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/0.1/G/1
```

/home/nicole/Jupyter/JG3/Data/0.1/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    = 7.831
vG      = 0.870
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 =  0.653
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.045
```

Out[34]: 0.6530756583330602

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

Out[35]: 11.285119854166668

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

Out[36]: 0.7876836044289044

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

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.367
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.896
```

Out[37]: 0.3668448684793828

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

Out[38]: 11.993996777777777

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

Out[39]: 1.501643462180493

```
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 =  0.634
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.079
```

Out[40]: 0.633636192991879

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

Out[41]: 11.121532871794871

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

Out[42]: 0.6229236372554608

```
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 =  0.571
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.868
```

Out[43]: 0.5709563354503714

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

Out[44]: 10.310185249999998

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

Out[45]: −0.0007157469570611921

```
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 =  0.472
         SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.942
```

Out[46]: 0.4715205139327561

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

Out[47]: 10.942740625000003

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

Out[48]: 0.3292868789316388

```
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 =  0.508
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.999
```

Out[49]: 0.5078944046146783

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

Out[50]: 11.215667624999998

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

Out[51]: 0.657612977058185

```
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 =  0.491
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.947
```

Out[52]: 0.49118196517539714

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

Out[53]: 11.4849005

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

Out[54]: 0.9641603984229964

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 =  0.479
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.960
```

Out[55]: 0.47940160753937

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

Out[56]: 11.742411499999998

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

Out[57]: 1.2418802037880765

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 =  0.309
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.982
```

Out[58]: 0.30855216564568544

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

Out[59]: 12.014813624999999

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

Out[60]: 1.5338769153295908

```
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 =  0.639
         SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.718
```

Out[61]: 0.6391889069115062

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

Out[62]: 11.595910000000002

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

Out[63]: 0.6326046884427587

```
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 =  0.741
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.990
```

Out[64]: 0.7409805205722675

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

Out[65]: 11.474039999999995

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

Out[66]: 0.9749967445638797

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 =  0.741
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.017
```

Out[67]: 0.7411536747947596

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

Out[68]: 11.749784999999997

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

Out[69]: 1.2701020319688603

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 =  0.678
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.909
```

Out[70]: 0.6776267759161401

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

Out[71]: 12.014095000000003

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

Out[72]: 1.511727096914488

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 =   0.418
SSBRJC from Gibbs – G4.Genotype.ID : regression of TBV on GEBV =   0.964
```

Out[73]: 0.4182344808282317

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

Out[74]: 12.30348

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

Out[75]: 1.8294486230485851

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 =   0.309
SSBRJC from Gibbs – G5.Genotype.ID : regression of TBV on GEBV =   0.982
```

Out[76]: 0.30855216564568544

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]: 12.014813624999999

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

Out[80]: 1.5338769153295908

```
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 =   0.554
         SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   2.014
```

Out[81]: 0.5538907265839111

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

Out[82]: 10.277217948717947

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

Out[83]: -0.016954732480133506

```
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 =   0.456
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   0.947
```

Out[84]: 0.4559466584606727

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

Out[85]: 10.929117564102565

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

Out[86]: 0.3127302157102993

```
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", cor15
         @printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 9
         JCAll = cor15
```

```
         SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.495
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.005
```

Out[87]: 0.494510935435858

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

Out[88]: 11.201972307692307

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

Out[89]: 0.6419081294963728

```
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", cor16
         @printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 9
         JCAll = cor16
```

```
         SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.479
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.948
```

Out[90]: 0.4789635976255355

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

Out[91]: 11.471331410256408

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

Out[92]: 0.9501202266668043

```
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", cor1
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =
         JCAll = cor17
```

```
         SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.472
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.960
```

Out[93]: 0.47219982475291106

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

Out[94]: 11.728025128205127

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

Out[95]: 1.2268143468839605

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

Out[96]: SSBR.NumSSBayes(54905,45905,9000,40000,39000,1000,0)