

```
In [1]: include("/home/nicole/Jupyter/SSBRnoJ/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/10  
        /home/nicole/Jupyter/JG3/Data/0.5a0/M/10
```

```
In [4]: ;ls
```

```
Correlation.G5.M.C*.txt
Correlation.G5.M.J.txt
Correlation.G5.M.JC*.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
MarNF.txt
MarNFcenter.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C*.txt
Regression.G5.M.J.txt
Regression.G5.M.JC*.txt
all.ID
alphaEstimatesJ
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
epsiEstimatesJ
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
genotype.ID
meanOfSNPMAll
meanOfSNPMG0
meanOfSNPMG1
meanOfSNPMG2
meanOfSNPMG3
meanOfSNPMG4
meanOfSNPMG5
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.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);
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(Z_Mats,M_Mats,numSSBayes) # no centering
nothing
```

```
In [31]: vRes      = 0.460
vG       = 0.460
nIter    = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter,
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
2570.695821 seconds (23.04 G allocations: 723.722 GB, 7.54% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
4.78714
```

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

```
Out[33]: 150-element Array{Float64,1}:  
  0.0569108  
 -0.0779066  
 -0.00731716  
  0.0317334  
 -0.0109867  
  0.0154325  
 -0.076753  
  0.240617  
 -0.016875  
 -0.0211948  
  0.0524002  
 -0.0060953  
  0.0399808  
  ⋮  
  0.0853784  
 -0.0275633  
 -0.028188  
  0.0748745  
 -0.0627129  
  0.0214018  
  0.0716789  
 -0.038667  
 -0.026943  
  0.0899177  
  0.0340414  
 -0.0197039
```

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

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

```
Out[35]: 45929-element Array{Float64,1}:
 -0.440228
 -0.00539274
 -0.259594
  0.0568937
  0.0749418
 -0.303341
 -0.270062
  0.0760442
  0.630202
 -0.11358
  0.184632
 -0.197715
 -0.29458
  ⋮
  0.390393
 -0.146461
 -0.140353
 -0.144192
  0.597904
  0.234402
 -0.316912
  0.157614
 -0.103611
 -0.324748
  0.208576
 -0.754279
```

```
In [36]: writedlm("epsiEstimatesC",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 = 0.899
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.958
```

```
Out[39]: 0.8994997894144385
```

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

```
Out[40]: 0.11227271621415844
```

```
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 = 0.890
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.975
```

```
Out[41]: 0.889866471203794
```

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

```
Out[42]: 1.0756887708022016
```

```
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 = 0.862
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.938
```

```
Out[43]: 0.862110898495159
```

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

```
Out[44]: -0.11005406561385149
```

```
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 = 0.632
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.711
```

```
Out[45]: 0.6321920065203251
```

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

```
Out[46]: -1.012239058729889
```

```
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 =  0.769
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.969
```

```
Out[47]: 0.7693392185929188
```

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

```
Out[48]: -0.5063176579907597
```

```
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 =  0.755
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.992
```

```
Out[49]: 0.7552046026316354
```

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

```
Out[50]: -0.03124969269618096
```

```
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 =  0.757
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.996
```

```
Out[51]: 0.7569605005963846
```



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

```
Out[52]: 0.36310253903725587
```

```
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 = 0.757
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.978
```

```
Out[53]: 0.7566386298650091
```

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

```
Out[54]: 0.7482547990768582
```

```
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 = 0.874
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.947
```

```
Out[55]: 0.8741733651738429
```

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

```
Out[56]: 1.1120853685876664
```

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

```
Out[57]: 1.618403026578426
```

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

```
Out[58]: 5-element Array{Float64,1}:
          -0.506318
          -0.0312497
           0.363103
           0.748255
           1.11209
```

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

```
Out[59]: 2-element Array{Float64,1}:
 4.85866
 0.947146
```

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

```
Out[60]: 0.26128758634959887
```

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

```
Out[61]: 0.30673105008526064
```

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

```
Out[62]: 0.24747756217563902
```

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

```
Out[63]: 0.947146267578582
```

```
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 = 0.887
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.969
```

```
Out[64]: 0.8867510126538868
```

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

```
Out[65]: 0.06332116533329336
```

```
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 = 0.876
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.959
```

```
Out[66]: 0.8760997022714049
```

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

```
Out[67]: 0.513621976954718
```

```
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 = 0.864
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.923
```

```
Out[68]: 0.8641471005665649
```

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

```
Out[69]: 0.7827931912355655
```

```
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 = 0.835
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.827
```

```
Out[70]: 0.8351575967612187
```

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

```
Out[71]: 1.1175764412034652
```

```
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 = 0.850
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.845
```

```
Out[72]: 0.8496972467392293
```

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

```
Out[73]: 1.4452671678653841
```

```
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)
         JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.874
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.947
```

```
Out[74]: 0.8741733651738429
```

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

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

```
In [77]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[77]: 1.1120853685876664
```

```
In [78]: 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)
         JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.610
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.703
```

```
Out[78]: 0.6095120064040181
```

```
In [79]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[79]: -1.0398175260135605
```

```
In [80]: 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 = 0.752
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.973
```

```
Out[80]: 0.7515085856648133
```

```
In [81]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[81]: -0.532469956322695
```

```
In [82]: 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 = 0.740
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.994
```

```
Out[82]: 0.7400483609081882
```

```
In [83]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[83]: -0.0521225871559693
```

```
In [84]: 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 = 0.742
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.995
```

```
Out[84]: 0.7421753994472757
```

```
In [85]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[85]: 0.3437570543663274
```

```
In [86]: 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 = 0.742
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.973
```

```
Out[86]: 0.7419310505912922
```

```
In [87]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[87]: 0.7303826870566397
```

```
In [88]: numSSBayes
```

```
Out[88]: SSBR.NumSSBayes(54929,45929,9000,40000,39000,1000,150)
```