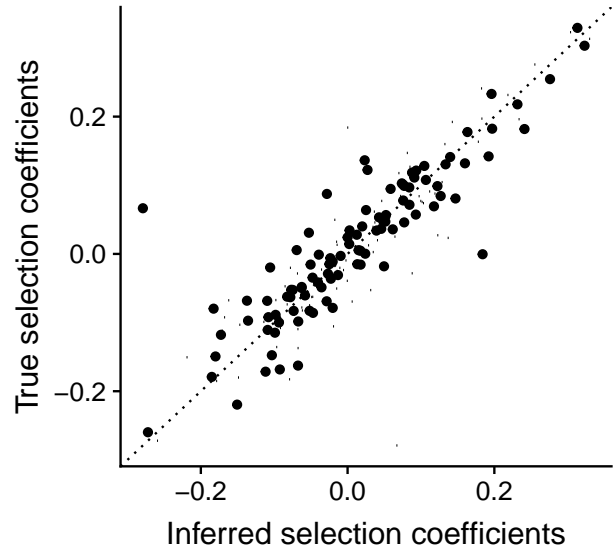
NAP

$$R^2 = 0.773, \beta = 0.823$$



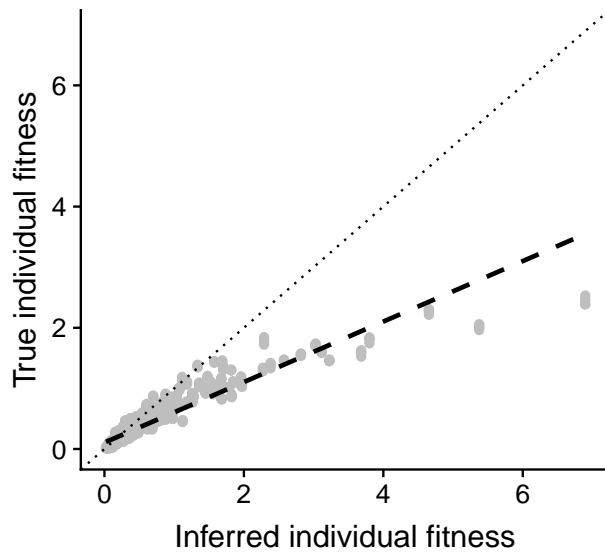
mGWA

$$R^2 = 0.773, \beta = 0.83$$



NAP

$$R^2 = 0.87, \beta = 0.499$$



mGWA

$$R^2 = 0.692, \beta = 0.27$$

