mcmccheck

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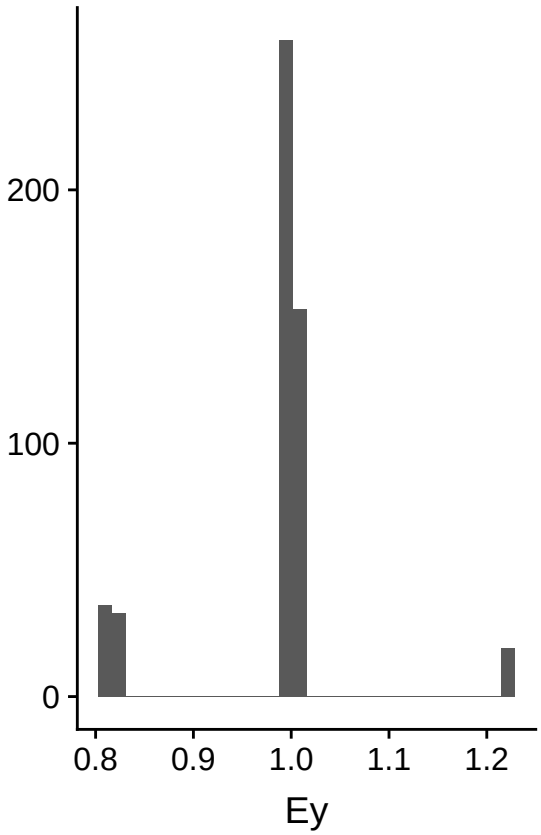
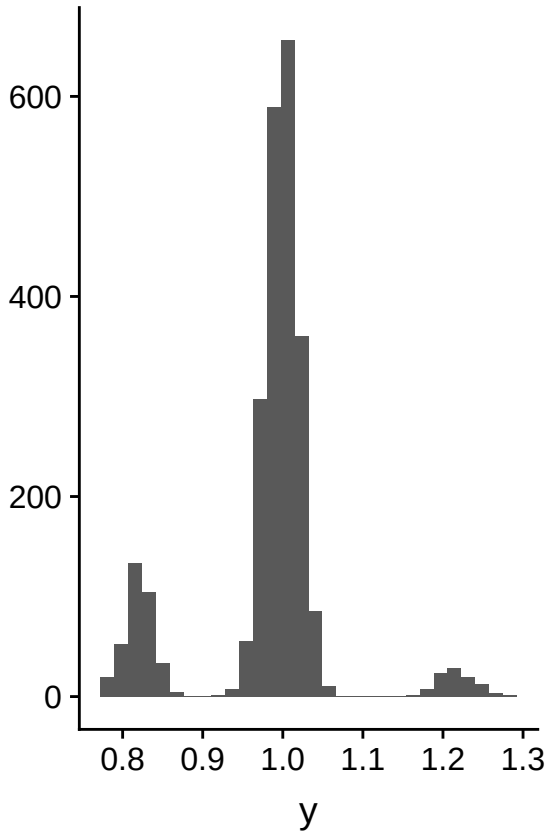
2019-04-04

Simple run with lognormal sampling of S

```
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=3)
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`.
