

```
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/0.5a0/G/9  
  
/home/nicole/Jupyter/JG3/Data/0.5a0/G/9
```

```
In [4]: ;ls  
  
GenNF.txt  
PedAll.txt  
Phe.txt  
PheAll.txt
```

```
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;wc G4.noGenotype.ID;wc G5.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 = 0.594
vG = 0.594
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 a
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.898
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.996
```

```
Out[34]: 0.8984477308647231
```

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

```
Out[35]: 2.6163576041666667
```

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

```
Out[36]: 1.3570703305516008
```

```
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 a
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n",
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.607
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.043
```

```
Out[37]: 0.6072294415193861
```

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

```
Out[38]: 3.8991563333333334
```

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

```
Out[39]: 2.635894727337599
```

```
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 ) ;
@printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg3)
JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.884
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[40]: 0.883601340665855
```

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

```
Out[41]: 2.320327128205128
```

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

```
Out[42]: 1.0619570082163703
```

```
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", reg4)
JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.687
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.822
```

```
Out[43]: 0.6873740401533486
```

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

```
Out[44]: 1.2755743750000004
```

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

```
Out[45]: 0.002907847128903057
```

```
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
JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.779
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.003
```

```
Out[46]: 0.7793954341584852
```

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

```
Out[47]: 1.7703276250000002
```

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

```
Out[48]: 0.5350383587931373
```

```
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 =  0.763
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.002
```

```
Out[49]: 0.7632421477240279
```

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

```
Out[50]: 2.344312625
```

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

```
Out[51]: 1.0905299732112568
```

```
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 = 0.786
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.047
```

```
Out[52]: 0.7863107875097429
```

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

```
Out[53]: 2.8908736250000002
```

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

```
Out[54]: 1.6303954304396329
```

```
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 = 0.753
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.017
```

```
Out[55]: 0.7534480467378328
```

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

```
Out[56]: 3.45945825
```

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

```
Out[57]: 2.18962793612043
```

```
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 = 0.458
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.079
```

```
Out[58]: 0.4582692145364429
```

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

```
Out[59]: 3.957599125
```

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

```
Out[60]: 2.6939224376162447
```

```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.912
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.009
```

```
Out[61]: 0.9116671895817529
```

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

```
Out[62]: 2.31163
```

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

```
Out[63]: 1.100025684841908
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.905
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.013
```

```
Out[64]: 0.9045554051164307
```

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

```
Out[65]: 2.9020149999999996
```

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

```
Out[66]: 1.6388041929940314
```

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.914
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.019
```

```
Out[67]: 0.9142290546323221
```

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

```
Out[68]: 3.4562049999999997
```

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

```
Out[69]: 2.172720628686574
```



```
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 = 0.908
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[70]: 0.9078760386021065
```

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

```
Out[71]: 4.02339
```

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

```
Out[72]: 2.7388924733031565
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=1)
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)
JCA12 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.581
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.179
```

```
Out[73]: 0.5814601805966787
```

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

```
Out[74]: 4.46483
```

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

```
Out[75]: 3.207922245716489
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.458
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.079
```

```
Out[76]: 0.4582692145364429
```

```
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]: 3.957599125
```

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

```
Out[80]: 2.6939224376162447
```

```
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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.665
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.808
```

```
Out[81]: 0.6645884311022129
```

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

```
Out[82]: 1.2490088461538464
```

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

```
Out[83]: -0.025223379479122714
```

```
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 = 0.762
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.000
```

```
Out[84]: 0.7618142345506285
```

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

```
Out[85]: 1.7413100000000001
```

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

```
Out[86]: 0.5067366707367043
```

```
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 = 0.743
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.998
```

```
Out[87]: 0.7428957205477477
```

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

```
Out[88]: 2.3158025641025644
```

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

```
Out[89]: 1.062781494865736
```

```
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 = 0.768
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.051
```

```
Out[90]: 0.7684601012996081
```

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

```
Out[91]: 2.861834743589743
```

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

```
Out[92]: 1.6019724293405684
```

```
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 = 0.741
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.019
```

```
Out[93]: 0.7411429498692089
```

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

```
Out[94]: 3.4336794871794876
```

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

```
Out[95]: 2.163517825617967
```

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

```
Out[96]: SSBR.NumSSBayes(54952,45952,9000,40000,39000,1000,0)
```