

```
In [1]: include("/home/nicole/Jupyter/SSBRJ/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/0.5a0/M/1  
  
/home/nicole/Jupyter/JG3/Data/0.5a0/M/1
```

```
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
MarNF.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}' MarNF.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("MarNF.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]: vRes    = 1.408
         vG      = 1.408
         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
         4714.286352 seconds (23.05 G allocations: 724.026 GB, 6.94% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          0.434455
         -3.22702
```

```
In [33]: mu  = betaHat[1]
         mug = betaHat[2]
```

```
Out[33]: -3.2270158362551307
```

```
In [34]: (mu+mug)/2
```

```
Out[34]: -1.3962802685775075
```

```
In [35]: alphaHat
```

```
Out[35]: 150-element Array{Float64,1}:
```

```
 0.0364927  
-0.0129516  
-0.0640389  
 0.130007  
 0.00849782  
-0.181069  
 0.116063  
-0.0445698  
-0.0361173  
-0.042879  
 0.0667434  
-0.0709046  
-0.0253674  
  ⋮  
 0.0296091  
-0.0783462  
-0.313272  
-0.137066  
 0.0101317  
 0.0628654  
-0.00325084  
-0.0214152  
 0.30177  
 0.105271  
-0.250044  
 0.146332
```

```
In [36]: writedlm("alphaEstimatesJC",alphaHat)
```

```
In [37]: epsiHat
```

```
Out[37]: 45950-element Array{Float64,1}:
 0.768954
-0.118742
 0.095415
-0.210688
 0.229329
-0.365026
 0.304917
-0.277013
 0.796331
-0.929515
 0.0233094
-0.217028
-0.850385
  ⋮
 0.0574391
 0.188845
 0.302055
 0.252593
 1.30836
 0.419361
 0.064543
-0.368995
 0.330128
-0.19536
-0.00928684
 0.112788
```

```
In [38]: writedlm("epsiEstimatesJC",epsiHat)
```

```
In [39]: using DataFrames
```

```
In [40]: 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 [41]: 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 = 0.903
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.985
```

```
Out[41]: 0.903126347897482
```

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

```
Out[42]: 2.2039594353042515
```

```
In [43]: 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 = 0.830
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.917
```

```
Out[43]: 0.8300098064455663
```

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

```
Out[44]: 3.6566839208083555
```



```
In [45]: 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 = 0.879
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.983
```

```
Out[45]: 0.8787802396412657
```

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

```
Out[46]: 1.868715323264843
```

```
In [47]: 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 = 0.793
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.084
```

```
Out[47]: 0.7931838825632644
```

```
In [48]: GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

```
Out[48]: 0.31360114220424906
```

```
In [49]: 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 = 0.773
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.007
```

```
Out[49]: 0.7728155357450661
```

```
In [50]: GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

```
Out[50]: 1.308127535941194
```

```
In [51]: 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 = 0.744
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.965
```

```
Out[51]: 0.7443808312347213
```

```
In [52]: GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

```
Out[52]: 2.02939506721883
```

```
In [53]: 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 = 0.735
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.963
```

```
Out[53]: 0.7353464661074123
```

```
In [54]: GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

```
Out[54]: 2.6638358824072217
```

```
In [55]: 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 = 0.740
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.954
```

```
Out[55]: 0.7402212640684102
```

```
In [56]: GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

```
Out[56]: 3.2060469257413104
```

```
In [57]: 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 =  0.810
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.887
```

```
Out[57]: 0.8100260793038764
```

```
In [58]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[58]: 2-element Array{Float64,1}:
         0.880761
         0.886563
```

```
In [59]: VarGEBV=var(aHat1[posAi])
```

```
Out[59]: 0.6018901989763202
```

```
In [60]: VarTBV=var(a[posAi])
```

```
Out[60]: 0.7210049007563287
```

```
In [61]: Cov=cov(aHat1[posAi], a[posAi])
```

```
Out[61]: 0.5336134228356152
```

```
In [62]: b=Cov/VarGEBV
```

```
Out[62]: 0.8865627380927145
```

```
In [63]: GEBV = aHat1[posAi]
        G5GEBV=mean(GEBV)
```

```
Out[63]: 3.702750058312705
```

```
In [64]: GEBVG5G1=G5GEBV-G1GEBV
```

```
Out[64]: 2.394622522371511
```

```
In [65]: GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]
```

```
Out[65]: 5-element Array{Float64,1}:  
 1.30813  
 2.0294  
 2.66384  
 3.20605  
 3.70275
```

