

```
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/9  
  
/home/nicole/Jupyter/JG3/Data/0.5g2k/G/9
```

```
In [4]: ;ls  
GENOTYPE.CAT  
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      = 0.682
         vRes    = 0.682
         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
7101.534771 seconds (23.87 G allocations: 737.327 GB, 2.79% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
          31.5823
```

```
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)
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.920
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.997
```

```
Out[35]: 0.9197799743227089
```

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

```
Out[36]: 0.15339732582538826
```

```
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)
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.916
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.094
```

```
Out[37]: 0.9162015860541391
```

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

```
Out[38]: 1.4753020036396822
```

```
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 = 0.886
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.979
```

```
Out[39]: 0.8861083474784182
```

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

```
Out[40]: -0.15165759982406415
```

```
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 = 0.709
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.859
```

```
Out[41]: 0.7086452865879931
```

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

```
Out[42]: -1.3395578785883744
```

```
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 = 0.781
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.002
```

```
Out[43]: 0.7812460940143859
```

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

```
Out[44]: -0.6802060246533074
```

```
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 = 0.773
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.026
```

```
Out[45]: 0.7734263325118542
```

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

```
Out[46]: -0.0710330469600977
```

```
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 = 0.773
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.056
```

```
Out[47]: 0.7733121859548205
```

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

```
Out[48]: 0.48316333338156014
```

```
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 = 0.786
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.061
```

```
Out[49]: 0.7856813509333345
```

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

```
Out[50]: 0.9977540739875305
```



```
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 =  0.898
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.083
```

```
Out[51]: 0.8979903794787689
```

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

```
Out[52]: 1.5302634977850185
```

```
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 =  0.941
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.079
```

```
Out[53]: 0.9408486289665171
```

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

```
Out[54]: 0.04641184027395306
```

```
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 =  0.933
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.062
```

```
Out[55]: 0.933111847192559
```

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

```
Out[56]: 0.5764004363018741
```

```
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 =  0.928
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.075
```

```
Out[57]: 0.9277481305773975
```

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

```
Out[58]: 1.0522668225764824
```

```
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 = 0.933
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.080
```

```
Out[59]: 0.9327267779087717
```

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

```
Out[60]: 1.4903573066635485
```

```
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 = 0.882
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.033
```

```
Out[61]: 0.8820155751078456
```

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

```
Out[62]: 2.012613846569097
```

```
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 =  0.898
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.083
```

```
Out[63]: 0.8979903794787689
```

```
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]: 1.5302634977850185
```

```
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 =  0.688
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.864
```

```
Out[67]: 0.688368722668774
```

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

```
Out[68]: -1.3750955636874083
```

```
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 =  0.764
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.009
```

```
Out[69]: 0.7638908255337125
```

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

```
Out[70]: -0.7124267031393378
```

```
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 =  0.755
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.025
```

```
Out[71]: 0.7552024200026751
```

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

```
Out[72]: -0.09983560771744587
```

```
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 =  0.757
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.056
```

```
Out[73]: 0.7568936407154426
```

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

```
Out[74]: 0.4573378468871502
```

```
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 =  0.770
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.059
```

```
Out[75]: 0.7701287055294739
```

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

```
Out[76]: 0.971732028536721
```

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

```
Out[77]: SSBR.NumSSBayes(54936,45936,9000,40000,39000,1000,2000)
```

