

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

```
In [2]: function getPos(ped,IDs)  
        posAi = Array{Int64,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/2  
  
/home/nicole/Jupyter/JG3/Data/0.5/G/2
```

```
In [4]: ;ls  
  
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  
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}' 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.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("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped,center=true);
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
J_Vecs = make_JVecs(numSSBayes,A_Mats)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(J_Vecs,Z_Mats,M_Mats,numSSBayes)
nothing
```

```
In [31]: vRes      = 0.714
vG       = 0.714
nIter    = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG)
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
2533.552047 seconds (23.06 G allocations: 724.116 GB, 7.52% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 13.3851
  4.57653
```

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

```
In [34]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ', header=:true,
a = Array{Float64,1}(undef, 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",
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.917
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.970
```

```
Out[35]: 0.917486106554202
```

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

```
Out[36]: -2.7004992749667576
```

```
In [37]: IDs = readtable("genotype.ID", eltypes=[UTF8String], separator = ' ', header=:true,
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",
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.980
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.046
```

```
Out[37]: 0.9795131046547053
```

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

```
Out[38]: -1.4656287972307858
```

```
In [39]: IDs = readtable("noGenotype.ID", eltypes=[UTF8String], separator = ' ', header=:true,
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",
JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.879
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.960
```

```
Out[39]: 0.8790070159154804
```

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

```
Out[40]: -2.9854693852135195
```

```
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 =  0.715
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.877
```

```
Out[41]: 0.7149064372800424
```

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

```
Out[42]: -4.115816189700654
```

```
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 =  0.777
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.981
```

```
Out[43]: 0.777496985926766
```

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

```
Out[44]: -3.4689955755567654
```

```
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 =  0.767
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.993
```

```
Out[45]: 0.7673549778547977
```

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

```
Out[46]: -2.907930484462935
```

```
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 =  0.757
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.969
```

```
Out[47]: 0.7572573238531817
```

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

```
Out[48]: -2.402151396396509
```

```
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 =  0.783
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.990
```

```
Out[49]: 0.783077663776796
```

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

```
Out[50]: -1.8913541444325446
```

```
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 =  0.976
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.044
```

```
Out[51]: 0.9764404904762257
```

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

```
Out[52]: -1.4167478592511356
```

```
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 = 0.979
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.075
```

```
Out[53]: 0.9785338211006752
```

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

```
Out[54]: -2.822294081664469
```

```
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 = 0.973
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.048
```

```
Out[55]: 0.9725961397611861
```

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

```
Out[56]: -2.287751260445244
```

```
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 = 0.973
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.046
```

```
Out[57]: 0.9728252593822369
```

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

```
Out[58]: -1.8359695735129935
```

```
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 = 0.976
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.024
```

```
Out[59]: 0.975958248320758
```

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

```
Out[60]: -1.3484510315051152
```

```
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 = 0.966
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.016
```

```
Out[61]: 0.9655815339008198
```

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

```
Out[62]: -0.9889155582121067
```

```
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 = 0.976
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.044
```

```
Out[63]: 0.9764404904762257
```

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



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

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

```
Out[66]: 11.93719025
```

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

```
Out[67]: -1.4167478592511356
```

```
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 = 0.694
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.875
```

```
Out[68]: 0.6940503625291776
```

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

```
Out[69]: -4.148983423240043
```

```
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]: 0.7604808203908006
```

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

```
Out[71]: -3.4992838913288553
```

```
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 = 0.750
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[72]: 0.7496056305858814
```

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

```
Out[73]: -2.9354166616667796
```

```
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 = 0.738
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.967
```

```
Out[74]: 0.7377219374006387
```

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

```
Out[75]: -2.429169354470647
```

```
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 = 0.769
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.988
```

```
Out[76]: 0.7689416662872751
```

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

```
Out[77]: -1.914493595361274
```

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

```
Out[78]: SSBR.NumSSBayes(54930,45930,9000,40000,39000,1000,200)
```

```
In [79]: J1 = sortrows(J_Vecs.J1)
```

```
Out[79]: 45930x1 Array{Float64,2}:  
  -0.990158  
  -0.987733  
  -0.986842  
  -0.985656  
  -0.985605  
  -0.985577  
  -0.985391  
  -0.985278  
  -0.985237  
  -0.985237  
  -0.984445  
  -0.984331  
  -0.98427  
  ⋮  
  6.10158e-17  
  6.6476e-17  
  6.95133e-17  
  7.39894e-17  
  7.40868e-17  
  8.14434e-17  
  8.86519e-17  
  1.00099e-16  
  1.11372e-16  
  1.16871e-16  
  1.22182e-16  
  1.4449e-16
```

```
In [80]: J1[J1 .< 0.0,:]
```

```
Out[80]: 43908x1 Array{Float64,2}:  
  -0.990158  
  -0.987733  
  -0.986842  
  -0.985656  
  -0.985605  
  -0.985577  
  -0.985391  
  -0.985278  
  -0.985237  
  -0.985237  
  -0.984445  
  -0.984331  
  -0.98427  
  ⋮  
 -1.26861e-35  
 -1.0855e-35  
 -7.35892e-36  
 -7.24634e-36  
 -7.24206e-36  
 -7.24206e-36  
 -7.22509e-36  
 -7.22509e-36  
 -7.21237e-36  
 -7.20816e-36  
 -5.42752e-36  
 -1.78112e-67
```