

```
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/4  
  
/home/nicole/Jupyter/JG3/Data/0.5a0/M/4
```

```
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  
MarNFCenter.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}' MarNFCenter.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("MarNFCenter.txt",numSSBayes) # genotype file - centered
M_Mats = make_MMats(df,A_Mats,ped); # M file centered already
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 = X_Mats - J_Vecs * M_Mats
nothing
```

```
In [31]: vRes = 1.991
vG = 1.991
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
3776.631085 seconds (23.02 G allocations: 723.337 GB, 6.97% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 11.2143
 -4.81467
```

```
In [33]: alphaHat
```

```
Out[33]: 150-element Array{Float64,1}:  
  0.118075  
  0.0333824  
  0.0388504  
  0.0514798  
  0.204284  
  0.0227794  
  0.0476496  
  0.162705  
  0.00413762  
 -0.0643155  
  0.0629572  
 -0.358294  
 -0.0673607  
  ⋮  
  0.0651682  
 -0.00447185  
 -0.177007  
 -0.104742  
 -0.0472155  
 -0.117765  
 -0.17385  
 -0.266862  
  0.0679653  
  0.00358609  
  0.225616  
  0.0509638
```

```
In [34]: writedlm("alphaEstimatesLeggaraJC",alphaHat)
```

```
In [35]: epsiHat
```

```
Out[35]: 45900-element Array{Float64,1}:
 -0.0565938
 -0.082323
 -0.944745
 -0.322442
 -1.48915
  1.04561
 -0.138484
 -0.163982
  0.681517
  0.314922
  1.03161
 -0.00225799
 -0.201168
  ⋮
  1.35515
 -0.718267
  0.114431
 -0.818262
  0.563252
  0.368207
 -0.183698
 -0.204138
  0.0773253
 -0.141563
 -0.508305
 -0.512529
```

```
In [36]: writedlm("epsiEstimatesLeggaraJC",epsiHat)
```

```
In [37]: using DataFrames
```

```
In [38]: 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 [39]: 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 correlation
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.919
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.012
```

```
Out[39]: 0.9194016258728039
```

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

```
Out[40]: 2.803578715044123
```

```
In [41]: 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 = 0.878
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[41]: 0.8782586104221654
```

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

```
Out[42]: 4.814670823948545
```

```
In [43]: 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 = 0.894
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.005
```

```
Out[43]: 0.8939467292267244
```

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

```
Out[44]: 2.3394805360661795
```

```
In [45]: 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 = 0.819
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.127
```

```
Out[45]: 0.819326609791292
```

```
In [46]: GEBV = aHat1[posAi]
         G1GEBV=mean(GEBV)
```

```
Out[46]: 0.23826827557588803
```

```
In [47]: 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 = 0.762
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.008
```

```
Out[47]: 0.7624495755530231
```

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

```
Out[48]: 1.602757267976493
```

```
In [49]: 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 = 0.762
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.035
```

```
Out[49]: 0.7617504329108596
```

```
In [50]: GEBV = aHat1[posAi]
         G2GEBV=mean(GEBV)
```

```
Out[50]: 2.523328028518438
```

```
In [51]: 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 = 0.755
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.012
```

```
Out[51]: 0.755408840614472
```

```
In [52]: GEBV = aHat1[posAi]
         G3GEBV=mean(GEBV)
```

```
Out[52]: 3.395521266201794
```

```
In [53]: 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 = 0.758
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.001
```

```
Out[53]: 0.7583253618131431
```

```
In [54]: GEBV = aHat1[posAi]
         G4GEBV=mean(GEBV)
```

```
Out[54]: 4.178936326181974
```

```
In [55]: 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 = 0.865
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.973
```

```
Out[55]: 0.8646373899519253
```

```
In [56]: GEBV = aHat1[posAi]
         G5GEBV=mean(GEBV)
```

```
Out[56]: 4.8826611258101495
```

```
In [57]: GEBVG5G1=G5GEBV-G1GEBV
```

```
Out[57]: 3.2799038578336566
```

```
In [58]: GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]
```

```
Out[58]: 5-element Array{Float64,1}:
 1.60276
 2.52333
 3.39552
 4.17894
 4.88266
```



```
In [59]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[59]: 2-element Array{Float64,1}:
 11.4472
 0.972509
```

```
In [60]: VarGEBV=var(aHat1[posAi])
```

```
Out[60]: 1.1357422371469499
```

```
In [61]: VarTBV=var(a[posAi])
```

```
Out[61]: 1.4368077632644083
```

```
In [62]: Cov=cov(aHat1[posAi], a[posAi])
```

```
Out[62]: 1.1045191080013346
```

```
In [63]: b=Cov/VarGEBV
```

```
Out[63]: 0.9725086132007826
```

```
In [64]: 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 )
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.835
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.902
```

```
Out[64]: 0.8346178880575138
```

```
In [65]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[65]: 3.0643453805998506
```

```
In [66]: 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 )
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.848
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.944
```

```
Out[66]: 0.8476708103297881
```

