In [1]:
```julia
include("/home/nicole/Jupyter/SSBRnoJ/src/SSBR.jl")
using SSBR
```

In [2]:
```julia
function getPos(ped,IDs)
    posAi = Array(Int64,size(IDs,1))
    for (i,id) = enumerate(IDs[:,1])
        posAi[i] = ped.idMap[id].seqID
    end
    return posAi
end
```

Out[2]: getPos (generic function with 1 method)

In [3]:
```julia
; cd Data/0.5/Q/9
```

/home/nicole/Jupyter/JG3/Data/0.5/Q/9

In [4]:
```
;ls
```

```
Correlation.G5.Q.J.txt
Correlation.G5.Q.JC.txt
G0.Genotype.ID
G0.ID
G0.noGenotype.ID
G1.Genotype.ID
G1.ID
G1.noGenotype.ID
G2.Genotype.ID
G2.ID
G2.noGenotype.ID
G3.Genotype.ID
G3.ID
G3.noGenotype.ID
G4.Genotype.ID
G4.ID
G4.noGenotype.ID
G5.Genotype.ID
G5.ID
G5.noGenotype.ID
PedAll.txt
Phe.txt
PheAll.txt
QTLNF.txt
Regression.G5.Q.J.txt
Regression.G5.Q.JC.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPQAll
meanOfSNPQG0
meanOfSNPQG1
meanOfSNPQG2
meanOfSNPQG3
meanOfSNPQG4
meanOfSNPQG5
noGenotype.ID
sim.bv
sim.phenotype
```

In [5]:
```
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```
;awk '{print $1}' QTLNF.txt | sort -b > genotype.ID
```

In [7]:
```
;join -v1 all.ID genotype.ID > noGenotype.ID
```

In [8]:
```
;awk '{print $1,$2}' Phe.txt > sim.phenotype
```

In [9]:
```
;awk '{print $1,$3}' PheAll.txt > sim.bv
```

In [10]:
```
; awk 'NR >=1 && NR <=8000 {print $1}' PedAll.txt | sort -b > G0.ID
```

```
In [11]:  ; awk 'NR >=8001 && NR <=16000 {print $1}' PedAll.txt | sort -b > G1.ID
```

```
In [12]:  ; awk 'NR >=16001 && NR <=24000 {print $1}' PedAll.txt | sort -b > G2.ID
```

```
In [13]:  ; awk 'NR >=24001 && NR <=32000 {print $1}' PedAll.txt | sort -b > G3.ID
```

```
In [14]:  ; awk 'NR >=32001 && NR <=40000 {print $1}' PedAll.txt | sort -b > G4.ID
```

```
In [15]:  ; awk 'NR >=40001 && NR <=48000 {print $1}' PedAll.txt | sort -b > G5.ID
```

```
In [16]:  ;join G0.ID genotype.ID > G0.Genotype.ID
```

```
In [17]:  ;join G1.ID genotype.ID > G1.Genotype.ID
```

```
In [18]:  ;join G2.ID genotype.ID > G2.Genotype.ID
```

```
In [19]:  ;join G3.ID genotype.ID > G3.Genotype.ID
```

```
In [20]:  ;join G4.ID genotype.ID > G4.Genotype.ID
```

```
In [21]:  ;join G5.ID genotype.ID > G5.Genotype.ID
```

```
In [22]:  ;join -v1 G0.ID genotype.ID > G0.noGenotype.ID
```

```
In [23]:  ;join -v1 G1.ID genotype.ID > G1.noGenotype.ID
```

```
In [24]:  ;join -v1 G2.ID genotype.ID > G2.noGenotype.ID
```

```
In [25]:  ;join -v1 G3.ID genotype.ID > G3.noGenotype.ID
```

```
In [26]:  ;join -v1 G4.ID genotype.ID > G4.noGenotype.ID
```

```
In [27]:  ;join -v1 G5.ID genotype.ID > G5.noGenotype.ID
```

```
In [28]:  ;wc G0.Genotype.ID;wc G1.Genotype.ID;wc G2.Genotype.ID;wc G3.Genotype.ID;wc (
          200   200 1200 G0.Genotype.ID
          200   200 1200 G1.Genotype.ID
          200   200 1200 G2.Genotype.ID
          200   200 1200 G3.Genotype.ID
          200   200 1200 G4.Genotype.ID
          8000  8000 48000 G5.Genotype.ID
```

In [29]:
```
;wc G0.noGenotype.ID;wc G1.noGenotype.ID;wc G2.noGenotype.ID;wc G3.noGenotype
```

```
  7800   7800 46800 G0.noGenotype.ID
  7800   7800 46800 G1.noGenotype.ID
  7800   7800 46800 G2.noGenotype.ID
  7800   7800 46800 G3.noGenotype.ID
  7800   7800 46800 G4.noGenotype.ID
 0 0 0 G5.noGenotype.ID
```

