

```
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/0.5/Q/6

/home/nicole/Jupyter/JG3/Data/0.5/Q/6
```

```
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
PedAll.txt
Phe.txt
PheAll.txt
QTLNF.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}' 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.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("QTLNF.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 W_Mats
nothing
```

```
In [31]: vRes = 0.912
vG = 0.912
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
4007.725115 seconds (22.98 G allocations: 722.799 GB, 8.32% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 14.6949
  7.45485
```

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

```
In [34]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ', header=:a
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 a
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.918
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.973
```

```
Out[35]: 0.9183588160890587
```

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

```
Out[36]: -4.4815453471938325
```

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

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.995
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.037
```

```
Out[37]: 0.9947873200232115
```

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

```
Out[38]: -3.1270787167718455
```

```
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 a
@printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n",
JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.881
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.970
```

```
Out[39]: 0.8810326315680646
```

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

```
Out[40]: -4.794114569598906
```

```
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 =  0.735
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.949
```

```
Out[41]: 0.7352273677816756
```

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

```
Out[42]: -6.068071043645748
```

```
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 =  0.985
```

```
Out[43]: 0.7749246332804737
```

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

```
Out[44]: -5.312415241073771
```

```
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 =  0.777
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.993
```

```
Out[45]: 0.7766745418826266
```

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

```
Out[46]: -4.6918442722495195
```

```
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 = 0.768
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.984
```

```
Out[47]: 0.7681357053731309
```

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

```
Out[48]: -4.139708377116666
```

```
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 = 0.780
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.982
```

```
Out[49]: 0.7797887656663036
```

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

```
Out[50]: -3.6030412116552655
```

```
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 = 0.994
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.037
```

```
Out[51]: 0.9941357770048744
```

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

```
Out[52]: -3.0741919374220243
```

```
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 = 0.994
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.046
```

```
Out[53]: 0.9940145786221434
```

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

```
Out[54]: -4.533414810829316
```

```
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 = 0.993
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.042
```

```
Out[55]: 0.9932266785303598
```

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

```
Out[56]: -4.023369523214245
```

```
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 = 0.993
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.032
```

```
Out[57]: 0.9933837232063174
```

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

```
Out[58]: -3.542926236057931
```

```
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 = 0.990
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.040
```

```
Out[59]: 0.9904537852220696
```

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

```
Out[60]: -3.0415681118942466
```

```
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 = 0.991
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.037
```

```
Out[61]: 0.9912206842302518
```

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

```
Out[62]: -2.6095860758563445
```

```
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 = 0.994
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.037
```

```
Out[63]: 0.9941357770048744
```

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



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

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

```
Out[66]: -3.0741919374220243
```

```
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 = 0.713
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.955
```

```
Out[67]: 0.713157802951574
```

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

```
Out[68]: -6.107421203461555
```

```
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 = 0.989
```

```
Out[69]: 0.7579733135200555
```

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

```
Out[70]: -5.345467695377861
```

```
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)
         JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.762
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.995
```

```
Out[71]: 0.7617344875065911
```

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

```
Out[72]: -4.721303709074945
```

```
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)
         JCall = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.753
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.984
```

```
Out[73]: 0.7532863266802505
```

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

```
Out[74]: -4.167865819814677
```

```
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)
         JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.766
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[75]: 0.765828294706425
```

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

```
Out[76]: -3.6285144202654944
```

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

```
Out[77]: SSBR.NumSSBayes(54914,45914,9000,40000,39000,1000,50)
```

```
In [78]: J1 = sortrows(J_Vecs.J1)
```

```
Out[78]: 45914x1 Array{Float64,2}:  
  -0.988953  
  -0.988323  
  -0.98701  
  -0.986736  
  -0.986206  
  -0.986162  
  -0.985593  
  -0.985589  
  -0.985292  
  -0.985236  
  -0.984509  
  -0.98444  
  -0.984398  
  ⋮  
  6.6665e-17  
  6.70766e-17  
  6.96733e-17  
  7.00697e-17  
  7.07202e-17  
  7.36787e-17  
  7.40941e-17  
  7.48391e-17  
  7.94004e-17  
  7.96053e-17  
  9.57602e-17  
  1.11476e-16
```

```
In [79]: J1[J1 .< 0.0,:]
```

```
Out[79]: 43909x1 Array{Float64,2}:  
  -0.988953  
  -0.988323  
  -0.98701  
  -0.986736  
  -0.986206  
  -0.986162  
  -0.985593  
  -0.985589  
  -0.985292  
  -0.985236  
  -0.984509  
  -0.98444  
  -0.984398  
  ⋮  
  -7.25056e-36  
  -7.23354e-36  
  -7.22085e-36  
  -7.22083e-36  
  -7.21871e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.21238e-36  
  -7.21238e-36  
  -5.38603e-36  
  -2.39868e-66  
  -1.77955e-67
```

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

```
Out[80]: 1285x1 Array{Float64,2}:  
 8.01438e-52  
 1.19594e-51  
 1.60147e-51  
 1.60241e-51  
 1.60241e-51  
 1.60288e-51  
 1.60335e-51  
 1.60335e-51  
 3.1819e-51  
 3.20388e-51  
 3.20481e-51  
 4.4058e-51  
 6.3638e-51  
 ⋮  
 6.6665e-17  
 6.70766e-17  
 6.96733e-17  
 7.00697e-17  
 7.07202e-17  
 7.36787e-17  
 7.40941e-17  
 7.48391e-17  
 7.94004e-17  
 7.96053e-17  
 9.57602e-17  
 1.11476e-16
```