```
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/0.5g2k/G/7
```

```
         /home/nicole/Jupyter/JG3/Data/0.5g2k/G/7
```

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

```
         GenNF.txt
         PedAll.txt
         Phe.txt
         PheAll.txt
```

```
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`

```
 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;wc G4.noGenotype.ID;wc G`

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

In [31]:
```
vG      = 0.910
vRes    = 0.910
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,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 epsilon
         @printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n", reg1)
         JCAll = cor1
```

```
         SSBRJC from Gibbs - all.ID : correlation =  0.896
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.989
```

Out[34]: 0.8963589776826291

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

Out[35]: 33.103910812500004

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

Out[36]: 1.620568960775255

```
In [37]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3f\n", reg2)
         JCAll = cor2
```

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.558
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.949
```

Out[37]: 0.5575932464454885

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

Out[38]: 34.55933366666667

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

Out[39]: 3.1002504813198635

In [40]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV = %6.3f\n", reg3)
JCAll = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.884
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.993
```

Out[40]: 0.8843380054268667

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

Out[41]: 32.768044

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

Out[42]: 1.27910399449573

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 epsilon
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.744
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.981
```

Out[43]: 0.7438901651559567

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

Out[44]: 31.488621875000003

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

Out[45]: −0.002317655630432568

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 epsilon
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.771
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.987
```

Out[46]: 0.7711689515776102

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

Out[47]: 32.19599624999999

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

Out[48]: 0.715602598655237

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 epsilon
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =   0.759
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   0.991
```

Out[49]: 0.7588563498578573

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

Out[50]: 32.84068424999999

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

Out[51]: 1.348162103041177

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 epsilon
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =   0.763
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.978
```

Out[52]: 0.7626410840014354

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

Out[53]: 33.425010249999985

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

Out[54]: 1.9312775152876591

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 epsilon
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =   0.730
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   0.958
```

Out[55]: 0.7302874391948042

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

Out[56]: 34.050391000000005

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

Out[57]: 2.5655138520960983

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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.391
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.900
```

Out[58]: 0.39063289308404775

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

Out[59]: 34.622761249999996

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

Out[60]: 3.1651753512017913

In [61]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.916
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.056
```

Out[61]: 0.9160399046860374

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

Out[62]: 32.917105

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

Out[63]: 1.4399155418713254

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
         JCAll = cor9
```

```
         SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.914
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.987
```

Out[64]: 0.9138921989697593

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

Out[65]: 33.48443999999999

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

Out[66]: 1.9894346413876094

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg10)
         JCAll = cor10
```

```
         SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.906
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.018
```

Out[67]: 0.9057027674554525

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

Out[68]: 34.001095

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

Out[69]: 2.524276771110211

In [70]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg11)
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.895
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.990
```

Out[70]: 0.8947210654232091

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

Out[71]: 34.67741

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

Out[72]: 3.1965542051117883

In [73]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.473
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.905
```

Out[73]: 0.4727833606986594

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

Out[74]: 35.179514999999995

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

Out[75]: 3.7540764518412537

In [76]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.391
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.900
```

Out[76]: 0.39063289308404775

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]: 34.622761249999996

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

Out[80]: 3.1651753512017913

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.722
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.978
```

Out[81]: 0.7216476497714616

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

Out[82]: 31.451994102564107

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

Out[83]: -0.039297994027913535

```
In [84]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.753
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.984
```

Out[84]: 0.7527696744715985

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

Out[85]: 32.16295923076923

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

Out[86]: 0.6829402385851763

In [87]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.742
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[87]: 0.7419063338898014

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

Out[88]: 32.81093012820512

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

Out[89]: 1.3180053166804326

In [90]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.744
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.977
```

Out[90]: 0.7435369184651303

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

```
Out[91]:  33.39289743589743
```

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

```
Out[92]:  1.8988345232408865
```

```
In [93]:  IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
          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 ) # with epsilon
          @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 =  0.717
          SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.959
```

```
Out[93]:  0.7173659153399721
```

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

```
Out[94]:  34.0214391025641
```

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

```
Out[95]:  2.5350378880000686
```

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

```
Out[96]:  SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,0)
```