In [30]:
```
ped,A_Mats,numSSBayes = calc_Ai("PedAll.txt","genotype.ID",calculateInbreedi
nothing
df      = read_genotypes("QTLNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                              # wit
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes);
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(Z_Mats,M_Mats,numSSBayes)           # no
nothing
```

In [31]:
```
vRes   = 0.547
vG     = 0.547
nIter  = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter,
nothing
```

```
This is iteration 5000
This is iteration 10000
This is iteration 15000
This is iteration 20000
This is iteration 25000
This is iteration 30000
This is iteration 35000
This is iteration 40000
This is iteration 45000
This is iteration 50000
3527.523007 seconds (23.01 G allocations: 723.503 GB, 7.61% gc time)
```

In [32]:
```
betaHat
```

Out[32]:
```
1-element Array{Float64,1}:
 10.0392
```

In [33]:
```
using DataFrames
```

In [34]:
```
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',hea
a  = Array(Float64,numSSBayes.num_ped)
for (i,ID) in enumerate(df[:,1])
    j = ped.idMap[ID].seqID
    a[j] = df[i,2]
end
```

In [35]:
```
IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor1 = cor(a[posAi],aHat1[posAi])[1,1]
reg1 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - all.ID : correlation = %6.3f\n", cor1 ) # with (
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
JCAll = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.906
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.987
```

Out[35]: 0.9059110708766369

In [36]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[36]: 1.376177245314627

In [37]:
```
IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=
posAi = getPos(ped,IDs)
cor2 = cor(a[posAi],aHat1[posAi])[1,1]
reg2 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - genotype.ID : correlation = %6.3f\n", cor2 ) # u
@printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3:
JCAll = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.929
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.159
```

Out[37]: 0.9291963111501821

In [38]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[38]: 2.4002114975850826

In [39]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
posAi = getPos(ped,IDs)
cor3 = cor(a[posAi],aHat1[posAi])[1,1]
reg3 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - noGenotype.ID : correlation = %6.3f\n", cor3 ) ;
@printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV = %6
JCAll = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.870
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.952
```

Out[39]: 0.869682374836503

In [40]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[40]: 1.1398616486368294

```
In [41]: IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false
         posAi = getPos(ped,IDs)
         cor4 = cor(a[posAi],aHat1[posAi])[1,1]
         reg4 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G0.ID : correlation = %6.3f\n", cor4 ) # with e]
         @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G0.ID : correlation =  0.673
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.786
```

Out[41]: 0.6730821824591874

```
In [42]: GEBV = aHat1[posAi]
         G1GEBV=mean(GEBV)
```

Out[42]: 0.1252846428453606

```
In [43]: IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=false
         posAi = getPos(ped,IDs)
         cor4 = cor(a[posAi],aHat1[posAi])[1,1]
         reg4 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G1.ID : correlation = %6.3f\n", cor4 ) # with e]
         @printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G1.ID : correlation =  0.773
         SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.980
```

Out[43]: 0.772976822727442

```
In [44]: GEBV = aHat1[posAi]
         G1GEBV=mean(GEBV)
```

Out[44]: 0.7152648753743329

```
In [45]: IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=false
         posAi = getPos(ped,IDs)
         cor5 = cor(a[posAi],aHat1[posAi])[1,1]
         reg5 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G2.ID : correlation = %6.3f\n", cor5 ) # with e]
         @printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor5
```

```
         SSBRJC from Gibbs - G2.ID : correlation =  0.764
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.011
```

Out[45]: 0.7642147625611125

```
In [46]: GEBV = aHat1[posAi]
         G2GEBV=mean(GEBV)
```

Out[46]: 1.2193292293314932

In [47]:
```
IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor6 = cor(a[posAi],aHat1[posAi])[1,1]
reg6 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G3.ID : correlation = %6.3f\n", cor6 ) # with e
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =   0.760
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.013
```

Out[47]: 0.7596087555022532

In [48]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[48]: 1.6724998790220134

In [49]:
```
IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat1[posAi])[1,1]
reg7 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.ID : correlation = %6.3f\n", cor7 ) # with e
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =   0.761
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.042
```

Out[49]: 0.7605485377248576

In [50]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[50]: 2.088160832650248

In [51]:
```
IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat1[posAi])[1,1]
reg8 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.ID : correlation = %6.3f\n", cor8 ) # with e
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.920
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.148
```

Out[51]: 0.9203896742115419

In [52]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[52]: 2.436524012664314

```
In [53]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat1[posAi])[1,1]
         #TBV = a[posAi]
         #GEBV = aHat1[posAi]
         #reg = linreg(X,Y)
         #reg = linreg(GEBV, TBV)[2,1]
         reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G0.Genotype.ID : correlation = %6.3f\n", cor9 )
         @printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor9
```

```
         SSBRJC from Gibbs - G0.Genotype.ID : correlation =   0.916
         SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =   1.079
```

Out[53]: 0.915655966660796

