

```
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/0.1/G/2  
/home/nicole/Jupyter/JG3/Data/0.1/G/2
```

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 = 0.705
          vG = 6.350
          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 = 0.478
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.201
```

```
Out[34]: 0.47828425364482363
```

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

```
Out[35]: 11.532842479166668
```

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

```
Out[36]: 1.326916366439797
```

```
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 = 0.251
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.149
```

```
Out[37]: 0.2509571796016595
```

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

```
Out[38]: 12.120473888888889
```

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

```
Out[39]: 3.7550595122509485
```

```
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 = 0.411
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.189
```

```
Out[40]: 0.41136900522365083
```

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

```
Out[41]: 11.397235230769232
```

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

```
Out[42]: 0.7665756404833771
```

```
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 = 0.663
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.498
```

```
Out[43]: 0.6634806624659868
```

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

```
Out[44]: 10.65073
```

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

```
Out[45]: 0.00728604400041945
```

```
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 = 0.325
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.123
```

```
Out[46]: 0.32523818511212166
```

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

```
Out[47]: 11.261764999999999
```

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

```
Out[48]: 0.6034683214090683
```

```
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 =  0.337
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.131
```

```
Out[49]: 0.3365819943501392
```

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

```
Out[50]: 11.491451625000002
```

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

```
Out[51]: 0.9074207094717426
```

```
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 =  0.322
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.123
```

```
Out[52]: 0.3216870172106156
```

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

```
Out[53]: 11.69377025
```

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

```
Out[54]: 1.0921323221372967
```

```
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 =  0.303
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.103
```

```
Out[55]: 0.30285010488891795
```

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

```
Out[56]: 11.964299125
```

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

```
Out[57]: 1.5394182653074884
```

```
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 =  0.215
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.136
```

```
Out[58]: 0.21471326361551973
```

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

```
Out[59]: 12.135038874999998
```

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

```
Out[60]: 3.8117725363127657
```



```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 = 0.645
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.737
```

```
Out[61]: 0.6451289492801979
```

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

```
Out[62]: 11.856909999999997
```

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

```
Out[63]: 1.6266745628749029
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.688
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.720
```

```
Out[64]: 0.6876752161894354
```

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

```
Out[65]: 11.74462
```

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

```
Out[66]: 2.6736227473992953
```

```
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 = 0.600
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.519
```

```
Out[67]: 0.5997877709591842
```

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

```
Out[68]: 11.890899999999998
```

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

```
Out[69]: 2.751577231542163
```

```
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 = 0.563
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.454
```

```
Out[70]: 0.5628809584436789
```

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

```
Out[71]: 12.230025000000003
```

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

```
Out[72]: 3.3935235247379416
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.256
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.197
```

```
Out[73]: 0.2557370159253663
```

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

```
Out[74]: 12.297315
```

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

```
Out[75]: 6.061378532227775
```

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

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.215
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.136
```

```
Out[76]: 0.21471326361551973
```

```
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]: 12.135038874999998
```

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

```
Out[80]: 3.8117725363127657
```

```
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 = 0.645
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.482
```

```
Out[81]: 0.6452700999619156
```

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

```
Out[82]: 10.619802307692307
```

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

```
Out[83]: -0.03423673853482375
```

```
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 = 0.314
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.119
```

```
Out[84]: 0.3136670430424741
```

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

```
Out[85]: 11.249384102564102
```

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

```
Out[86]: 0.5503874386913702
```

```
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 = 0.328
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.127
```

```
Out[87]: 0.32802246889949727
```

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

```
Out[88]: 11.48120935897436
```

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

```
Out[89]: 0.8601346448032703
```

```
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 = 0.307
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.117
```

```
Out[90]: 0.3072770059317323
```

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

```
Out[91]: 11.680020128205127
```

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

```
Out[92]: 1.033122291301383
```

```
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 = 0.298
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.106
```

```
Out[93]: 0.2981540980451135
```

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

```
Out[94]: 11.955760256410256
```

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

```
Out[95]: 1.4234705661556863
```

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

```
Out[96]: SSBR.NumSSBayes(54914,45914,9000,40000,39000,1000,0)
```