

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

```
In [2]: function getPos(ped,IDs)
        posAi = Array{Int64,1}(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]: ; cd Data/0.5/Q/10

        /home/nicole/Jupyter/JG3/Data/0.5/Q/10
```

```
In [4]: ;ls

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.JC.txt
all.ID
genotype.ID
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 G4.Genotype.ID;wc G5.Genotype.ID
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.ID;wc G4.noGenotype.ID;wc G5.noGenotype.ID
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",calculateInbreedingCoefficients,
nothing
df = read_genotypes("QTLNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped,center=true); # with centering
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 centering
nothing
```

```
In [31]: vRes = 0.583
vG = 0.583
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
2241.174170 seconds (22.99 G allocations: 723.033 GB, 8.85% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
 9.64884
```

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

```
In [34]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ', header=:a
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 a
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.901
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.014
```

```
Out[35]: 0.9011383230167215
```

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

```
Out[36]: 0.14473291034394242
```

```
In [37]: IDs = readtable("genotype.ID", eltypes=[UTF8String], separator = ' ', header=:false)
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) # with a
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n",
JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.834
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.155
```

```
Out[37]: 0.834121358665204
```

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

```
Out[38]: 1.206702023035731
```

```
In [39]: IDs = readtable("noGenotype.ID", eltypes=[UTF8String], separator = ' ', header=:false)
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) # with a
@printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n",
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.871
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.966
```

```
Out[39]: 0.8713095778569397
```

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

```
Out[40]: -0.10033688489262432
```

```
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", r
         JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.676
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.790
```

```
Out[41]: 0.6756542201341477
```

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

```
Out[42]: -1.2239288741090397
```

```
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", r
         JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.763
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.982
```

```
Out[43]: 0.7633855686489827
```

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

```
Out[44]: -0.5383516002719734
```

```
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", r
         JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.753
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.033
```

```
Out[45]: 0.7526885002774317
```

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

```
Out[46]: 0.02708938823332143
```

```
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", r
         JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.761
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.096
```

```
Out[47]: 0.7606165201346942
```

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

```
Out[48]: 0.48771540003020813
```

```
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", r
         JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.759
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.117
```

```
Out[49]: 0.7585869639780348
```

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

```
Out[50]: 0.8748952722078815
```

```
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", r
         JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.814
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.115
```

```
Out[51]: 0.8138376524280027
```

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

```
Out[52]: 1.2409778759732562
```

```
In [53]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat1[posAi])[1,1]
         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 = %6.3f\n", reg9 )
         JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.847
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.156
```

```
Out[53]: 0.8467527565223302
```

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

```
Out[54]: 0.2534167110993605
```

```
In [55]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat1[posAi])[1,1]
         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 = %6.3f\n", reg9 )
         JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.776
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.917
```

```
Out[55]: 0.7759147124367287
```

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

```
Out[56]: 0.6850207940636569
```

```
In [57]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         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 = %6.3f\n", reg10 )
         JCall = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.780
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.009
```

```
Out[57]: 0.779623303791962
```

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

```
Out[58]: 0.9830867316645511
```

```
In [59]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         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 = %6.3f\n", reg11)
         JCall = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.783
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.965
```

```
Out[59]: 0.7831420896022111
```

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

```
Out[60]: 1.2032064799299105
```

```
In [61]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         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 = %6.3f\n", reg12)
         JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.676
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.778
```

```
Out[61]: 0.6764546227237799
```

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

```
Out[62]: 1.5377452809201784
```

```
In [63]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         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 = %6.3f\n", reg13)
         JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.814
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.115
```

```
Out[63]: 0.8138376524280027
```

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



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

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

```
Out[66]: 1.2409778759732562
```

```
In [67]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg14)
         JCall = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.655
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.803
```

```
Out[67]: 0.6554542586302264
```

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

```
Out[68]: -1.261809530140024
```

```
In [69]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg14)
         JCall = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.745
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.991
```

```
Out[69]: 0.7447509819881796
```

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

```
Out[70]: -0.5697201232036562
```

```
In [71]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg15)
         JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.737
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.034
```

```
Out[71]: 0.7369398020383328
```

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

```
Out[72]: 0.002576635837648907
```

```
In [73]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg16)
         JCall = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.748
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.086
```

```
Out[73]: 0.7482794271809122
```

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

```
Out[74]: 0.46936947490457476
```

```
In [75]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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 = %6.3f\n", reg17)
         JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.748
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.106
```

```
Out[75]: 0.7479326846095843
```

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

```
Out[76]: 0.8578991181383353
```

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

```
Out[77]: SSBR.NumSSBayes(54932,45932,9000,40000,39000,1000,50)
```