In [1]:
```julia
include("/home/nicole/Jupyter/SSBRnoJ/src/SSBR.jl")
using SSBR
```

In [2]:
```julia
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]:
```julia
; cd Data/0.5g2k/G/9
```

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/9

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

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

In [5]:
```julia
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```julia
;awk '{print $1}' GenNF.txt | sort -b > genotype.ID
```

In [7]:
```julia
;join -v1 all.ID genotype.ID > noGenotype.ID
```

In [8]:
```julia
;awk '{print $1,$2}' Phe.txt > sim.phenotype
```

In [9]:
```julia
;awk '{print $1,$3}' PheAll.txt > sim.bv
```

In [10]:
```julia
; awk 'NR >=1 && NR <=8000 {print $1}' PedAll.txt | sort -b > G0.ID
```

In [11]:
```julia
; 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    = 0.682
vRes  = 0.682
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 =  0.897
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.005
```

Out[34]: 0.8972303052257922

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

Out[35]: 31.740460895833337

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

Out[36]: 1.4154635453345705

```
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 =  0.593
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.054
```

Out[37]: 0.5929838898212956

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

Out[38]: 33.07933477777778

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

Out[39]: 2.7230255896398337

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 =   0.883
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.994
```

Out[40]: 0.8830973820203187

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

Out[41]: 31.431490000000004

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

Out[42]: 1.1137184581872022

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 =   0.708
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   0.873
```

Out[43]: 0.7079151076949128

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

Out[44]: 30.3241715

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

Out[45]: -0.0048188898199469435

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 =  0.779
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.993
```

Out[46]: 0.7787657804157004

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

Out[47]: 30.86662312499999

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

Out[48]: 0.5678176750388377

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 =  0.771
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.011
```

Out[49]: 0.771342369269932

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

Out[50]: 31.47034175

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

Out[51]: 1.1613613218946361

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 =  0.765
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.026
```

Out[52]: 0.7651367178027951

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

Out[53]: 32.05523775

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

Out[54]: 1.7271378536576696

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 =  0.747
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.035
```

Out[55]: 0.747102929519337

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

Out[56]: 32.58414175000001

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

Out[57]: 2.260071991201482

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 =  0.438
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.055
```

Out[58]: 0.4378601728333228

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

Out[59]: 33.142249500000005

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

Out[60]: 2.781211320034745

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 =  0.903
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.969
```

Out[61]: 0.9030830623823363

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

Out[62]: 31.40948

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

Out[63]: 1.1658711248220235

```
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 =  0.902
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.000
```

Out[64]: 0.9018995733073214

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

Out[65]: 32.04329

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

Out[66]: 1.7444669073432817

```
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 =  0.881
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.970
```

Out[67]: 0.881848223745489

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

Out[68]: 32.625765

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

Out[69]: 2.2854400764337104

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 =  0.884
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[70]: 0.8843719766048918

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

Out[71]: 33.108585

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

Out[72]: 2.7908209239512587

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 =  0.596
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.129
```

Out[73]: 0.5960575048764228

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

Out[74]: 33.692964999999994

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

Out[75]: 3.3010996998524416

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 =  0.438
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.055
```

Out[76]: 0.4378601728333228

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]: 33.142249500000005

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

Out[80]: 2.781211320034745

```
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 =  0.688
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.866
```

Out[81]: 0.6878347911588525

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

Out[82]: 30.29634307692307

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

Out[83]: -0.03483658250307439

```
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 =  0.762
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.992
```

Out[84]: 0.761504571666154

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

Out[85]: 30.836452179487175

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

Out[86]: 0.5376471819028263

```
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 = 0.754
          SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.010

Out[87]: 0.7536659356615208

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

Out[88]: 31.44071551282051

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

Out[89]: 1.1325387897269674

```
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 = 0.749
          SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.029

Out[90]: 0.7489962301378303

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

Out[91]: 32.02822884615385

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

Out[92]: 1.6998639287783468

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 =  0.732
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.031
```

Out[93]: 0.7321587094798405

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

Out[94]: 32.555710384615395

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

Out[95]: 2.233378973030945

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

Out[96]: SSBR.NumSSBayes(54936,45936,9000,40000,39000,1000,0)