

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

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 G
          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
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",calculateInbreedin
nothing
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
nothing
```

```
In [31]: vRes = 0.547
vG = 0.547
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 = ' ',head
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 e
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.882
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.964
```

```
Out[34]: 0.8823604036369287
```

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

```
Out[35]: 11.428397729166667
```

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

```
Out[36]: 1.1902140594687267
```

```
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 ) # w
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.563
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.966
```

```
Out[37]: 0.5633551946139531
```

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

```
Out[38]: 12.488875555555556
```

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

```
Out[39]: 2.2923327984963335
```

```
In [40]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
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 = 0.868
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.964
```

```
Out[40]: 0.8677167276188983
```

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

```
Out[41]: 11.183672076923077
```

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

```
Out[42]: 0.9358789658469713
```

```
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 ep
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.672
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.800
```

```
Out[43]: 0.6724673158600225
```

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

```
Out[44]: 10.275937750000002
```

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

```
Out[45]: -0.002940086237395844
```

```
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 ep
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.775
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.976
```

```
Out[46]: 0.7752378206635424
```

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

```
Out[47]: 10.713453375
```

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

```
Out[48]: 0.4890785739960332
```

```
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 ep
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.762
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.986
```

```
Out[49]: 0.7619958884528764
```

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

```
Out[50]: 11.205781749999998
```

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

```
Out[51]: 0.965256883050352
```

```
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 ep
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.755
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.972
```

```
Out[52]: 0.7551305652467674
```

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

```
Out[53]: 11.694766500000002
```

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

```
Out[54]: 1.4443297310302645
```

```
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 ep
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.715
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.952
```

```
Out[55]: 0.7150493011981555
```

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

```
Out[56]: 12.144875125
```

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

```
Out[57]: 1.9043834206593604
```

```
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 ep
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.407
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.945
```

```
Out[58]: 0.4074384297144443
```

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

```
Out[59]: 12.535571875
```

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

```
Out[60]: 2.3411758343137454
```



```
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.
JCall = cor9
```

SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.921

SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.025

Out[61]: 0.9213723769103497

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

Out[62]: 11.166174999999999

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

Out[63]: 1.00585922843889

```
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.
JCall = cor9
```

SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.894

SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.995

Out[64]: 0.8940231740016384

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

Out[65]: 11.69979

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

Out[66]: 1.442036876984904

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.888
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.985
```

```
Out[67]: 0.8877903082970064
```

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

```
Out[68]: 12.181799999999999
```

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

```
Out[69]: 1.9186161827153063
```

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.843
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.892
```

```
Out[70]: 0.8430312396113313
```

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

```
Out[71]: 12.595339999999998
```

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

```
Out[72]: 2.3637888348445664
```

```
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.
JCall = cor12
```

SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.517

SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.973

Out[73]: 0.5172545256822579

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

Out[74]: 12.933420000000002

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

Out[75]: 2.7776414368014968

```
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.
JCall = cor13
```

SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.407

SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.945

Out[76]: 0.4074384297144443

```
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]: 12.535571875

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

Out[80]: 2.3411758343137454

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', he
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 = %
JCall = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.651
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.789
```

```
Out[81]: 0.6513878494336921
```

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

```
Out[82]: 10.253111153846152
```

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

```
Out[83]: -0.028806735331659585
```

```
In [84]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', he
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 = %
JCall = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.759
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.970
```

```
Out[84]: 0.759403697857883
```

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

```
Out[85]: 10.688162692307694
```

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

```
Out[86]: 0.4646437457142674
```

```
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 = 0.744
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.983
```

```
Out[87]: 0.7442860309125761
```

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

```
Out[88]: 11.180755641025641
```

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

```
Out[89]: 0.9408117728025327
```

```
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 = 0.740
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.973
```

```
Out[90]: 0.7399278536261467
```

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

```
Out[91]: 11.671674871794874
```

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

```
Out[92]: 1.4207538565734874
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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 = %
JCall = cor17
```

SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.703

SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.957

Out[93]: 0.7032905817883089

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

Out[94]: 12.124656025641027

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

Out[95]: 1.8819921894762284

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

Out[96]: SSBR.NumSSBayes(54966,45966,9000,40000,39000,1000,0)