

```
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/1  
  
/home/nicole/Jupyter/JG3/Data/0.5/Q/1
```

In [4]: ;ls

```
Correlation.G5.Q.J.txt
Correlation.G5.Q.JC.txt
Correlation.G5.Q.N.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
Regression.G5.Q.N.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPQA11
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 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
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
nothing
df      = read_genotypes("QTLNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped,center=true);           # with
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      = 0.668
vG        = 0.668
nIter     = 50000
@time aHat1,alphaHat,betaHat,epsHat =
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
2104.267346 seconds (22.98 G allocations: 722.674 GB, 9.05% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
11.2352
```

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

```
In [34]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ',head
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",
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.909
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.986
```

```
Out[35]: 0.9092793924920715
```

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

```
Out[36]: 0.14483591433013424
```

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

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.945
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.161
```

```
Out[37]: 0.945443709192305
```

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

```
Out[38]: 1.2493938765498742
```

```
In [39]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=
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 = %6.3f\n",
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.874
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.955
```

```
Out[39]: 0.8738528142239895
```

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

```
Out[40]: -0.11006207695134435
```

```
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 = 0.708
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.844
```

```
Out[41]: 0.7076591245263194
```

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

```
Out[42]: -1.2246541450993478
```

```
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 = 0.775
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.991
```

```
Out[43]: 0.7749415601089006
```

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

```
Out[44]: -0.5631337845008101
```

```
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 = 0.766
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.007
```

```
Out[45]: 0.7660559331613697
```

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

```
Out[46]: -0.007507964138409179
```

```
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 = 0.766
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.019
```

```
Out[47]: 0.7659339242425324
```

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

```
Out[48]: 0.4750485956265219
```

```
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 = 0.779
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.039
```

```
Out[49]: 0.7787807141997974
```

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

```
Out[50]: 0.902643315969096
```

```
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 = 0.938
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.147
```

```
Out[51]: 0.9384101914451651
```

```
In [52]: writedlm("Correlation.G5.Q.C.txt",cor13)
```

```
LoadError: UndefVarError: cor13 not defined
while loading In[52], in expression starting on line 1
```

```
In [53]: writedlm("Regression.G5.Q.C.txt",reg13)
```

```
LoadError: UndefVarError: reg13 not defined
while loading In[53], in expression starting on line 1
```

```
In [54]: GEBV = aHat1[posAi]
         G5GEBV=mean(GEBV)
```

```
Out[54]: 1.2866194681237544
```

```
In [55]: 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 = 0.939
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.109
```

```
Out[55]: 0.9391026558321032
```

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

```
Out[56]: 0.17797796275308586
```

```
In [57]: 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 = 0.953
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.102
```

```
Out[57]: 0.9529067771803542
```

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

```
Out[58]: 0.6280022707298288
```



```
In [59]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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)
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.938
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.130
```

```
Out[59]: 0.9381405633078309
```

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

```
Out[60]: 1.0088301045670138
```

```
In [61]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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)
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.922
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.077
```

```
Out[61]: 0.9222427792311599
```

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

```
Out[62]: 1.3170628216145948
```

```
In [63]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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)
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.924
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.096
```

```
Out[63]: 0.9240091038843435
```

```
In [64]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[64]: 1.626072560129655
```

```
In [65]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 = 0.938

SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.147

Out[65]: 0.9384101914451651

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

Out[66]: 1.2866194681237544

```
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 = 0.690

SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.855

Out[67]: 0.6897511651109006

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

Out[68]: -1.2606190709417178

```
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 = 0.758

SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.997

Out[69]: 0.7581643645886982

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

Out[70]: -0.593675734634929

```
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)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.749
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.004
```

```
Out[71]: 0.7485807895820472
```

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

```
Out[72]: -0.03356791461803537
```

```
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)
JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.751
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.011
```

```
Out[73]: 0.7505915859751889
```

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

```
Out[74]: 0.4534584872678534
```

```
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)
JCA11 = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.767
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.031
```

```
Out[75]: 0.7672746038227632
```

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

```
Out[76]: 0.884093848170107
```

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

```
Out[77]: SSBR.NumSSBayes(54906,45906,9000,40000,39000,1000,50)
```