

```
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/M/9  
  
/home/nicole/Jupyter/JG3/Data/0.5/M/9
```

```
In [4]: ;ls  
  
MarNF.txt  
PedAll.txt  
Phe.txt  
PheAll.txt
```

```
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.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("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 W_Mats
nothing
```

```
In [31]: vRes    = 0.547
         vG      = 0.547
         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
2527.479479 seconds (23.06 G allocations: 724.246 GB, 7.57% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          10.1803
          -1.76665
```

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

```
Out[33]: -1.7666467691121197
```

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

```
Out[34]: 4.206803468383339
```

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

```
Out[35]: 150-element Array{Float64,1}:
 -0.102956
  0.109034
 -0.048072
  0.0213814
 -0.00671735
 -0.00523747
  0.00889648
 -0.000454847
 -0.0900504
 -0.0305042
 -0.0938203
 -0.222272
  0.00261831
  ⋮
  0.0670105
  0.198002
 -0.110046
 -0.0654577
 -0.0787913
 -0.00619985
 -0.0454541
  0.00697404
  0.0181941
  0.0885831
  0.0614874
  0.050434
```

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

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

```
Out[37]: 45966-element Array{Float64,1}:
 -0.0880113
  0.384315
  0.235476
 -0.370653
 -0.202885
  0.518342
 -0.731194
 -1.39796
  0.0666706
 -0.570645
 -0.451848
  0.372595
 -0.412094
  ⋮
 -0.335771
 -0.320156
 -0.32004
  0.385437
 -0.0239607
 -0.472013
 -0.438429
 -0.630246
  0.0778032
 -0.794494
  0.360835
  0.271185
```

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

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

```
In [40]: 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 [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 cor1
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.891
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.995
```

```
Out[41]: 0.8908204308896311
```

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

```
Out[42]: 1.2205646161645192
```

```
In [43]: 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 ) # 1
         @printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.783
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.991
```

```
Out[43]: 0.7832461337620293
```

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

```
Out[44]: 2.1786613555166316
```

```
In [45]: 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", reg3)
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.864
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.956
```

```
Out[45]: 0.8637172866468947
```

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

```
Out[46]: 0.9994653686217239
```

```
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 e
         @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
         JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.670
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.776
```

```
Out[47]: 0.6703613580821131
```

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

```
Out[48]: -0.01830116116215784
```

```
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 e
         @printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.763
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.970
```

```
Out[49]: 0.7627034829626822
```

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

```
Out[50]: 0.6006583275699926
```

```
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 e
         @printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.753
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.006
```

```
Out[51]: 0.7528212176335657
```

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

```
Out[52]: 1.0880350476555205
```

```
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 e
         @printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.745
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.003
```

```
Out[53]: 0.744834250190467
```

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

```
Out[54]: 1.5293488206352048
```

```
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 e
         @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.727
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.013
```

```
Out[55]: 0.7274340872885336
```

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

```
Out[56]: 1.9154928380037264
```

```
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 e
         @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.759
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.944
```

```
Out[57]: 0.7587382056203532
```

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

```
Out[58]: 2-element Array{Float64,1}:
         10.4512
         0.943946
```

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

```
Out[59]: 0.25803054606508363
```

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

```
Out[60]: 0.39937518948266976
```

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

```
Out[61]: 0.24356677997429968
```



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

```
Out[62]: 0.9439455277239318
```

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

```
Out[63]: 2.2081538242848286
```

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

```
Out[64]: 1.607495496714836
```

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

```
Out[65]: 5-element Array{Float64,1}:
          0.600658
          1.08804
          1.52935
          1.91549
          2.20815
```

```
In [66]: 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 = 0.823
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.964
```

```
Out[66]: 0.8229320127688459
```

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

```
Out[67]: 1.3426907667390993
```

```
In [68]: 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 = 0.769
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.844
```

```
Out[68]: 0.7688404064857874
```

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

```
Out[69]: 1.6597297846815418
```

```
In [70]: 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 = 0.762
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.837
```

```
Out[70]: 0.7617697444367485
```

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

```
Out[71]: 1.980338747270013
```

```
In [72]: 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 = 0.710
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.756
```

```
Out[72]: 0.7098775281961797
```

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

```
Out[73]: 2.251054205654206
```

```
In [74]: 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 = 0.675
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.776
```

```
Out[74]: 0.6746603221283978
```

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

```
Out[75]: 2.4797945225104296
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 = 0.759
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.944
```

```
Out[76]: 0.7587382056203532
```

```
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]: 12.535571875
```

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

```
Out[80]: 2.2081538242848286
```

```
In [81]: 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 = 0.652
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.788
```

```
Out[81]: 0.6521882490806752
```

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

```
Out[82]: -0.0531983900827029
```

```
In [83]: 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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.748
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.976
```

```
Out[83]: 0.7479350677048784
```

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

```
Out[84]: 0.5735026491825171
```

```
In [85]: 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 = 0.737
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[85]: 0.7370008213908631
```

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

```
Out[86]: 1.065155465614123
```

```
In [87]: 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 = 0.732
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.994
```

```
Out[87]: 0.7320596959614789
```

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

```
Out[88]: 1.5108435543526662
```

```
In [89]: 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 = 0.717
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.002
```

```
Out[89]: 0.7172513644915262
```

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

```
Out[90]: 1.9010235640420163
```

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

```
Out[91]: SSBR.NumSSBayes(54966,45966,9000,40000,39000,1000,150)
```

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

```
Out[92]: 45966x1 Array{Float64,2}:
-0.990145
-0.986216
-0.985984
-0.985915
-0.985665
-0.985546
-0.985536
-0.985405
-0.985217
-0.984727
-0.984479
-0.984386
-0.983639
⋮
6.76027e-17
7.10931e-17
7.14323e-17
7.52907e-17
7.54313e-17
7.75322e-17
7.92816e-17
8.88178e-17
9.02541e-17
9.40576e-17
9.99201e-17
1.2259e-16
```

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

```
Out[93]: 43930x1 Array{Float64,2}:  
  -0.990145  
  -0.986216  
  -0.985984  
  -0.985915  
  -0.985665  
  -0.985546  
  -0.985536  
  -0.985405  
  -0.985217  
  -0.984727  
  -0.984479  
  -0.984386  
  -0.983639  
  ⋮  
  -7.22508e-36  
  -7.2166e-36  
  -7.2166e-36  
  -4.91411e-36  
  -7.60646e-65  
  -3.80323e-65  
  -2.34411e-65  
  -1.17206e-65  
  -9.00332e-67  
  -4.50166e-67  
  -3.55912e-67  
  -3.55912e-67
```

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

```
Out[94]: 1367x1 Array{Float64,2}:  
 2.60249e-81  
 8.44487e-81  
 1.60289e-51  
 1.60289e-51  
 1.61185e-51  
 3.07671e-51  
 3.20102e-51  
 3.20294e-51  
 3.20577e-51  
 3.95084e-51  
 4.05474e-51  
 4.05474e-51  
 4.6261e-51  
 ⋮  
 6.76027e-17  
 7.10931e-17  
 7.14323e-17  
 7.52907e-17  
 7.54313e-17  
 7.75322e-17  
 7.92816e-17  
 8.88178e-17  
 9.02541e-17  
 9.40576e-17  
 9.99201e-17  
 1.2259e-16
```