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

```
Out[67]: 3.532067973417997
```

```
In [68]: 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 = 0.873
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.940
```

```
Out[68]: 0.8729239749608928
```

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

```
Out[69]: 4.320864860284924
```

```
In [70]: 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 = 0.861
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.900
```

```
Out[70]: 0.8614296293450425
```

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

```
Out[71]: 4.907119267218364
```

```
In [72]: 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 = 0.837
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.892
```

```
Out[72]: 0.8368932917313261
```

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

```
Out[73]: 5.529344563757409
```

```
In [74]: 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 = 0.865
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.973
```

```
Out[74]: 0.8646373899519253
```

```
In [75]: writedlm("Correlation.G5.M.JC*.txt",cor13)
```

```
In [76]: writedlm("Regression.G5.M.JC*.txt",reg13)
```

```
In [77]: TBVG5Gall = a[posAi]
         TBVG5G=mean(TBVG5Gall)
```

```
Out[77]: 16.195634
```

```
In [78]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[78]: 4.8826611258101495
```

```
In [79]: 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 = 0.808
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 1.194
```

```
Out[79]: 0.8076936746008647
```

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

```
Out[80]: 0.16580476006245304
```

```
In [81]: 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 = 1.019
```

```
Out[81]: 0.7479529364100913
```

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

```
Out[82]: 1.553287762708762
```

```
In [83]: 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 = 0.745
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.039
```

```
Out[83]: 0.7452081326529096
```

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

```
Out[84]: 2.477237340524426
```

```
In [85]: 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 = 0.740
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.007
```

```
Out[85]: 0.7395808795159067
```

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

```
Out[86]: 3.3567623430988047
```

```
In [87]: 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 = 0.747
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.997
```

```
Out[87]: 0.746613751702854
```

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

```
Out[88]: 4.14431047393645
```

```
In [89]: numSSBayes
```

```
Out[89]: SSBR.NumSSBayes(54900,45900,9000,40000,39000,1000,150)
```

```
In [90]: J1 = sortrows(J_Vecs.J1)
```

```
Out[90]: 45900x1 Array{Float64,2}:
-1.00243
-0.988969
-0.986889
-0.986202
-0.985957
-0.985613
-0.985452
-0.985433
-0.985377
-0.985375
-0.985203
-0.984978
-0.984763
⋮
6.48833e-17
6.52495e-17
6.6039e-17
6.62586e-17
6.66651e-17
6.81721e-17
7.40486e-17
8.89238e-17
8.91103e-17
8.9262e-17
9.99488e-17
1.29767e-16
```

```
In [91]: J1[J1 .< 0.0,:]
```

```
Out[91]: 43906x1 Array{Float64,2}:  
  -1.00243  
  -0.988969  
  -0.986889  
  -0.986202  
  -0.985957  
  -0.985613  
  -0.985452  
  -0.985433  
  -0.985377  
  -0.985375  
  -0.985203  
  -0.984978  
  -0.984763  
  ⋮  
  -7.27634e-36  
  -7.25083e-36  
  -7.25083e-36  
  -7.22083e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.21128e-36  
  -7.05063e-36  
  -2.42284e-67  
  -1.79376e-67  
  -1.77772e-67  
  -8.88859e-68
```

```
In [92]: J1[J1 .> 0.0,:]
```

```
Out[92]: 1320x1 Array{Float64,2}:  
 8.00613e-52  
 8.07836e-52  
 1.60123e-51  
 1.60241e-51  
 1.60335e-51  
 1.61001e-51  
 1.61001e-51  
 1.61567e-51  
 1.62435e-51  
 2.1823e-51  
 2.38745e-51  
 4.43215e-51  
 4.64621e-51  
 ⋮  
 6.48833e-17  
 6.52495e-17  
 6.6039e-17  
 6.62586e-17  
 6.66651e-17  
 6.81721e-17  
 7.40486e-17  
 8.89238e-17  
 8.91103e-17  
 8.9262e-17  
 9.99488e-17  
 1.29767e-16
```