

```
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/0.5g2k/G/2  
  
/home/nicole/Jupyter/JG3/Data/0.5g2k/G/2
```

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

```
Correlation.G5.G.C.txt
Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.N.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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.C.txt
Regression.G5.G.J.txt
Regression.G5.G.JC.txt
Regression.G5.G.N.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPGAll
meanOfSNPGG0
meanOfSNPGG1
meanOfSNPGG2
meanOfSNPGG3
meanOfSNPGG4
meanOfSNPGG5
noGenotype.ID
```

```
sim.bv  
sim.phenotype
```

```
In [5]: ;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

```
In [6]: ;awk '{print $1}' GenNF.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
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
nothing
```

```
In [31]: vG      = 0.806
         vRes    = 0.806
         aHat3=SSBR.PBLUP(y_Vecs,Z_Mats,A_Mats,numSSBayes,vRes,vG);
```

```
In [32]: using DataFrames
```

```
In [33]: 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 [34]: IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor1 = cor(a[posAi],aHat3[posAi])[1,1]
         reg1 = linreg(aHat3[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)
         JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.893
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV =  0.983
```

```
Out[34]: 0.8927301197131253
```

```
In [35]: TBV = a[posAi]
         mean(TBV)
```

```
Out[35]: 33.45646697916667
```

```
In [36]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[36]: 1.5524359899569415
```

```
In [37]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor2 = cor(a[posAi],aHat3[posAi])[1,1]
reg2 = linreg(aHat3[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)
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.577
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.998
```

```
Out[37]: 0.5769180610734326
```

```
In [38]: TBV = a[posAi]
mean(TBV)
```

```
Out[38]: 34.82397588888889
```

```
In [39]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[39]: 2.9589607479158655
```

```
In [40]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor3 = cor(a[posAi],aHat3[posAi])[1,1]
reg3 = linreg(aHat3[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)
JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.882
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.987
```

```
Out[40]: 0.881515455789616
```

```
In [41]: TBV = a[posAi]
mean(TBV)
```

```
Out[41]: 33.140888000000004
```

```
In [42]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[42]: 1.227853353504882
```

```
In [43]: IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor4 = cor(a[posAi],aHat3[posAi])[1,1]
         reg4 = linreg(aHat3[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 =  0.727
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.913
```

```
Out[43]: 0.7269527168008468
```

```
In [44]: TBV = a[posAi]
         mean(TBV)
```

```
Out[44]: 31.9281865
```

```
In [45]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[45]: 0.0004639543240959787
```

```
In [46]: IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor4 = cor(a[posAi],aHat3[posAi])[1,1]
         reg4 = linreg(aHat3[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)
         JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.780
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.015
```

```
Out[46]: 0.7802584465301706
```

```
In [47]: TBV = a[posAi]
         mean(TBV)
```

```
Out[47]: 32.629996125000005
```

```
In [48]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[48]: 0.708743967363405
```

```
In [49]: IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor5 = cor(a[posAi],aHat3[posAi])[1,1]
         reg5 = linreg(aHat3[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 =  0.781
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.022
```

```
Out[49]: 0.7810823532217924
```

```
In [50]: TBV = a[posAi]
         mean(TBV)
```

```
Out[50]: 33.182511500000001
```

```
In [51]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[51]: 1.2791028849135968
```



```
In [52]: IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor6 = cor(a[posAi],aHat3[posAi])[1,1]
reg6 = linreg(aHat3[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 = 0.756
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.993
```

```
Out[52]: 0.7559512777667722
```

```
In [53]: TBV = a[posAi]
mean(TBV)
```

```
Out[53]: 33.77602525
```

```
In [54]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[54]: 1.8715978864298355
```

```
In [55]: IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat3[posAi])[1,1]
reg7 = linreg(aHat3[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 = 0.745
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.983
```

```
Out[55]: 0.7446191901889756
```

```
In [56]: TBV = a[posAi]
mean(TBV)
```

```
Out[56]: 34.339634499999995
```

```
In [57]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[57]: 2.434397571366167
```

```
In [58]: IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor8 = cor(a[posAi],aHat3[posAi])[1,1]
         reg8 = linreg(aHat3[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)
         JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.446
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.016
```

```
Out[58]: 0.4463086822518445
```

```
In [59]: TBV = a[posAi]
         mean(TBV)
```

```
Out[59]: 34.882447999999999
```

```
In [60]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[60]: 3.0203096753445475
```