## `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 = 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)
```

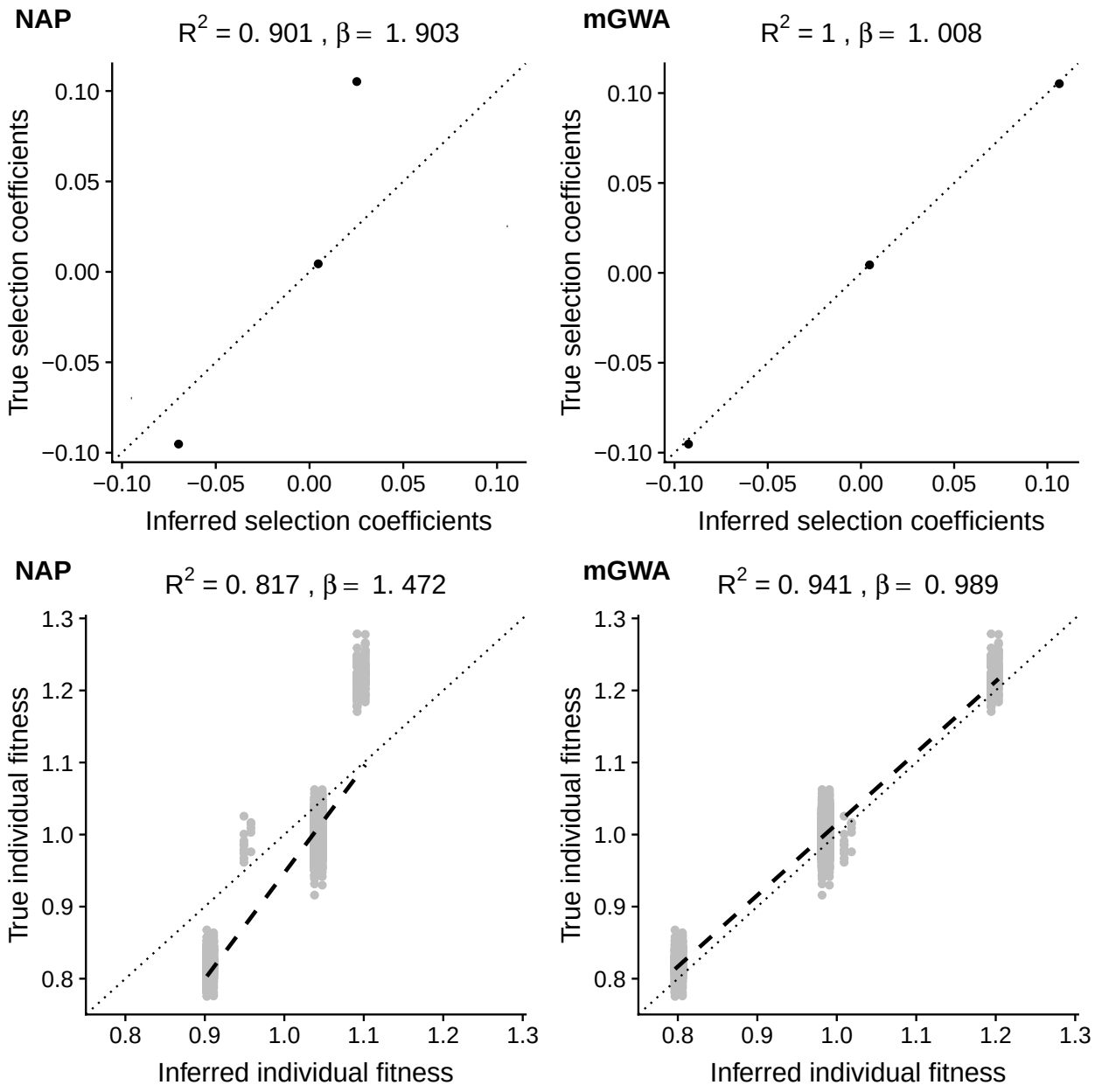
```
pnap<-scorplot(s,x$shat)
pgwa<-scorplot(s,BMridge(X,My(y,h)))
pfinal<-plot_grid(
          pnap$psel,
          pgwa$psel,
          labels=c("NAP","mGWA")
          )
# print(pfinal)


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).