```
In [66]: 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)  
JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.834  
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.908
```

```
Out[66]: 0.8341839738762856
```

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

```
Out[67]: 2.4129253304958445
```

```
In [68]: 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 =  0.876
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.915
```

```
Out[68]: 0.8755758010999546
```

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

```
Out[69]: 2.8155715834131665
```

```
In [70]: 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 =  0.847
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.910
```

```
Out[70]: 0.847390178309569
```

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

```
Out[71]: 3.3271455101527105
```

```
In [72]: 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 =  0.822
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.986
```

```
Out[72]: 0.821623812622889
```

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

```
Out[73]: 3.741934629564944
```

```
In [74]: 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 =  0.713
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.711
```

```
Out[74]: 0.7127412978368958
```

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

```
Out[75]: 4.143197050241114
```

```
In [76]: 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 =  0.810
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.887
```

```
Out[76]: 0.8100260793038764
```

```
In [77]: writedlm("Correlation.G5.M.JC.txt",cor13)
```

```
In [78]: writedlm("Regression.G5.M.JC.txt",reg13)
```

```
In [79]: TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

```
Out[79]: 4.163481125000001
```

```
In [80]: GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

```
Out[80]: 3.702750058312705
```

```
In [81]: 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 =  0.784
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.136
```

```
Out[81]: 0.7839461959674618
```



```
In [82]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[82]: 0.2597723168634389
```

```
In [83]: 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 = 0.759
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.014
```

```
Out[83]: 0.7586464740894945
```

```
In [84]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[84]: 1.269475124467553
```

```
In [85]: 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 = 0.730
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.965
```

```
Out[85]: 0.7298335168532315
```

```
In [86]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[86]: 1.9961194148359098
```

```
In [87]: 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 =  0.722
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.957
```

```
Out[87]: 0.7224160765763717
```

```
In [88]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[88]: 2.636192324787793
```

```
In [89]: 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 =  0.730
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.950
```

```
Out[89]: 0.7303675872122872
```

```
In [90]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[90]: 3.182017435369521
```

```
In [91]: numSSBayes
```

```
Out[91]: SSBR.NumSSBayes(54950,45950,9000,40000,39000,1000,150)
```

```
In [92]: J1 = sortrows(J_Vecs.J1)
```

```
Out[92]: 45950x1 Array{Float64,2}:
```

```
-0.998128  
-0.989112  
-0.986218  
-0.986069  
-0.98556  
-0.985539  
-0.985398  
-0.985287  
-0.984751  
-0.983664  
-0.983657  
-0.983607  
-0.983579  
:  
7.22383e-17  
7.40727e-17  
7.42191e-17  
7.46619e-17  
7.52197e-17  
8.88923e-17  
8.92435e-17  
8.94813e-17  
1.18284e-16  
1.22329e-16  
1.44477e-16  
1.47425e-16
```

```
In [93]: J1[J1 .< 0.0,:]
```

```
Out[93]: 43902x1 Array{Float64,2}:
```

```
-0.998128  
-0.989112  
-0.986218  
-0.986069  
-0.98556  
-0.985539  
-0.985398  
-0.985287  
-0.984751  
-0.983664  
-0.983657  
-0.983607  
-0.983579  
:  
-7.21238e-36  
-7.2121e-36  
-7.20816e-36  
-7.20371e-36  
-7.18073e-36  
-2.1823e-51  
-3.19403e-65  
-2.57004e-65  
-5.46188e-67  
-2.73094e-67  
-1.79614e-67  
-1.78856e-67
```

```
In [94]: J1[J1 .> 0.0,:]
```

```
Out[94]: 1371x1 Array{Float64,2}:
```

```
6.06391e-83  
8.05497e-52  
8.08909e-52  
1.60053e-51  
1.60147e-51  
1.60241e-51  
1.60567e-51  
1.60617e-51  
1.60859e-51  
1.61099e-51  
1.61782e-51  
2.21192e-51  
2.45981e-51  
:  
7.22383e-17  
7.40727e-17  
7.42191e-17  
7.46619e-17  
7.52197e-17  
8.88923e-17  
8.92435e-17  
8.94813e-17  
1.18284e-16  
1.22329e-16  
1.44477e-16  
1.47425e-16
```