

```
In [1]: include("/home/nicole/Jupyter/SSBRnoJ/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/G/4  
  
/home/nicole/Jupyter/JG3/Data/0.5/G/4
```

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 G
          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
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",calculateInbreedin
nothing
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
nothing
```

```
In [31]: vRes = 0.759
vG = 0.759
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 = ' ',head
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 e
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.895
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.989
```

```
Out[34]: 0.8949350914114739
```

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

```
Out[35]: 10.471534229166668
```

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

```
Out[36]: 1.4838002798718413
```

```
In [37]: IDs = readtable("genotype.ID", eltypes=[UTF8String], separator = ' ',header=
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 ) # v
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.574
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.982
```

```
Out[37]: 0.5740746779016379
```

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

```
Out[38]: 11.824753222222222
```

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

```
Out[39]: 2.8397722613140397
```

```
In [40]: IDs = readtable("noGenotype.ID", eltypes=[UTF8String], separator = ' ',heade
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 ) #
@printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.
JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.881
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.985
```

```
Out[40]: 0.8811653687884569
```

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

```
Out[41]: 10.159252923076924
```

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

```
Out[42]: 1.1708836687697954
```

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

```
SSBRJC from Gibbs - G0.ID : correlation = 0.721
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.908
```

```
Out[43]: 0.7212422580935137
```

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

```
Out[44]: 9.017859375
```

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

```
Out[45]: 0.002465054960012266
```

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

```
SSBRJC from Gibbs - G1.ID : correlation = 0.775
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.002
```

```
Out[46]: 0.7745964955220455
```

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

```
Out[47]: 9.608738375000001
```

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

```
Out[48]: 0.6344625424304675
```

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

```
SSBRJC from Gibbs - G2.ID : correlation =  0.772
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.016
```

```
Out[49]: 0.7724334527067311
```

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

```
Out[50]: 10.183037250000002
```

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

```
Out[51]: 1.202866143015828
```

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

```
SSBRJC from Gibbs - G3.ID : correlation =  0.763
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.987
```

```
Out[52]: 0.7627675032122285
```

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

```
Out[53]: 10.773109375
```

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

```
Out[54]: 1.7876206471642657
```

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

```
SSBRJC from Gibbs - G4.ID : correlation =  0.728
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.983
```

```
Out[55]: 0.7284631787285037
```

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

```
Out[56]: 11.359387625
```

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

```
Out[57]: 2.375624017184832
```

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

```
SSBRJC from Gibbs - G5.ID : correlation =  0.407
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.938
```

```
Out[58]: 0.4072218569151642
```

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

```
Out[59]: 11.887073375
```

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

```
Out[60]: 2.899763274475641
```



```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6.
JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.910
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.037
```

```
Out[61]: 0.9099508305165308
```

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

```
Out[62]: 10.192884999999997
```

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

```
Out[63]: 1.269275259658478
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6.
JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.911
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.000
```

```
Out[64]: 0.9107117414397974
```

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

```
Out[65]: 10.736695
```

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

```
Out[66]: 1.7615578687453666
```

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.895
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.954
```

```
Out[67]: 0.8952042706536661
```

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

```
Out[68]: 11.3590550000000001
```

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

```
Out[69]: 2.3737098381020076
```

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.867
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.946
```

```
Out[70]: 0.8674310601259959
```

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

```
Out[71]: 11.9364400000000003
```

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

```
Out[72]: 2.9674354465970767
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.471
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.926
```

```
Out[73]: 0.4712850515779606
```

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

```
Out[74]: 12.4058850000000001
```

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

```
Out[75]: 3.427242367003219
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.
JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.407
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.938
```

```
Out[76]: 0.4072218569151642
```

```
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]: 11.887073375
```

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

```
Out[80]: 2.899763274475641
```

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.701
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.904
```

```
Out[81]: 0.7009792299634106
```

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

```
Out[82]: 8.987730512820514
```

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

```
Out[83]: -0.030017257980974023
```

```
In [84]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.759
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.002
```

```
Out[84]: 0.7592151448718636
```

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

```
Out[85]: 9.57981641025641
```

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

```
Out[86]: 0.6055626622685472
```

```
In [87]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.756
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.019
```

```
Out[87]: 0.7558533747385638
```

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

```
Out[88]: 10.15288294871795
```

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

```
Out[89]: 1.1728445098084903
```

```
In [90]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.745
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.988
```

```
Out[90]: 0.7450944608421075
```

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

```
Out[91]: 10.743280384615385
```

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

```
Out[92]: 1.7573689856403474
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.715
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.983
```

```
Out[93]: 0.7153795097824844
```

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

```
Out[94]: 11.33255435897436
```

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

```
Out[95]: 2.3486594441125663
```

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

```
Out[96]: SSBR.NumSSBayes(54918,45918,9000,40000,39000,1000,0)
```