```

```
plot_grid(pfinal,pfin2,ncol=1)
```



With mixture lognormal prior of S

```
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=3)
y=sampleW(Ey,a,b,p,rep = replicates)
h=sort(rep.int(1:n,replicates))
plot_grid(qplot(Ey),qplot(y))
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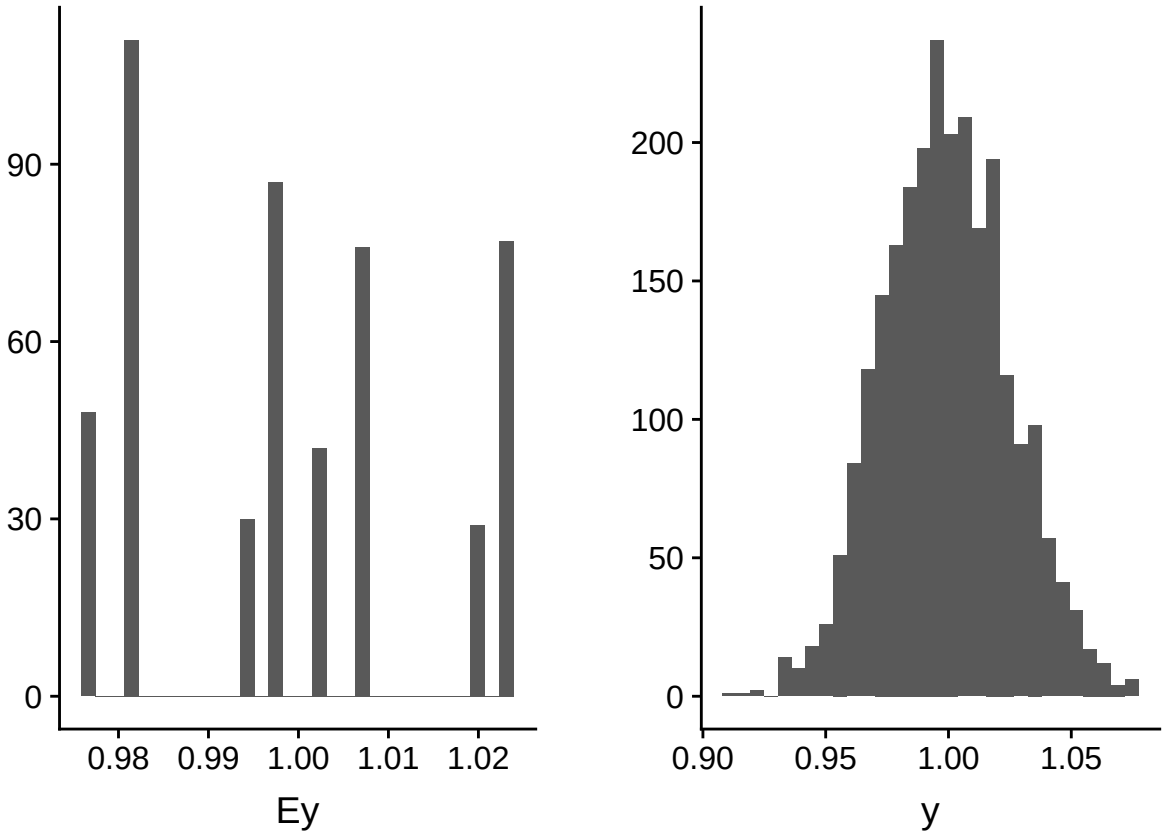


```
x<-napMCMC(y,h,X,m=1:m,n=1:n,rnorm(m,0,0.1),
           test=F,
           verbose=F,
```

```
            iterations=1000,
            FITmode = 3,
