

```
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/0.3/G/9  
  
/home/nicole/Jupyter/JG3/Data/0.3/G/9
```

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

```
Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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.J.txt
Regression.G5.G.JC.txt
Regression.G5.G.PBLUP.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPGA11
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      = 0.746
         vRes    = 1.742
         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)
         JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.805
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV =  0.983
```

```
Out[34]: 0.8051847485307807
```

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

```
Out[35]: 11.418315708333331
```

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

```
Out[36]: 1.0993110350169657
```

```
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)
JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.471
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.921
```

```
Out[37]: 0.4708246117899099
```

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

```
Out[38]: 12.31398022222222
```

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

```
Out[39]: 2.0691553552928164
```

```
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)
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.790
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.013
```

```
Out[40]: 0.7899888782764969
```

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

```
Out[41]: 11.211623897435897
```

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

```
Out[42]: 0.8755008072610002
```

```
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 =  0.706
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.244
```

```
Out[43]: 0.7055664809826873
```

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

```
Out[44]: 10.314537125000001
```

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

```
Out[45]: 0.0014634129830954725
```

```
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 =  0.669
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.029
```

```
Out[46]: 0.6687055647769407
```

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

```
Out[47]: 10.866148375
```

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

```
Out[48]: 0.506347772629009
```

```
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 =  0.644
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.972
```

```
Out[49]: 0.6444946678805444
```

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

```
Out[50]: 11.313845874999997
```

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

```
Out[51]: 0.9674318077644887
```



```
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 = 0.625
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.938
```

```
Out[52]: 0.6247921954171057
```

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

```
Out[53]: 11.650402374999995
```

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

```
Out[54]: 1.3121810355365977
```

```
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 = 0.607
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.930
```

```
Out[55]: 0.6073401715700245
```

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

```
Out[56]: 12.017476874999995
```

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

```
Out[57]: 1.698498668333778
```

```
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 =  0.375
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.958
```

```
Out[58]: 0.3751072298524801
```

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

```
Out[59]: 12.347483624999992
```

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

```
Out[60]: 2.1099435128548256
```

```
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 =  0.826
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.949
```

```
Out[61]: 0.8256064597638404
```

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

```
Out[62]: 11.393729999999998
```

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

```
Out[63]: 0.9912279926012196
```

```
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)
         JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.830
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.960
```

```
Out[64]: 0.8297464486021761
```

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

```
Out[65]: 11.78747
```

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

```
Out[66]: 1.4319419190168232
```

```
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 = 0.783
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.890
```

```
Out[67]: 0.7834247023913924
```

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

```
Out[68]: 11.98991
```

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

```
Out[69]: 1.6733846114819502
```

```
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 = 0.820
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.971
```

```
Out[70]: 0.8196137782948641
```

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

```
Out[71]: 12.374974999999997
```

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

```
Out[72]: 2.0944223301058718
```

```
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 = 0.477
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.028
```

```
Out[73]: 0.4766403395883764
```

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

```
Out[74]: 12.683680000000003
```

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

```
Out[75]: 2.523273620777815
```

```
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 = 0.375
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.958
```

```
Out[76]: 0.3751072298524801
```

```
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]: 12.347483624999992
```

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

```
Out[80]: 2.1099435128548256
```

```
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 =  0.690
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.273
```

```
Out[81]: 0.6899459237915372
```

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

```
Out[82]: 10.286865512820512
```

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

```
Out[83]: -0.02391516598147182
```

```
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 = 0.651
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.034
```

```
Out[84]: 0.6512246634495952
```

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

```
Out[85]: 10.842524743589742
```

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

```
Out[86]: 0.4826145893882958
```

```
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 = 0.633
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.975
```

```
Out[87]: 0.6333254232165827
```

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

```
Out[88]: 11.296510897435894
```

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

```
Out[89]: 0.9493304538230151
```

```
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 = 0.609
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.938
```

```
Out[90]: 0.6087284919260029
```

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

```
Out[91]: 11.631823589743584
```

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

```
Out[92]: 1.2921235664450779
```

```
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 = 0.599
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.938
```

```
Out[93]: 0.5991686987371352
```



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

```
Out[94]: 12.00039474358974
```

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

```
Out[95]: 1.6773505926300847
```

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

```
Out[96]: SSBR.NumSSBayes(54907,45907,9000,40000,39000,1000,0)
```