

```
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/0.5g2k/G/3  
  
/home/nicole/Jupyter/JG3/Data/0.5g2k/G/3
```

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

```
Correlation.G5.G.J.txt
Correlation.G5.G.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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.J.txt
Regression.G5.G.JC.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      = 0.852
         vRes    = 0.852
         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 =  0.891
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV =  0.997
```

```
Out[34]: 0.8911374745981071
```

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

```
Out[35]: 32.058456729166664
```

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

```
Out[36]: 1.5510816785986326
```

```
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 = 0.568
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.006
```

```
Out[37]: 0.568102353940207
```

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

```
Out[38]: 33.481461555555555
```

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

```
Out[39]: 2.995659043892474
```

```
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 = 0.881
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[40]: 0.8809393321220971
```

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

```
Out[41]: 31.730070999999995
```

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

```
Out[42]: 1.2177176712231308
```

```
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)
         JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.738
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.942
```

```
Out[43]: 0.7375338655084247
```

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

```
Out[44]: 30.509905500000006
```

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

```
Out[45]: -0.00021897656161562606
```

```
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)
         JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.769
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.006
```

```
Out[46]: 0.7685363018453091
```

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

```
Out[47]: 31.175604374999995
```

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

```
Out[48]: 0.6773403720236415
```

```
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 =  0.765
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.017
```

```
Out[49]: 0.7650110757904571
```

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

```
Out[50]: 31.796001874999995
```

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

```
Out[51]: 1.278929374473039
```



```
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 = 0.772
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.018
```

```
Out[52]: 0.7723833109819288
```

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

```
Out[53]: 32.369343875
```

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

```
Out[54]: 1.8477545824633756
```

```
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 = 0.757
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.017
```

```
Out[55]: 0.7570401180581237
```

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

```
Out[56]: 32.9534035
```

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

```
Out[57]: 2.441299202260163
```

```
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 =  0.437
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.028
```

```
Out[58]: 0.4368072518917469
```

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

```
Out[59]: 33.54648125
```

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

```
Out[60]: 3.061385516933191
```

```
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 =  0.887
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.073
```

```
Out[61]: 0.8874677323749762
```

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

```
Out[62]: 31.800485
```

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

```
Out[63]: 1.3435548199018315
```

```
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 =  0.882
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.960
```

```
Out[64]: 0.8817154756214599
```

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

```
Out[65]: 32.421325
```

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

```
Out[66]: 1.8702979706643197
```

```
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 = 0.878
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.961
```

```
Out[67]: 0.8784114196017472
```

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

```
Out[68]: 32.936285
```

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

```
Out[69]: 2.4301807337415
```

```
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 = 0.900
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.006
```

```
Out[70]: 0.8998550213005433
```

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

```
Out[71]: 33.533654999999996
```

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

```
Out[72]: 3.024963282541859
```

```
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 =  0.489
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.939
```

```
Out[73]: 0.4890769261093047
```

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

```
Out[74]: 34.11477
```

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

```
Out[75]: 3.680239490984184
```

```
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 =  0.437
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.028
```

```
Out[76]: 0.4368072518917469
```

```
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]: 33.54648125
```

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

```
Out[80]: 3.061385516933191
```

```
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 = 0.719  
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.938
```

```
Out[81]: 0.7185311037040879
```

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

```
Out[82]: 30.47681371794872
```

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

```
Out[83]: -0.03467471493247323
```

```
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)
JCall = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.752
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.003
```

```
Out[84]: 0.7516923462188144
```

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

```
Out[85]: 31.143662820512812
```

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

```
Out[86]: 0.6467517156482395
```

```
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)
JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.750
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.020
```

```
Out[87]: 0.7502330262366426
```

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

```
Out[88]: 31.76676384615384
```

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

```
Out[89]: 1.249410108850771
```

```
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 =  0.757
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.021
```

```
Out[90]: 0.7568720088074454
```

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

```
Out[91]: 32.33948974358974
```

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

```
Out[92]: 1.8175697439998246
```

```
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 =  0.747
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.026
```

```
Out[93]: 0.747281370987716
```



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

```
Out[94]: 32.92362487179487
```

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

```
Out[95]: 2.409531502549291
```

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

```
Out[96]: SSBR.NumSSBayes(54897,45897,9000,40000,39000,1000,0)
```