

```
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/0.5g2k/G/5  
  
/home/nicole/Jupyter/JG3/Data/0.5g2k/G/5
```

In [4]: ;ls

```
Correlation.G5.G.PBLUP.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.PBLUP.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
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)
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) # with J
nothing
```

```
In [31]: vG      = 0.704
         vRes    = 0.704
         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,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
         7088.478253 seconds (23.84 G allocations: 736.501 GB, 2.83% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          35.2737
           3.23277
```

```
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 = 0.916
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.992
```

```
Out[35]: 0.9162337958934708
```

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

```
Out[36]: -1.857020554852373
```

```
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 = 0.907
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.105
```

```
Out[37]: 0.9071271449444995
```

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

```
Out[38]: -0.5841605169284093
```

```
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 = 0.884
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.969
```

```
Out[39]: 0.8842001263179008
```

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

```
Out[40]: -2.15075748668098
```

```
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 = 0.710
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.862
```

```
Out[41]: 0.7103806243904698
```

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

```
Out[42]: -3.3676440344162084
```

```
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 = 0.786
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.001
```

```
Out[43]: 0.785842319548925
```

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

```
Out[44]: -2.652344243431408
```

```
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 = 0.771
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.998
```

```
Out[45]: 0.7705543294742967
```

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

```
Out[46]: -2.050803306872118
```



```
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 = 0.777
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.036
```

```
Out[47]: 0.7769206560544959
```

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

```
Out[48]: -1.522760562930204
```

```
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 = 0.767
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.049
```

```
Out[49]: 0.767398178324782
```

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

```
Out[50]: -1.0129005595186664
```

```
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 = 0.890
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.095
```

```
Out[51]: 0.8896102323033726
```

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

```
Out[52]: -0.5356706219456339
```

```
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 = 1.086
```

```
Out[53]: 0.9427134499270754
```

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

```
Out[54]: -1.8845418997650305
```

```
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 =  0.932
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.001
```

```
Out[55]: 0.9324166161602709
```

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

```
Out[56]: -1.391877499837726
```

```
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 =  0.932
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.073
```

```
Out[57]: 0.93187971408171
```

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

```
Out[58]: -0.9655682036252741
```

```
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 = 0.934

SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.108

Out[59]: 0.9340315433003825

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

Out[60]: -0.5064230296465436

```
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 = 0.869

SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.993

Out[61]: 0.8689232496881254

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

Out[62]: -0.1119877510784904

```
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 = 0.890
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.095
```

```
Out[63]: 0.8896102323033726
```

```
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]: 34.768634500000005
```

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

```
Out[67]: -0.5356706219456339
```

```
In [68]: 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 = 0.869
```

```
Out[68]: 0.688307956736098
```

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

```
Out[69]: -3.405672294279059
```

```
In [70]: 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)
         JCall = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.768
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.006
```

```
Out[70]: 0.7680925147123159
```

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

```
Out[71]: -2.6846639035235533
```

```
In [72]: 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)
         JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.753
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.994
```

```
Out[72]: 0.7525794830439658
```

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

```
Out[73]: -2.078629847981011
```

```
In [74]: 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 =  0.761
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.033
```

```
Out[74]: 0.7610958719045126
```

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

```
Out[75]: -1.5488204996810668
```

```
In [76]: 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 =  0.753
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.045
```

```
Out[76]: 0.7528555807977821
```

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

```
Out[77]: -1.0360008879402092
```

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

```
Out[78]: SSBR.NumSSBayes(54875,45875,9000,40000,39000,1000,2000)
```

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

```
Out[79]: 45875x1 Array{Float64,2}:
```

```
-1.00013  
-0.989406  
-0.989104  
-0.988687  
-0.986955  
-0.986772  
-0.98594  
-0.985627  
-0.985612  
-0.985601  
-0.985574  
-0.985536  
-0.985534  
:  
6.10569e-17  
6.32562e-17  
6.62234e-17  
6.63866e-17  
6.66704e-17  
7.02019e-17  
7.43747e-17  
7.69405e-17  
8.8762e-17  
8.89062e-17  
8.99651e-17  
1.07791e-16
```



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

```
Out[80]: 43858x1 Array{Float64,2}:
```

```
-1.00013  
-0.989406  
-0.989104  
-0.988687  
-0.986955  
-0.986772  
-0.98594  
-0.985627  
-0.985612  
-0.985601  
-0.985574  
-0.985536  
-0.985534  
:  
-7.21236e-36  
-7.20815e-36  
-7.20799e-36  
-7.19558e-36  
-7.17281e-36  
-7.16503e-36  
-5.41067e-36  
-7.17032e-66  
-3.55806e-67  
-1.78322e-67  
-1.78322e-67  
-1.78112e-67
```