```
In [54]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[54]: 1.3855302706435324

```
In [55]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat1[posAi])[1,1]
         #TBV = a[posAi]
         #GEBV = aHat1[posAi]
         #reg = linreg(X,Y)
         #reg = linreg(GEBV, TBV)[2,1]
         reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G1.Genotype.ID : correlation = %6.3f\n", cor9 )
         @printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor9
```

```
         SSBRJC from Gibbs - G1.Genotype.ID : correlation =   0.906
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =   1.030
```

Out[55]: 0.9057573521366803

```
In [56]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[56]: 1.79406915296006

```
In [57]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         posAi = getPos(ped,IDs)
         cor10 = cor(a[posAi],aHat1[posAi])[1,1]
         reg10 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G2.Genotype.ID : correlation = %6.3f\n", cor10
         @printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor10
```

```
         SSBRJC from Gibbs - G2.Genotype.ID : correlation =   0.898
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.044
```

Out[57]: 0.8980001160611681

In [58]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[58]: 2.1462803512780693

In [59]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor11 = cor(a[posAi],aHat1[posAi])[1,1]
reg11 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G3.Genotype.ID : correlation = %6.3f\n", cor11
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =   0.878
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   1.003
```

Out[59]: 0.8777551853226561

In [60]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[60]: 2.4753255557877925

In [61]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor12 = cor(a[posAi],aHat1[posAi])[1,1]
reg12 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.Genotype.ID : correlation = %6.3f\n", cor12
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =   0.893
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   1.079
```

Out[61]: 0.8928988752045394

In [62]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[62]: 2.7473515540867193

In [63]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor13 = cor(a[posAi],aHat1[posAi])[1,1]
reg13 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.Genotype.ID : correlation = %6.3f\n", cor13
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =   0.920
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   1.148
```

Out[63]: 0.9203896742115419

In [64]:
```
writedlm("Correlation.G5.Q.N.txt",cor13)
```

```
In [65]:  writedlm("Regression.G5.Q.N.txt",reg13)
```

```
In [66]:  GEBVG5Gall = aHat1[posAi]
          GEBVG5G=mean(GEBVG5Gall)
```

Out[66]: 2.436524012664314

```
In [67]:  IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          posAi = getPos(ped,IDs)
          cor14 = cor(a[posAi],aHat1[posAi])[1,1]
          reg14 = linreg(aHat1[posAi], a[posAi])[2,1]
          @printf("SSBRJC from Gibbs - G0.noGenotype.ID : correlation = %6.3f\n", cor14
          @printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 9
          JCAll = cor14
```

```
          SSBRJC from Gibbs - G0.noGenotype.ID : correlation =   0.653
          SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.789
```

Out[67]: 0.6525804742898854

```
In [68]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[68]: 0.09297065238899724

```
In [69]:  IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          posAi = getPos(ped,IDs)
          cor14 = cor(a[posAi],aHat1[posAi])[1,1]
          reg14 = linreg(aHat1[posAi], a[posAi])[2,1]
          @printf("SSBRJC from Gibbs - G1.noGenotype.ID : correlation = %6.3f\n", cor14
          @printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 9
          JCAll = cor14
```

```
          SSBRJC from Gibbs - G1.noGenotype.ID : correlation =   0.757
          SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   0.986
```

Out[69]: 0.7568062632457984

```
In [70]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[70]: 0.6876032272311091

```
In [71]:  IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          posAi = getPos(ped,IDs)
          cor15 = cor(a[posAi],aHat1[posAi])[1,1]
          reg15 = linreg(aHat1[posAi], a[posAi])[2,1]
          @printf("SSBRJC from Gibbs - G2.noGenotype.ID : correlation = %6.3f\n", cor15
          @printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 9
          JCAll = cor15
```

```
          SSBRJC from Gibbs - G2.noGenotype.ID : correlation =   0.747
          SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   1.007
```

Out[71]: 0.7465400270630191

```
In [72]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[72]: 1.1955612518456837

```
In [73]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         posAi = getPos(ped,IDs)
         cor16 = cor(a[posAi],aHat1[posAi])[1,1]
         reg16 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G3.noGenotype.ID : correlation = %6.3f\n", cor16
         @printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = %
         JCAll = cor16
```

```
         SSBRJC from Gibbs - G3.noGenotype.ID : correlation =   0.745
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =   1.005
```

Out[73]: 0.7446142523502168

```
In [74]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[74]: 1.6519146052587883

```
In [75]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         posAi = getPos(ped,IDs)
         cor17 = cor(a[posAi],aHat1[posAi])[1,1]
         reg17 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : correlation = %6.3f\n", cor17
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = %
         JCAll = cor17
```

```
         SSBRJC from Gibbs - G4.noGenotype.ID : correlation =   0.747
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   1.033
```

Out[75]: 0.7472980968034276

```
In [76]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[76]: 2.071258506459569

```
In [77]: numSSBayes
```

Out[77]: SSBR.NumSSBayes(54966,45966,9000,40000,39000,1000,50)