## mcmccheck

Moi Exposito-Alonso 2019-04-05

## Simple run without sampling variance

Hyperparameters are fixed

```
a=0.1
b=0
p=0
mu=1
svar=0.1
ss=0
epi=1
replicates=5
ss=0
n=50
m=10
FITmode=2
maf=mafsim(m)
X=A <- Xsim(n,m,maf)</pre>
s= ssim(m,svar)
Ey=wsim(X,s,mode=FITmode,epi = epi,mu = mu)
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')</pre>
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 = 0.94
                                               30
9
                                               20
6
                                               10
3
                                                0
     0.5
                1.0
                           1.5
                                                      0.5
                                                                1.0
                                                                         1.5
                                                                                  2.0
                   Ey
                                                                    У
x<-napMCMCwrap()</pre>
## The provided vector s is a good start
## Starting c++ MCMC
## rGWA start for vector s is better than proposed start
## Starting c++ MCMC
LIKELIHOOD(y,h-1,wC(X,BMridge(X,My(y,h)),FITmode),b,a,p,mu,epi,verbose = F)
## [1] 204.4449
LIKELIHOOD(y,h-1,wC(X,x$shat,FITmode),b,a,p,mu,epi,verbose = F)
## [1] 201.7672
LIKELIHOOD(y,h-1,wC(X,s,FITmode),b,a,p,mu,epi,verbose = F)
## [1] 212.7335
# x < -napMCMC(y,h,X,m=1:m,n=1:n,
#
             rnorm(m, 0, 0.1),
#
             \# BMridge(X,My(y,h), lambda=10),
             # s+rnorm(m,0,0.01),
#
#
             test = F,
#
             verbose=F,
#
             iterations=5000 * m,
#
             FITmode = FITmode, PRImode = 1, LIKmode = 2,
#
             bw=0.001)
```

```
\# LIKELIHOOD(y,h-1,wC(X,BMridge(X,My(y,h)),FITmode),b,a,p,mu,epi,verbose = F)
# LIKELIHOOD(y,h-1,wC(X,x\$shat,FITmode),b,a,p,mu,epi,verbose = F)
# LIKELIHOOD(y,h-1,wC(X,s,FITmode),b,a,p,mu,epi,verbose = F)
#
# x < -napMCMC(y,h,X,m=1:m,n=1:n,
#
             x$shat,
#
             test=F,
#
             verbose=F,
#
             iterations=5000 * m,
#
             FITmode = FITmode, PRImode = 1, LIKmode = 2,
#
             bw=0.05)
#
 \# \ LIKELIHOOD(y,h-1,wC(X,BMridge(X,My(y,h)),FITmode),b,a,p,mu,epi,verbose = F) \\
# LIKELIHOOD(y,h-1,wC(X,x\$shat,FITmode),b,a,p,mu,epi,verbose = F)
# LIKELIHOOD(y,h-1,wC(X,s,FITmode),b,a,p,mu,epi,verbose = F)
\# qplot(x\$shat,BMridge(X,My(y,h)), xlab = "NAP",ylab="rGWA") +
      # geom_abline(slope = 1,intercept = 0, color=transparent("grey"))
pnap<-scorplot(s,x$shat)</pre>
pgwa<-scorplot(s,BMridge(X,My(y,h)))</pre>
pfinal<-plot_grid(</pre>
          pnap$psel,
          pgwa$psel,
          labels=c("NAP","mGWA")
# pfinal
inap<-indplot(y,h,wC(X,x$shat,FITmode,epi = x$par["epi",] ,mu= x$par["mu",]))</pre>
igwa<-indplot(y,h,X %*% BMridge(X,My(y,h))+mu)</pre>
trueplot<-indplot(y,h,wC(X,s,FITmode,epi = epi ,mu= mu))</pre>
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_smooth).
## Warning: Removed 1 rows containing missing values (geom_hline).
## Warning: Removed 1 rows containing missing values (geom_vline).
# pfin2
plo<-plot_grid(pfinal,pfin2,ncol=1)</pre>
print(plo)
```

```
mGWA<sup>2</sup> = 0. 984 , \beta = 1. 034 , a = 0. 047
         R^2 = 0.985, \beta = 0.988, a = 0.043
True selection coefficients
                                                       True selection coefficients
                                                            0.1
     0.1
                                                            0.0
     0.0
     -0.1
                                                            -0.1
    -0.2
                                                           -0.2
             -0.2
                       -0.1
                                  0.0
                                            0.1
                                                                    -0.2
                                                                              -0.1
                                                                                         0.0
                                                                                                    0.1
             Inferred selection coefficients
                                                                     Inferred selection coefficients
                                                          mG₩A
         R^2 = 0.887, \beta = 0.934, a = 0.021
                                                                    = 0. 864 , \beta = 0. 963 , a = 0. 024
    2.0
                                                           2.0
True individual fitness
                                                       True individual fitness
    1.5
                                                           1.5
                                                           1.0
    1.0
                                                           0.5
    0.5
              0.5
                          1.0
                                     1.5
                                                 2.0
                                                                     0.5
                                                                                 1.0
                                                                                             1.5
                                                                                                        2.0
               Inferred individual fitness
                                                                       Inferred individual fitness
#What it should be
inap<-indplot(y,h,wC(X,x$shat,FITmode,epi = x$par["epi",] ,mu= x$par["mu",]))</pre>
inapfalse<-indplot(y,h,wC(X,x$shat,1,epi = x$par["epi",] ,mu= x$par["mu",]))</pre>
igwa<-indplot(y,h,X %*% BMridge(X,My(y,h))+mu)</pre>
trueplot<-indplot(y,h,wC(X,s,FITmode,epi = epi ,mu= mu))</pre>
plot_grid(inap,igwa,trueplot,ncol=1,labels=c("NAP","mGWA","Truth"))
## 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_smooth).
```

```
## 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).
```

