

R script for the simulations

```
library(parallel)
rm(list=ls())

## Inbreeding measures
Funi <- function(x,hObs,pObs,m){
  rowMeans( sapply(1:m,function(j) {
    (x[,j]^2-(1+2*pObs[j])*x[,j]+2*pObs[j]*pObs[j])/(hObs[j])
  }
  ),na.rm=TRUE)
}

Fhom <- function(h,hObs){
  1-rowSums(h)/sum(hObs)
}

## Fixed simulations parameters
m <- 1000      ## Number of causal variants
p1 <- 0.3      ## Allele frequency in Population 1
a <- sqrt(5)   ## Additive effect
d <- sqrt(a^2/5) ## Dominance effect
N <- 10000     ## Sample size
ax <- a*(-1)^(1:m) ## a_j: additive effect sizes
hsq <- 0.8     ## Heritability

sim <- function(r=0.1,fst=0.0){
  n1 <- (1-r)*N
  n2 <- r*n1
  p2 <- p1 + fst

  h1 <- 2*p1*(1-p1)
  h2 <- 2*p2*(1-p2)

  d1 <- d
  d2 <- d
```

```

b <- -((1-r)*d1 + r*d2)
X1 <- matrix(rbinom(n1*m,size=2,prob=p1),nrow=n1)
X2 <- matrix(rbinom(n2*m,size=2,prob=p2),nrow=n2)

H1 <- X1*(2-X1)
H2 <- X2*(2-X2)

## scaled
x1 <- (X1-2*p1)/sqrt(h1)
x2 <- (X2-2*p2)/sqrt(h2)

H1 <- (H1-h1)/h1
H2 <- (H2-h2)/h2

g1 <- c(x1%*%ax)/m + d1*rowMeans(H1)
g2 <- c(x2%*%ax)/m + d2*rowMeans(H2)

ve1 <- var(g1)*(1/hsq-1)
ve2 <- var(g2)*(1/hsq-1)

y1 <- rnorm(n1,mean=g1,sd=sqrt(ve1))
y2 <- rnorm(n2,mean=g2,sd=sqrt(ve2))

y <- c(y1,y2)
x <- rbind(X1,X2)
H <- x*(2-x)

pObs <- 0.5*colMeans(x)
pObs <- ifelse(pObs>0.5,1-pObs,pObs)
hObs <- 2*pObs*(1-pObs)
funi <- Funi(x,hObs,pObs,m)
fhom <- Fhom(H,hObs)

return( c(Truth=b,

```

```
        Funi=as.numeric(lm(y~funi)$coefficients[2]),
        Fhom=as.numeric(lm(y~fhom)$coefficients[2]))
    )
}

B <- 10 ## Number of simulation replicates
r <- 0.25 ## Proportion of samples from Population 2 in the data
R00 <- do.call("rbind",mclapply(1:B,function(b) sim(r=r,fst= 0.00)))
Rp1 <- do.call("rbind",mclapply(1:B,function(b) sim(r=r,fst=+0.05)))
Rp2 <- do.call("rbind",mclapply(1:B,function(b) sim(r=r,fst=+0.10)))
Rn1 <- do.call("rbind",mclapply(1:B,function(b) sim(r=r,fst=-0.05)))
Rn2 <- do.call("rbind",mclapply(1:B,function(b) sim(r=r,fst=-0.10)))
```