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/8
```

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/8

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]:
```julia
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]:
```julia
vG      = 0.719
vRes    = 0.719
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
7090.153087 seconds (23.86 G allocations: 736.943 GB, 2.67% gc time)
```

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

Out[32]:
```
1-element Array{Float64,1}:
 30.7559
```

In [33]:
```julia
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 =  0.907
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.987
```

Out[35]: 0.9067110835431677

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

Out[36]: 1.4933594100813543

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 =  0.901
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.101
```

Out[37]: 0.9014667064204843

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

Out[38]: 2.6849326072609974

```
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 =  0.874
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.974
```

Out[39]: 0.8736412637900408

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

Out[40]: 1.218380979962975

```
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 =  0.722
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.878
```

Out[41]: 0.7215373366377543

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

Out[42]: 0.11931614133302375

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 =  0.772
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.999
```

Out[43]: 0.7716888757606274

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

Out[44]: 0.7673074533366308

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 =  0.771
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.023
```

Out[45]: 0.770831092219199

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

Out[46]: 1.2849483504212562

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 =  0.777
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.028
```

Out[47]: 0.7773141302648642

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

Out[48]: 1.773866096159468

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 =  0.769
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.039
```

Out[49]: 0.7693792604789037

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

Out[50]: 2.2833357827537117

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 =  0.886
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.099
```

Out[51]: 0.8858317905290762

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

Out[52]: 2.7313826364840343

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 =  0.927
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.136
```

Out[53]: 0.9266415963510755

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

Out[54]: 1.4971626318682016

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 =  0.924
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.084
```

Out[55]: 0.9243683733753473

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

Out[56]: 1.8699477866235825

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 =  0.945
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.112
```

Out[57]: 0.9446250435424699

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

Out[58]: 2.289147819872157

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 =  0.911
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.063
```

Out[59]: 0.9105837115110702

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

Out[60]: 2.7784552078149836

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 =  0.821
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.993
```

Out[61]: 0.8209489536372043

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

Out[62]: 3.1319484212045876

```
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 =   0.886
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   1.099
```

Out[63]: 0.8858317905290762

```
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]: 33.47593925000001

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

Out[67]: 2.7313826364840343

```
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 =   0.702
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.881
```

Out[68]: 0.7021786176354893

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

Out[69]: 0.08398674413981407

```
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 =  0.757
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.002
```

Out[70]: 0.757231888358677

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

Out[71]: 0.739034624277991

```
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 =  0.756
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.025
```

Out[72]: 0.7559858903957258

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

Out[73]: 1.2591996460763615

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 =  0.763
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.027
```

Out[74]: 0.7628067215768851

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

Out[75]: 1.748107400988814

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 =  0.758
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.038
```

Out[76]: 0.7580738649660059

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

Out[77]: 2.261576484331894

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

Out[78]: SSBR.NumSSBayes(54908,45908,9000,40000,39000,1000,2000)