            PRImode = 2,
            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)
```

```
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")
          )
```

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```
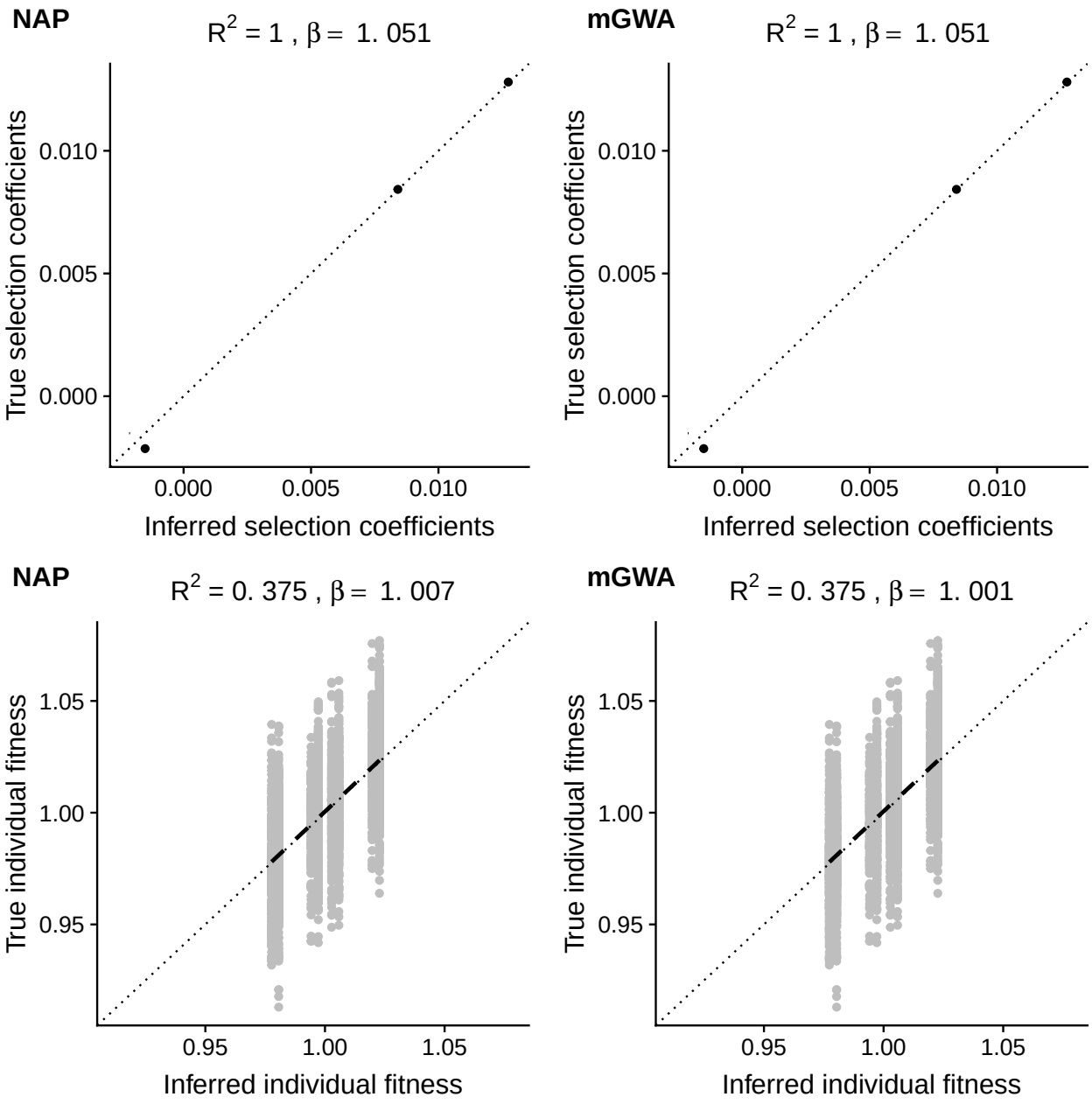

```
plot_grid(pfinal,pfin2,ncol=1)
```



With mixture lognormal prior of S and lognormal sampling of S

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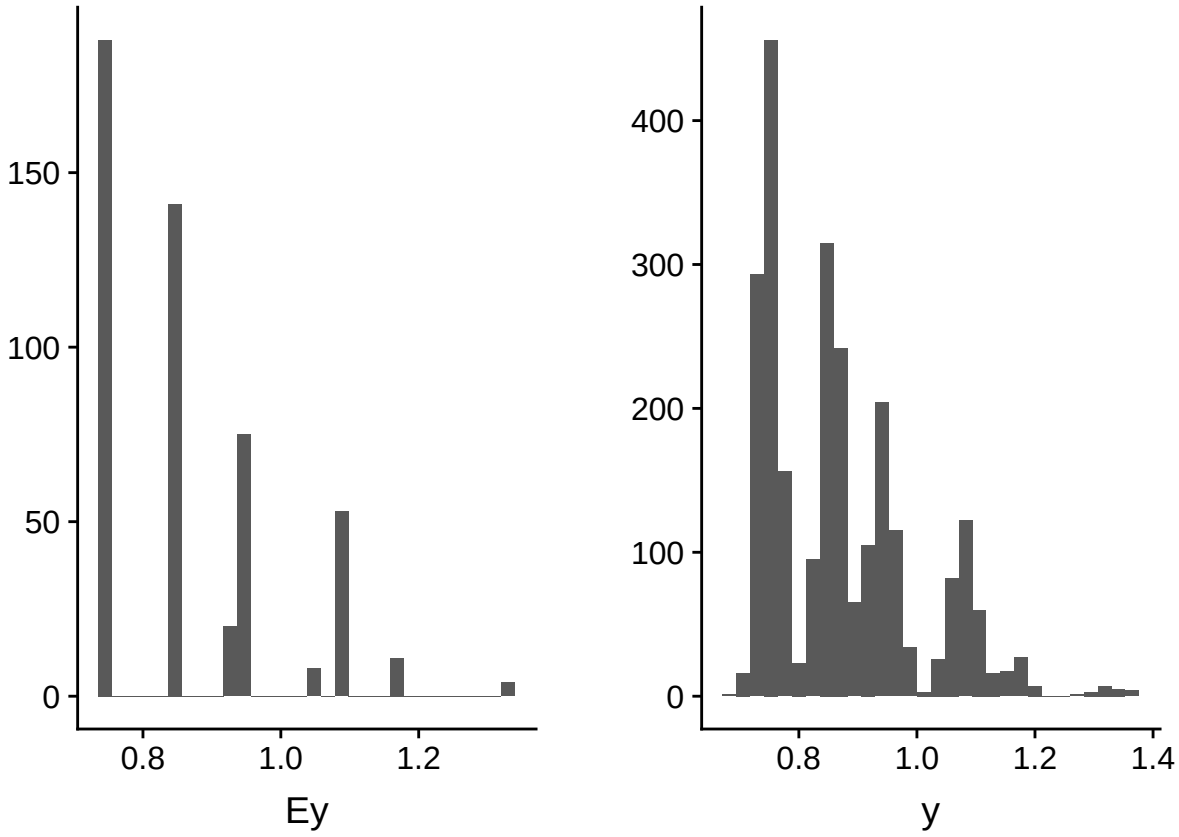


```
