```
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/1
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/G/1
```

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

```
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.JC.txt
Regression.G5.G.N.txt
all.ID
genotype.ID
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
```
```
  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    = 1.408
vG      = 1.408
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
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
JCAll = cor1
```
```
SSBRJC from Gibbs - all.ID : correlation =  0.887
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.968
```

Out[34]: 0.8874508056578726

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

Out[35]: 2.642914354166667

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

Out[36]: 1.8124993169693728

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

```
         SSBRJC from Gibbs - genotype.ID : correlation =   0.556
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   0.878
```

Out[37]: 0.555818145385672

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

Out[38]: 4.108706222222223

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

Out[39]: 3.410962489128093

```
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 =   0.877
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.995
```

Out[40]: 0.8767379006697824

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

Out[41]: 2.3046546923076923

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

Out[42]: 1.4436232003173604

```
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 =  0.799
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.130
```

Out[43]: 0.7990127756656066

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

Out[44]: 0.8388541249999999

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

Out[45]: -0.0006331634645465405

```
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 =  0.776
         SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.003
```

Out[46]: 0.7760287925348034

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

Out[47]: 1.7074885

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

Out[48]: 0.8220206254046252

```
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", re
         JCAll = cor5
```

```
         SSBRJC from Gibbs - G2.ID : correlation =  0.745
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.961
```

Out[49]: 0.7451269979704263

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

Out[50]: 2.43677575

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

Out[51]: 1.552212611450559

```
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", re
         JCAll = cor6
```

```
         SSBRJC from Gibbs - G3.ID : correlation =  0.734
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.935
```

Out[52]: 0.7339263078700347

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

Out[53]: 3.0633003750000003

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

Out[54]: 2.2106905765327056

```
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", re
         JCAll = cor7
```

```
         SSBRJC from Gibbs - G4.ID : correlation =  0.705
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.874
```

Out[55]: 0.7052909069954982

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

Out[56]: 3.6475862500000003

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

Out[57]: 2.812858983270985

```
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", re
         JCAll = cor8
```

```
         SSBRJC from Gibbs - G5.ID : correlation =  0.420
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.867
```

Out[58]: 0.4202985326544734

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

Out[59]: 4.163481125000001

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

Out[60]: 3.4778462686219083

```
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 =  0.889
         SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.960
```

Out[61]: 0.888746080232019

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

Out[62]: 2.558755

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

Out[63]: 1.6339367750739304

```
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 =  0.882
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.012
```

Out[64]: 0.8815735773861826

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

Out[65]: 3.1442850000000004

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

Out[66]: 2.285290935091015

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 =  0.879
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.971
```

Out[67]:  0.8793439736010608

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

Out[68]:  3.7104500000000002

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

Out[69]:  2.869155254594426

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 =  0.882
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.999
```

Out[70]:  0.8821532131454335

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

Out[71]:  4.21913

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

Out[72]:  3.4468936026894776

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 =   0.438
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.750
```

Out[73]: 0.43803154239800746

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

Out[74]: 4.719915

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

Out[75]: 4.144184698439014

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 =   0.420
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   0.867
```

Out[76]: 0.4202985326544734

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]: 4.163481125000001

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

Out[80]: 3.4778462686219083

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 =  0.785
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.142
```

Out[81]: 0.7851397821006547

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

Out[82]: 0.7947541025641025

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

Out[83]: -0.04254521317066133

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 =  0.762
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.005
```

Out[84]: 0.7618454066814878

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

Out[85]: 1.6706475641025644

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

Out[86]: 0.784500873874205

```
In [87]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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", cor1!
         @printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = !
         JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.730
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.960
```

Out[87]: 0.7300473075312068

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

Out[88]: 2.4041174358974358

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

Out[89]: 1.5184448513699473

```
In [90]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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", cor1(
         @printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = !
         JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.720
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.934
```

Out[90]: 0.7195284806143848

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

Out[91]: 3.033663717948718

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

Out[92]: 2.178993063041506

```
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 =  0.695
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.881
```

Out[93]: 0.6949663101798487

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

Out[94]: 3.6200906410256413

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

Out[95]: 2.7787224264718047

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

Out[96]: SSBR.NumSSBayes(54950,45950,9000,40000,39000,1000,0)