

```
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/G/3  
  
/home/nicole/Jupyter/JG3/Data/0.5/G/3
```

In [4]: ;ls

```
Correlation.G5.G.C.txt
Correlation.G5.G.J.txt
Correlation.G5.G.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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.C.txt
Regression.G5.G.J.txt
Regression.G5.G.JC.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPGA11
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 (
          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("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped); # 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      = 0.664
vG       = 0.664
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
2538.987203 seconds (23.03 G allocations: 723.220 GB, 7.37% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
 9.65927
```

```
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",
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.912
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.981
```

```
Out[35]: 0.9120368075943468
```

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

```
Out[36]: 1.4776567773616889
```

```
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",
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.965
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.074
```

```
Out[37]: 0.9649998295985445
```

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

```
Out[38]: 2.614606610486485
```

```
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",
JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.873
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.963
```

```
Out[39]: 0.8734826037302009
```

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

```
Out[40]: 1.2152837389482745
```

```
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
JCA11 = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.701
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.865
```

```
Out[41]: 0.7010972678568946
```

```
In [42]: GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

```
Out[42]: 0.12442564890863389
```

```
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
JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.777
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.980
```

```
Out[43]: 0.7766902365110032
```

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

```
Out[44]: 0.7669409177378552
```

```
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
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.756
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.994
```

```
Out[45]: 0.7563540356988375
```

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

```
Out[46]: 1.3066239657515955
```

```
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 = 0.751
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.003
```

```
Out[47]: 0.7508655400239576
```

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

```
Out[48]: 1.7834037008548842
```

```
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 = 0.767
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.996
```

```
Out[49]: 0.7666145644679409
```

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

```
Out[50]: 2.227692164612667
```

```
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 = 0.960
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.065
```

```
Out[51]: 0.9602176989760197
```

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

```
Out[52]: 2.656854266304497
```

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

SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.963

SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.095

Out[53]: 0.9625622274838107

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

Out[54]: 1.4461102633006118

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

SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.959

SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.089

Out[55]: 0.9590128111502637

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

Out[56]: 1.907746916476871

```
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 = 0.958

SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.086

Out[57]: 0.958477805064759


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

```
Out[58]: 2.2965894884234546
```

```
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 = 0.963
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.054
```

```
Out[59]: 0.9631670641239795
```

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

```
Out[60]: 2.697477294966186
```

```
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 = 0.947
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.044
```

```
Out[61]: 0.94737578827399
```

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

```
Out[62]: 3.0352028565448115
```

```
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 = 0.960
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.065
```

```
Out[63]: 0.9602176989760197
```

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

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

```
In [66]: TBVG5Gall = a[posAi]
         TBVG5G=mean(TBVG5Gall)
```

```
Out[66]: 12.321140625
```

```
In [67]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[67]: 2.656854266304497
```

```
In [68]: 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 = 0.678
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.863
```

```
Out[68]: 0.6775019639338414
```

```
In [69]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[69]: 0.09053629982166009
```

```
In [70]: 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 = 0.760
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.983
```

```
Out[70]: 0.7596738317385966
```

```
In [71]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[71]: 0.7376894818727522
```

```
In [72]: 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 = 0.739
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.994
```

```
Out[72]: 0.7394347214814653
```

```
In [73]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[73]: 1.281240234401035
```

```
In [74]: 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 = 0.734
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.002
```

```
Out[74]: 0.7337235107545137
```

```
In [75]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[75]: 1.759965916390492
```

```
In [76]: 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 = 0.751
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.988
```

```
Out[76]: 0.7511715631044276
```

```
In [77]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[77]: 2.2069867622554327
```

```
In [78]: numSSBayes
```

```
Out[78]: SSBR.NumSSBayes(54866,45866,9000,40000,39000,1000,200)
```