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/10
```

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/10

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

```
Correlation.G5.G.C.txt
Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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.PBLUP.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 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
df      = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                        # without centering
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes);
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(Z_Mats,M_Mats,numSSBayes)     # no J
nothing
```

In [31]:
```
vG     = 0.858
vRes   = 0.858
nIter  = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter, outFreq=5000);
nothing
```

```
This is iteration 5000
This is iteration 10000
This is iteration 15000
This is iteration 20000
This is iteration 25000
This is iteration 30000
This is iteration 35000
This is iteration 40000
This is iteration 45000
This is iteration 50000
7069.317270 seconds (23.86 G allocations: 736.887 GB, 2.67% gc time)
```

In [32]:
```
betaHat
```

Out[32]:
```
1-element Array{Float64,1}:
 32.3886
```

In [33]:
```
using DataFrames
```

```
In [34]: 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 [35]: IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor1 = cor(a[posAi],aHat1[posAi])[1,1]
         reg1 = linreg(aHat1[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 =  0.912
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.981
```

```
Out[35]: 0.9121916787963351
```

```
In [36]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[36]: 1.7180686080809255
```

```
In [37]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor2 = cor(a[posAi],aHat1[posAi])[1,1]
         reg2 = linreg(aHat1[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 =  0.913
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.075
```

```
Out[37]: 0.913211611865203
```

```
In [38]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[38]: 2.9943680667476436
```

In [39]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor3 = cor(a[posAi],aHat1[posAi])[1,1]
reg3 = linreg(aHat1[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 =  0.881
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.965
```

Out[39]: 0.8813540170973876

In [40]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[40]: 1.4235379637732213

In [41]:
```
IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat1[posAi])[1,1]
reg4 = linreg(aHat1[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 =  0.750
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.937
```

Out[41]: 0.7497820593783163

In [42]:
```
GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

Out[42]: 0.14364839465462462

In [43]:
```
IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat1[posAi])[1,1]
reg4 = linreg(aHat1[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 =  0.776
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.994
```

Out[43]: 0.7761383694756393

In [44]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[44]: 0.9064160499426044

In [45]:
```
IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor5 = cor(a[posAi],aHat1[posAi])[1,1]
reg5 = linreg(aHat1[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 =  0.764
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.996
```

Out[45]: 0.7640211925518545

In [46]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[46]: 1.5469463839825

In [47]:
```
IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor6 = cor(a[posAi],aHat1[posAi])[1,1]
reg6 = linreg(aHat1[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 =  0.755
SSBRJC from Gibbs – G3.ID : regression of TBV on GEBV =  0.996
```

Out[47]: 0.754535003531951

In [48]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[48]: 2.0723503187200243

In [49]:
```
IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat1[posAi])[1,1]
reg7 = linreg(aHat1[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 =  0.756
SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV =  0.987
```

Out[49]: 0.7557376007250507

In [50]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[50]: 2.5997400579670122

In [51]:
```
IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat1[posAi])[1,1]
reg8 = linreg(aHat1[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 =   0.899
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.061
```

Out[51]: 0.8994476603758066

In [52]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[52]: 3.0393104432187874

In [53]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
#TBV = a[posAi]
#GEBV = aHat1[posAi]
#reg = linreg(X,Y)
#reg = linreg(GEBV, TBV)[2,1]
reg9 = linreg(aHat1[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 =   0.922
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =   1.064
```

Out[53]: 0.9220343592901366

In [54]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[54]: 1.7385030467994025

```
In [55]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat1[posAi])[1,1]
         #TBV = a[posAi]
         #GEBV = aHat1[posAi]
         #reg = linreg(X,Y)
         #reg = linreg(GEBV, TBV)[2,1]
         reg9 = linreg(aHat1[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 =  0.936
SSBRJC from Gibbs – G1.Genotype.ID : regression of TBV on GEBV =  1.084
```

Out[55]: 0.9356334855919276

```
In [56]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[56]: 2.226403611289677

```
In [57]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor10 = cor(a[posAi],aHat1[posAi])[1,1]
         reg10 = linreg(aHat1[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 =  0.928
SSBRJC from Gibbs – G2.Genotype.ID : regression of TBV on GEBV =  1.063
```

Out[57]: 0.9275343415390254

```
In [58]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[58]: 2.6404283118260867

In [59]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor11 = cor(a[posAi],aHat1[posAi])[1,1]
reg11 = linreg(aHat1[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 =  0.930
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.096
```

Out[59]: 0.929529966340576

In [60]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[60]: 3.1351576865710684

In [61]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor12 = cor(a[posAi],aHat1[posAi])[1,1]
reg12 = linreg(aHat1[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 =  0.859
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.030
```

Out[61]: 0.8588677487412726

In [62]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[62]: 3.4336526184062235

In [63]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor13 = cor(a[posAi],aHat1[posAi])[1,1]
reg13 = linreg(aHat1[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 =  0.899
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.061
```

Out[63]: 0.8994476603758066

In [64]:
```
writedlm("Correlation.G5.G.N.txt",cor13)
```

In [65]:
```
writedlm("Regression.G5.G.N.txt",reg13)
```

In [66]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[66]: 35.44119087500001

In [67]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[67]: 3.0393104432187874

In [68]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat1[posAi])[1,1]
reg14 = linreg(aHat1[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 =  0.732
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.952
```

Out[68]: 0.7323625679627958

In [69]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[69]: 0.10275468562527135

In [70]:
```
IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat1[posAi])[1,1]
reg14 = linreg(aHat1[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 =  0.760
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.002
```

Out[70]: 0.7599583236977312

In [71]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[71]: 0.8725702150362693

In [72]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor15 = cor(a[posAi],aHat1[posAi])[1,1]
reg15 = linreg(aHat1[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 =  0.749
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.996
```

Out[72]: 0.7488102296698593

In [73]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[73]: 1.5189083858326644

In [74]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor16 = cor(a[posAi],aHat1[posAi])[1,1]
reg16 = linreg(aHat1[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 =  0.737
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[74]: 0.7372784969894896

In [75]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[75]: 2.0450988477494847

In [76]:
```
IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor17 = cor(a[posAi],aHat1[posAi])[1,1]
reg17 = linreg(aHat1[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 =  0.744
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.980
```

Out[76]: 0.7435566190996441

In [77]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[77]: 2.578357684622417

In [78]:
```
numSSBayes
```

Out[78]: SSBR.NumSSBayes(54904,45904,9000,40000,39000,1000,2000)