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/0.3/G/3
```

/home/nicole/Jupyter/JG3/Data/0.3/G/3

```
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     = 0.505
         vRes   = 1.180
         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
2491.773022 seconds (23.05 G allocations: 723.868 GB, 7.90% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
          10.1741
```

```
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 =  0.876
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.980
```

Out[35]: 0.8758495796669156

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

Out[36]: 1.2288019453190266

```
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 =  0.960
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.095
```

Out[37]: 0.9597147739727834

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

Out[38]: 2.176284242658336

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 =  0.822
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.966
```

Out[39]: 0.8220481926497609

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

Out[40]: 1.0101521843945707

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 =  0.640
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.016
```

Out[41]: 0.639755372668038

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

Out[42]: 0.10050420062425727

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 =  0.686
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.020
```

Out[43]: 0.686190993978076

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

Out[44]: 0.6435923789073075

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 =  0.697
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.025
```

Out[45]: 0.6966417243207778

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

Out[46]: 1.0769214248675179

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 =  0.696
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.047
```

Out[47]: 0.6961595491979984

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

Out[48]: 1.4666722083850696

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 =  0.730
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.075
```

Out[49]: 0.7295287530674844

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

Out[50]: 1.8717906418714179

In [51]:
```julia
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 =  0.956
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.094
```

Out[51]: 0.9562979793869235

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

Out[52]: 2.213330817258591

In [53]:
```julia
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 =  0.944
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.049
```

Out[53]: 0.9442180371594641

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

Out[54]: 1.2172041833530143

```
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 =  0.947
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.047
```

Out[55]: 0.9466527473822145

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

Out[56]: 1.523022362657579

```
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 =  0.953
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.085
```

Out[57]: 0.953431274830908

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

Out[58]: 1.8654016242458777

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 =  0.950
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.062
```

Out[59]: 0.9502842489077291

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

Out[60]: 2.277565498807083

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 =  0.952
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.086
```

Out[61]: 0.9515476766437865

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

Out[62]: 2.516364560217944

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 =  0.956
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.094
```

Out[63]: 0.9562979793869235

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]: 12.3666555

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

Out[67]: 2.213330817258591

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 =  0.620
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.066
```

Out[68]: 0.6196999060362526

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

Out[69]: 0.07187086773377632

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 =   0.666
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   1.031
```

Out[70]: 0.6657192429887392

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

Out[71]: 0.6210428921444799

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 =   0.678
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   1.027
```

Out[72]: 0.6777201164408874

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

Out[73]: 1.0567039838578165

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 =  0.676
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.048
```

Out[74]: 0.6755835000694912

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

Out[75]: 1.4458800727332228

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 =  0.716
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.075
```

Out[76]: 0.7164241285018749

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

Out[77]: 1.8552631055035584

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

Out[78]: SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,200)