```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat3[posAi])[1,1]
         reg9 = linreg(aHat3[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 =  0.907
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.025
```

```
Out[61]: 0.906829801823165
```

```
In [62]: TBV = a[posAi]
         mean(TBV)
```

```
Out[62]: 33.316475000000004
```

```
In [63]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[63]: 1.4188862085029337
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat3[posAi])[1,1]
         reg9 = linreg(aHat3[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)
         JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.915
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.016
```

```
Out[64]: 0.914806614716605
```

```
In [65]: TBV = a[posAi]
         mean(TBV)
```

```
Out[65]: 33.738085
```

```
In [66]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[66]: 1.8494166768260831
```

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor10 = cor(a[posAi],aHat3[posAi])[1,1]
reg10 = linreg(aHat3[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 = 0.883
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.006
```

```
Out[67]: 0.8828352696074719
```

```
In [68]: TBV = a[posAi]
mean(TBV)
```

```
Out[68]: 34.389979999999994
```

```
In [69]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[69]: 2.47009848738101
```

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor11 = cor(a[posAi],aHat3[posAi])[1,1]
reg11 = linreg(aHat3[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 = 0.904
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.997
```

```
Out[70]: 0.9042661448736632
```

```
In [71]: TBV = a[posAi]
mean(TBV)
```

```
Out[71]: 34.901525
```

```
In [72]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[72]: 2.9922285161931885
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor12 = cor(a[posAi],aHat3[posAi])[1,1]
         reg12 = linreg(aHat3[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 = 0.574
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.108
```

```
Out[73]: 0.5739781386351581
```

```
In [74]: TBV = a[posAi]
         mean(TBV)
```

```
Out[74]: 35.43493
```

```
In [75]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[75]: 3.610216753528821
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor13 = cor(a[posAi],aHat3[posAi])[1,1]
         reg13 = linreg(aHat3[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 = 0.446
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.016
```

```
Out[76]: 0.4463086822518445
```

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

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

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

```
Out[79]: 34.882447999999999
```

```
In [80]: EBV = aHat3[posAi]  
mean(EBV)
```

```
Out[80]: 3.0203096753445475
```

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)  
posAi = getPos(ped,IDs)  
cor14 = cor(a[posAi],aHat3[posAi])[1,1]  
reg14 = linreg(aHat3[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)  
JCall = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.702  
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.903
```

```
Out[81]: 0.7020324420608203
```

```
In [82]: TBV = a[posAi]  
mean(TBV)
```

```
Out[82]: 31.89258935897436
```

```
In [83]: EBV = aHat3[posAi]  
mean(EBV)
```

```
Out[83]: -0.03590584706510498
```

```
In [84]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat3[posAi])[1,1]
reg14 = linreg(aHat3[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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.767
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.018
```

```
Out[84]: 0.7667460151962542
```

```
In [85]: TBV = a[posAi]
mean(TBV)
```

```
Out[85]: 32.60158358974359
```

```
In [86]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[86]: 0.6794959491720544
```

```
In [87]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor15 = cor(a[posAi],aHat3[posAi])[1,1]
reg15 = linreg(aHat3[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)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.766
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.023
```

```
Out[87]: 0.7660113644444273
```

```
In [88]: TBV = a[posAi]
mean(TBV)
```

```
Out[88]: 33.151550769230774
```

```
In [89]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[89]: 1.2485645361323812
```

```
In [90]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor16 = cor(a[posAi],aHat3[posAi])[1,1]
         reg16 = linreg(aHat3[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 =  0.738
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.992
```

```
Out[90]: 0.7380141634933739
```

```
In [91]: TBV = a[posAi]
         mean(TBV)
```

```
Out[91]: 33.74716628205128
```

```
In [92]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[92]: 1.8428637677179545
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor17 = cor(a[posAi],aHat3[posAi])[1,1]
         reg17 = linreg(aHat3[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 =  0.733
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.987
```

```
Out[93]: 0.7328667461375308
```



```
In [94]: TBV = a[posAi]  
         mean(TBV)
```

```
Out[94]: 34.31155
```

```
In [95]: EBV = aHat3[posAi]  
         mean(EBV)
```

```
Out[95]: 2.4042483615671246
```

```
In [96]: numSSBayes
```

```
Out[96]: SSBR.NumSSBayes(54938,45938,9000,40000,39000,1000,0)
```