

```
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/G/7  
/home/nicole/Jupyter/JG3/Data/0.5a0/G/7
```

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

```
In [31]: vRes = 0.738
          vG = 0.738
          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{Float64,1}(zeros(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 correlation
          @printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
          JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.890
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.980
```

```
Out[34]: 0.8901211799083555
```

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

```
Out[35]: 2.6270850208333334
```

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

```
Out[36]: 1.4070626483393
```

```
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 ) # 1
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3:
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.575
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[37]: 0.5749530240338646
```

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

```
Out[38]: 3.8989498888888887
```

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

```
Out[39]: 2.7082305854892303
```

```
In [40]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',head
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 = 0.876
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.980
```

```
Out[40]: 0.8759512695433169
```

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

```
Out[41]: 2.3335777435897436
```

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

```
Out[42]: 1.1067931243816238
```

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

```
SSBRJC from Gibbs - G0.ID : correlation =  0.719
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.895
```

```
Out[43]: 0.7188971886694375
```

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

```
Out[44]: 1.242720875
```

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

```
Out[45]: -0.0020853722211218112
```

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

```
SSBRJC from Gibbs - G1.ID : correlation =  0.767
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.975
```

```
Out[46]: 0.7666444018188885
```

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

```
Out[47]: 1.806066625
```

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

```
Out[48]: 0.585321250552222
```

```
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 e
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.765
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.994
```

```
Out[49]: 0.7647733431863895
```

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

```
Out[50]: 2.3675376249999998
```

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

```
Out[51]: 1.149384000363274
```

```
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 e
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.763
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.993
```

```
Out[52]: 0.7627819875990384
```

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

```
Out[53]: 2.9335720000000003
```

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

```
Out[54]: 1.7083824860113277
```

```
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 e
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.715
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.966
```

```
Out[55]: 0.7151329832377464
```

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

```
Out[56]: 3.4565102499999996
```

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

```
Out[57]: 2.2353172277048654
```

```
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 e
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.424
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.987
```

```
Out[58]: 0.42366568934981763
```

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

```
Out[59]: 3.9561027499999994
```

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

```
Out[60]: 2.766056297625235
```



```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 = %6.3f\n", reg9 )
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.887
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.043
```

```
Out[61]: 0.8867558349762482
```

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

```
Out[62]: 2.353905
```

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

```
Out[63]: 1.184799575267387
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 = %6.3f\n", reg9 )
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.901
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.971
```

```
Out[64]: 0.9008816583366337
```

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

```
Out[65]: 2.9259999999999997
```

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

```
Out[66]: 1.7136115874718494
```

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 = %6.3f\n", reg10)
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.880
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.999
```

```
Out[67]: 0.8800716355611855
```

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

```
Out[68]: 3.5142349999999998
```

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

```
Out[69]: 2.274252385059967
```

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 = %6.3f\n", reg11)
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.840
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.944
```

```
Out[70]: 0.8396762234921895
```

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

```
Out[71]: 3.953035
```

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

```
Out[72]: 2.7581962364387045
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head = 1000)
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 = %6.3f\n", reg12)
JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.583
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.103
```

```
Out[73]: 0.5829551906157323
```

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

```
Out[74]: 4.46146
```

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

```
Out[75]: 3.2972646577680798
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', head = 1000)
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 = %6.3f\n", reg13)
JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.424
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.987
```

```
Out[76]: 0.42366568934981763
```

```
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]: 3.9561027499999994
```

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

```
Out[80]: 2.766056297625235
```

```
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 = 0.889
```

```
Out[81]: 0.7005965854773608
```

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

```
Out[82]: 1.2142289743589743
```

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

```
Out[83]: -0.03251831959262204
```

```
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 = 0.750
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.974
```

```
Out[84]: 0.7501524619289174
```

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

```
Out[85]: 1.7773503846153844
```

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

```
Out[86]: 0.5563907290927442
```

```
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)
JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.747
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[87]: 0.7469845278801275
```

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

```
Out[88]: 2.338135128205128
```

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

```
Out[89]: 1.1205412212684869
```

```
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)
JCall = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.749
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.995
```

```
Out[90]: 0.7486640854403901
```

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

```
Out[91]: 2.907431923076923
```

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

```
Out[92]: 1.681464184718318
```

```
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 = 0.700
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.967
```

```
Out[93]: 0.7000930971590186
```

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

```
Out[94]: 3.4307423076923076
```

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

```
Out[95]: 2.2080878064211924
```

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

```
Out[96]: SSBR.NumSSBayes(54885,45885,9000,40000,39000,1000,0)
```