

```
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/5  
  
/home/nicole/Jupyter/JG3/Data/0.3/G/5
```

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

```
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
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      = 0.754
vRes     = 1.760
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 = 0.835
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.013
```

```
Out[34]: 0.8352187238223079
```

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

```
Out[35]: 11.5422205625
```

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

```
Out[36]: 1.2737528359678347
```

```
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 = 0.483
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.947
```

```
Out[37]: 0.4831427965926574
```

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

```
Out[38]: 12.668443
```

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

```
Out[39]: 2.40524979050061
```

```
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 = 0.820
```

```
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.025
```

```
Out[40]: 0.8202913834127287
```

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

```
Out[41]: 11.282323076923076
```

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

```
Out[42]: 1.0126381541525789
```

```
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 = 0.708
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.214
```

```
Out[43]: 0.7083633880025051
```

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

```
Out[44]: 10.232199249999999
```

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

```
Out[45]: 0.0014749372163922602
```

```
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 = 0.677
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.020
```

```
Out[46]: 0.6767767568120728
```

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

```
Out[47]: 10.883167999999998
```

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

```
Out[48]: 0.5694291729443988
```

```
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)
         JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.676
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.023
```

```
Out[49]: 0.6758999481723583
```

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

```
Out[50]: 11.342879875000001
```

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

```
Out[51]: 1.068058878175012
```

```
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)
         JCA11 = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.675
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.004
```

```
Out[52]: 0.6747669222912224
```



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

```
Out[53]: 11.785422499999997
```

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

```
Out[54]: 1.5277933618369908
```

```
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 =  0.651
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.026
```

```
Out[55]: 0.6508271249401921
```

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

```
Out[56]: 12.294639625
```

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

```
Out[57]: 2.021471137512307
```

```
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 = 0.358
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.933
```

```
Out[58]: 0.3579857959515831
```

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

```
Out[59]: 12.715014125
```

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

```
Out[60]: 2.454289528121908
```

```
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 = 0.842
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.918
```

```
Out[61]: 0.8416830981885104
```

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

```
Out[62]: 11.500845000000002
```

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

```
Out[63]: 1.12943573783844
```

```
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 = 0.871
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.047
```

```
Out[64]: 0.8706267248763141
```

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

```
Out[65]: 11.801710000000003
```

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

```
Out[66]: 1.569339407885495
```

```
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 = 0.869
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.998
```

```
Out[67]: 0.8694956951724772
```

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

```
Out[68]: 12.237335
```

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

```
Out[69]: 1.9771599796438353
```

```
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 =  0.847
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.012
```

```
Out[70]: 0.8470404951279562
```

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

```
Out[71]: 12.791765000000003
```

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

```
Out[72]: 2.5019646340019666
```

```
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 = 0.344
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.619
```

```
Out[73]: 0.3435022205686357
```

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

```
Out[74]: 13.147714999999998
```

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

```
Out[75]: 2.886759688281379
```

```
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 = 0.358
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.933
```

```
Out[76]: 0.3579857959515831
```

```
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]: 12.715014125
```

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

```
Out[80]: 2.454289528121908
```

```
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)
         JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.686
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.240
```

```
Out[81]: 0.6863184226191319
```

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

```
Out[82]: 10.199669871794873
```

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

```
Out[83]: -0.02744713459442948
```

```
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 = 0.660
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.028
```

```
Out[84]: 0.6596429348755971
```

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

```
Out[85]: 10.859615641025638
```

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

```
Out[86]: 0.5437904489715499
```

```
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 = 0.660
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.027
```

```
Out[87]: 0.6596647540118499
```

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

```
Out[88]: 11.31994512820513
```

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

```
Out[89]: 1.0447485935219651
```

```
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 =  0.655
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.001
```

```
Out[90]: 0.6551176410354592
```

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

```
Out[91]: 11.759618846153845
```

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

```
Out[92]: 1.5028146112686582
```

```
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 =  0.643
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.034
```

```
Out[93]: 0.6429975158844818
```



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

```
Out[94]: 12.272765897435896
```

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

```
Out[95]: 1.9992842515951512
```

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

```
Out[96]: SSBR.NumSSBayes(54883,45883,9000,40000,39000,1000,0)
```