

```
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/0.5/G/7  
/home/nicole/Jupyter/JG3/Data/0.5/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",calculateInbreeding)
          nothing
          y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
          Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
          nothing
```

```
In [31]: vRes = 0.711
          vG = 0.711
          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 = 0.883
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.973
```

```
Out[34]: 0.8829439837607918
```

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

```
Out[35]: 11.218311875
```

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

```
Out[36]: 1.3500838093845131
```

```
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 = 0.563
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[37]: 0.563447535015066
```

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

```
Out[38]: 12.409567111111111
```

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

```
Out[39]: 2.59580907226698
```

```
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 = 0.871
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.980
```

```
Out[40]: 0.8714452696473725
```

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

```
Out[41]: 10.943406820512822
```

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

```
Out[42]: 1.0626087487193285
```

```
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 =  0.710
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.896
```

```
Out[43]: 0.7102823922176044
```

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

```
Out[44]: 9.911972250000002
```

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

```
Out[45]: 0.0011050894418207847
```

```
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 =  0.773
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.997
```

```
Out[46]: 0.7733038351608958
```

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

```
Out[47]: 10.446048125
```

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

```
Out[48]: 0.5711696569760965
```

```
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 = 0.774
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.016
```

```
Out[49]: 0.7736525198477531
```

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

```
Out[50]: 10.958247499999999
```

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

```
Out[51]: 1.0931136043276533
```

```
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 = 0.762
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.990
```

```
Out[52]: 0.7616368763010631
```

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

```
Out[53]: 11.531684875
```

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

```
Out[54]: 1.64946097553186
```

```
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
JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.731
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.986
```

```
Out[55]: 0.7305650548928745
```

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

```
Out[56]: 11.999897374999996
```

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

```
Out[57]: 2.1344515360157112
```

```
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
JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.425
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.010
```

```
Out[58]: 0.42548827682461937
```

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

```
Out[59]: 12.462021125
```

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

```
Out[60]: 2.6512019940139373
```



```
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 = 0.913
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.055
```

```
Out[61]: 0.9126120057485598
```

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

```
Out[62]: 10.996195
```

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

```
Out[63]: 1.160600057714882
```

```
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 = 0.895
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.020
```

```
Out[64]: 0.8950391097416087
```

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

```
Out[65]: 11.449715
```

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

```
Out[66]: 1.6115045467705187
```

```
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 = 0.893
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.973
```

```
Out[67]: 0.8932001169795858
```

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

```
Out[68]: 12.099385
```

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

```
Out[69]: 2.199941972710145
```

```
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 = 0.854
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.028
```

```
Out[70]: 0.8543548481601531
```

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

```
Out[71]: 12.470485000000002
```

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

```
Out[72]: 2.626181058117034
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.468
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.897
```

```
Out[73]: 0.4681328077629016
```

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

```
Out[74]: 12.933895000000001
```

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

```
Out[75]: 3.165100856144045
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.425
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.010
```

```
Out[76]: 0.42548827682461937
```

```
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]: 12.462021125
```

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

```
Out[80]: 2.6512019940139373
```

```
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 = 0.691
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.889
```

```
Out[81]: 0.6905362053676302
```

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

```
Out[82]: 9.884171666666667
```

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

```
Out[83]: -0.028625550770309004
```

```
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 = 0.760
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.999
```

```
Out[84]: 0.7600223841693486
```

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

```
Out[85]: 10.420313076923078
```

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

```
Out[86]: 0.544494403391624
```

```
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 = 0.756
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.015
```

```
Out[87]: 0.756268726818335
```

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

```
Out[88]: 10.928987564102563
```

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

```
Out[89]: 1.0647333897537432
```

```
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 = 0.991
```

```
Out[90]: 0.7488589801318093
```

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

```
Out[91]: 11.507613076923077
```

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

```
Out[92]: 1.624416870850189
```

```
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 = 0.721
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.994
```

```
Out[93]: 0.720612873877329
```

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

```
Out[94]: 11.975948717948715
```

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

```
Out[95]: 2.108024630371395
```

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

```
Out[96]: SSBR.NumSSBayes(54917,45917,9000,40000,39000,1000,0)
```