x<-napMCMC(y,h,X,m=1:m,n=1:n,rnorm(m,0,0.1),
           test=F,
           verbose=F,
           iterations=1000,
           FITmode = 3,
           PRImode = 2,
           Smode = 2,
           bmin=b,bmax=b,
           amin=b,amax=a,
           pmin=p,pmax=p,
           svarmin=svar,svarmax=svar,
           ssmin=ss,ssmax=ss,
           mumin=mu,mumax=mu)
```

```
pnap<-scorplot(s,x$shat)
pgwa<-scorplot(s,BMridge(X,My(y,h)))
pfinal<-plot_grid(
          pnap$psel,
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inap<-indplot(y,h,x$w)
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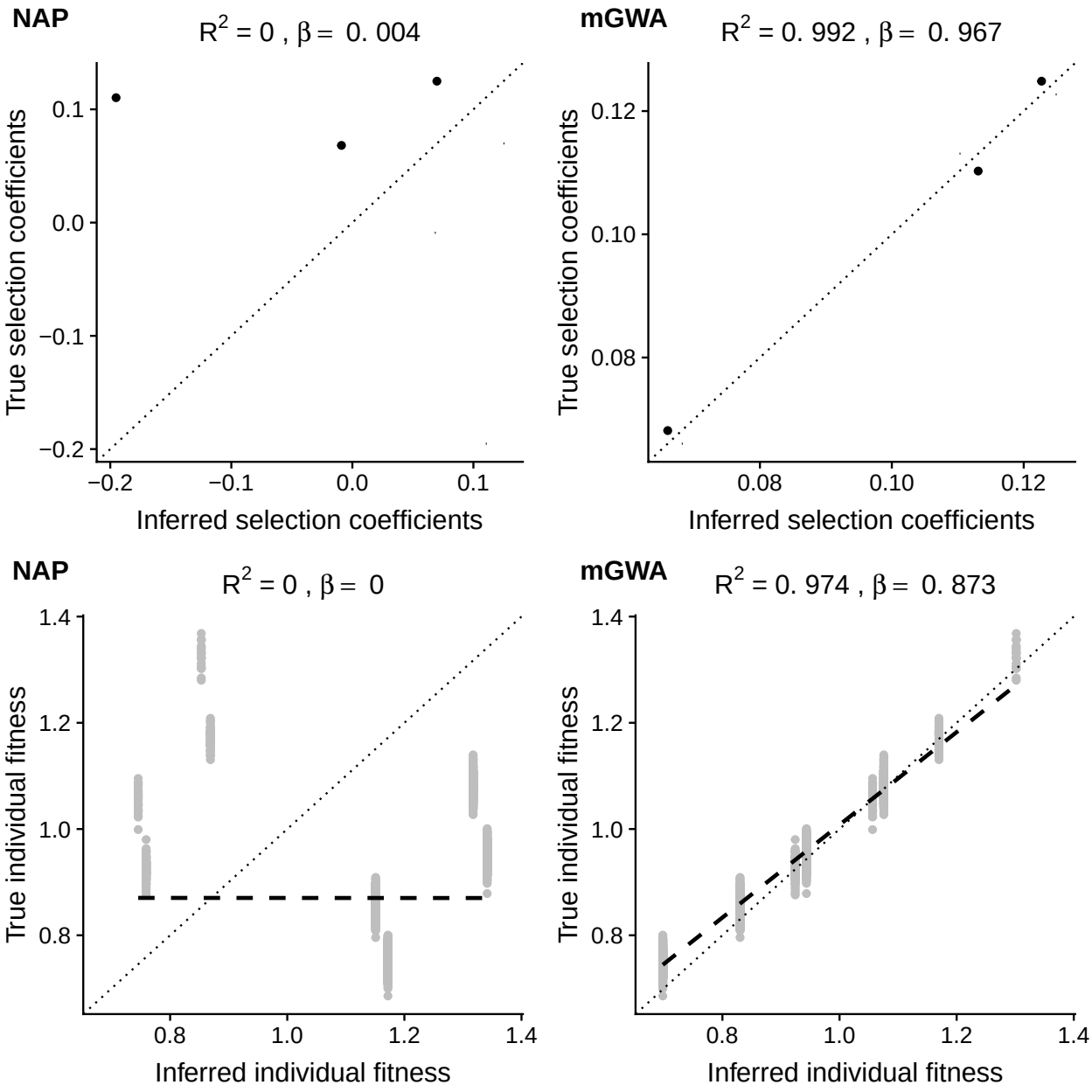
NAP
R^2 = 0 , β = 0. 004
True selection coefficients
Inferred selection coefficients
mGWA
R^2 = 0. 992 , β = 0. 967
True selection coefficients
Inferred selection coefficients
NAP
R^2 = 0 , β = 0
True individual fitness
Inferred individual fitness
mGWA
R^2 = 0. 974 , β = 0. 873
True individual fitness
Inferred individual fitness