

```
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/0.5g2k/G/7

        /home/nicole/Jupyter/JG3/Data/0.5g2k/G/7
```

```
In [4]: ;ls
        GENR.txt
        PedAll.txt
        Phe.txt
        PheAll.txt
        Regression.G5.G.J.txt
        Regression.G5.G.JC.txt
        Regression.G5.G.PBLUP.txt
        all.ID
        alphaEstimates
        genotype.ID
        meanOfSNPGAll
        meanOfSNPGG0
        meanOfSNPGG1
        meanOfSNPGG2
        meanOfSNPGG3
        meanOfSNPGG4
        meanOfSNPGG5
        noGenotype.ID
        sim.bv
        sim.phenotype
```

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

```
In [6]: ;awk '{print $1}' GenNF.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
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 G
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",calculateInbreeding=false)
nothing
df      = read_genotypes("GenNF.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 J
nothing
```

```
In [31]: vG      = 0.910
         vRes    = 0.910
         nIter   = 50000
         @time aHat1,alphaHat,betaHat,epsiHat =
         ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter, outFreq=5000);
         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
         7090.648692 seconds (23.86 G allocations: 737.010 GB, 2.79% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
          32.9262
```

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

```
In [34]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',header=false)
         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 epsilon
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.920
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.992
```

```
Out[35]: 0.9198278049747344
```

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

```
Out[36]: 0.17802720414575932
```

```
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 epsilon
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.915
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.068
```

```
Out[37]: 0.9154303127796041
```

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

```
Out[38]: 1.6213362683858907
```

```
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 epsilon
@printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg3)
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.888
```

```
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.976
```

```
Out[39]: 0.8875897773700231
```

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

```
Out[40]: -0.1550441183711941
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCA11 = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.744
```

```
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.960
```

```
Out[41]: 0.7438252069660316
```

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

```
Out[42]: -1.5178974639255118
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.774
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.991
```

```
Out[43]: 0.7744014892995562
```

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

```
Out[44]: -0.6965814135975855
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.762
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.001
```

```
Out[45]: 0.7618524030514678
```

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

```
Out[46]: -0.052101404935098704
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.769
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.999
```

```
Out[47]: 0.7688306218646838
```

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

```
Out[48]: 0.5246789464452924
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.770
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.010
```

```
Out[49]: 0.770314124092582
```

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

```
Out[50]: 1.1327761334217996
```



```
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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.899
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.057
```

```
Out[51]: 0.8988903527939056
```

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

```
Out[52]: 1.6772884274656599
```

```
In [53]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.943
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.105
```

```
Out[53]: 0.9427311653879228
```

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

```
Out[54]: 0.18428098075956853
```

```
In [55]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.943
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.026
```

```
Out[55]: 0.9427496745382086
```

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

```
Out[56]: 0.6593135877647647
```

```
In [57]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg10)
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.939
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.044
```

```
Out[57]: 0.9394378973360891
```

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

```
Out[58]: 1.1394714477296046
```

```
In [59]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg11)
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.928
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.026
```

```
Out[59]: 0.9277028855059453
```

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

```
Out[60]: 1.7206829349275734
```

```
In [61]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg12)
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.874
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.009
```

```
Out[61]: 0.8742742227412368
```

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

```
Out[62]: 2.1648460275571733
```

```
In [63]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg13)
JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.899
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.057
```

```
Out[63]: 0.8988903527939056
```

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

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

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

```
Out[66]: 1.6772884274656599
```

```
In [67]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.722
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.976
```

```
Out[67]: 0.7220890353106016
```

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

```
Out[68]: -1.5615430650712834
```

```
In [69]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.756
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.995
```

```
Out[69]: 0.7558139664033644
```

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

```
Out[70]: -0.7313479520940559
```

```
In [71]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg15)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.744
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.003
```

```
Out[71]: 0.7444777969456522
```

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

```
Out[72]: -0.08265455500342443
```

```
In [73]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg16)
JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.750
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.993
```

```
Out[73]: 0.74981778547866
```

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

```
Out[74]: 0.49401217750984944
```

```
In [75]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg17)
JCA11 = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.756
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.003
```

```
Out[75]: 0.7555057061985012
```

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

```
Out[76]: 1.106312802802944
```

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

```
Out[77]: SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,2000)
```

