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/0.5/M/6
```

/home/nicole/Jupyter/JG3/Data/0.5/M/6

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

```
Correlation.G5.M.J.txt
Correlation.G5.M.JC.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
MarNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.J.txt
Regression.G5.M.JC.txt
all.ID
alphaEstimatesJ
alphaEstimatesJC
epsiEstimatesJ
epsiEstimatesJC
genotype.ID
meanOfSNPMAll
meanOfSNPMG0
meanOfSNPMG1
meanOfSNPMG2
meanOfSNPMG3
meanOfSNPMG4
meanOfSNPMG5
noGenotype.ID
sim.bv
sim.phenotype
```

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

```
In [6]:  ;awk '{print $1}' MarNF.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 G
```
```
 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
```

```
   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",calculateInbreedi
nothing
df      = read_genotypes("MarNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped,center=true);                    # wit
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
nothing
```

In [31]:
```
vRes    = 0.912
vG      = 0.912
nIter   = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter,
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
2391.221988 seconds (23.03 G allocations: 723.515 GB, 7.70% gc time)
```

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

Out[32]:
```
1-element Array{Float64,1}:
 10.0299
```

```
In [33]: alphaHat
```

```
Out[33]: 150-element Array{Float64,1}:
         -0.109073
         -0.112823
          0.0700685
         -0.0295701
          0.223503
         -0.165391
          0.190131
          0.0212746
         -0.0437051
          0.0157644
          0.0394169
         -0.193112
         -0.12263
          ⋮
         -0.31675
          0.0899542
          0.291244
         -0.00342189
         -0.0467829
          0.144069
         -0.0204526
          0.00120288
          0.00892093
          0.114696
         -0.109853
         -0.104477
```

```
In [34]: writedlm("alphaEstimatesC",alphaHat)
```

```
In [35]:  epsiHat
```

```
Out[35]:  45914-element Array{Float64,1}:
           0.742887
          -0.302637
           0.0164402
          -0.696152
           0.265281
          -0.490629
          -0.641596
          -0.423299
          -0.350943
          -0.126072
          -0.1136
          -0.147156
          -0.80024
           ⋮
           0.680833
          -1.06398
           0.698929
          -0.172274
          -0.851137
           0.736458
          -0.436471
          -0.606308
          -0.656381
           0.585583
          -0.107579
           0.818677
```

```
In [36]:  writedlm("epsiEstimatesC",epsiHat)
```

```
In [37]:  using DataFrames
```

```
In [38]:  df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',hea
          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 [39]:  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
          @printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
          JCAll = cor1

          SSBRJC from Gibbs - all.ID : correlation =  0.902
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.991
```

```
Out[39]:  0.9022353862181784
```

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

Out[40]: 0.16284369985431957

In [41]:
```
IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=
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 ) # w
@printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3:
JCAll = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.831
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.971
```

Out[41]: 0.8313074290439278

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

Out[42]: 1.4234445747429219

In [43]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
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 ) ;
@printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV = %6
JCAll = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.874
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.976
```

Out[43]: 0.8742720471968083

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

Out[44]: −0.12806419435074237

In [45]:
```
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 e
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.730
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.931
```

Out[45]: 0.7296930997196134

In [46]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[46]: -1.4223146095173855

In [47]:
```
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 e
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.761
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.990
```

Out[47]: 0.7606464223953626

In [48]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[48]: -0.6072546321363875

In [49]:
```
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 e
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.762
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.003
```

Out[49]: 0.7619194047294771

In [50]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[50]: 0.0004962272956668556

In [51]:
```
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 e
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.750
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.000
```

Out[51]: 0.7498885340622794

In [52]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[52]: 0.5187119789649655

In [53]:
```
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 e
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", r
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =   0.744
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   0.984
```

Out[53]: 0.7442384456311179

In [54]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[54]: 1.0206527490650943

In [55]:
```
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 e
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", r
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.809
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.937
```

Out[55]: 0.8090425136093125

In [56]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[56]: 1.4667704854539643

In [57]:
```
GEBVG5G1=G5GEBV-G1GEBV
```

Out[57]: 2.074025117590352

In [58]:
```
GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]
```

Out[58]:
```
5-element Array{Float64,1}:
 -0.607255
  0.000496227
  0.518712
  1.02065
  1.46677
```

In [59]:
```
reg8 = linreg(aHat1[posAi], a[posAi])
```

Out[59]: 2-element Array{Float64,1}:
  10.1864
   0.936747

In [60]:
```
VarGEBV=var(aHat1[posAi])
```

Out[60]: 0.4155798013786917

In [61]:
```
VarTBV=var(a[posAi])
```

Out[61]: 0.5571294135864484

In [62]:
```
Cov=cov(aHat1[posAi], a[posAi])
```

Out[62]: 0.38929300746271145

In [63]:
```
b=Cov/VarGEBV
```

Out[63]: 0.936746699842549

In [64]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G0.Genotype.ID : correlation = %6.3f\n", cor9 )
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.844
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.002
```

Out[64]: 0.8442051974128242

In [65]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[65]: 0.29555451012955414

In [66]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G1.Genotype.ID : correlation = %6.3f\n", cor9 )
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.835
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.931
```

Out[66]: 0.8345959772267084

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

Out[67]: 0.6786845362551379

```
In [68]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
         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
         @printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor10
```

```
         SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.825
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.942
```

Out[68]: 0.8248381989738629

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

Out[69]: 1.0650327381202478

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
         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
         @printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor11
```

```
         SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.792
         SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.821
```

Out[70]: 0.7921534510697101

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

Out[71]: 1.5045061955101269

```
In [72]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
         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
         @printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor12
```

```
         SSBRJC from Gibbs - G4.Genotype.ID : correlation =  0.746
         SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.784
```

Out[72]: 0.7461910296120533

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

Out[73]: 1.8404084652578316

In [74]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =  0.809
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.937
```

Out[74]: 0.8090425136093125

In [75]:
```
writedlm("Correlation.G5.M.C.txt",cor13)
```

In [76]:
```
writedlm("Regression.G5.M.C.txt",reg13)
```

In [77]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[77]: 1.4667704854539643

In [78]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = %
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.711
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.952
```

Out[78]: 0.7112325918219534

In [79]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[79]: -1.466362535662179

In [80]:
```
IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = '
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.746
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.998
```

Out[80]: 0.7457042497465852

In [81]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[81]: -0.6402274313259139

In [82]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = '
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.749
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   1.003
```

Out[82]: 0.7489150723956445

In [83]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[83]: -0.026799580674194197

In [84]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = '
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.737
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.998
```

Out[84]: 0.7368772699521462

In [85]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[85]: 0.4934352041817562

```
In [86]:  IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          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", cor1
          @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 
          JCAll = cor17
```

```
          SSBRJC from Gibbs - G4.noGenotype.ID : correlation =   0.733
          SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   0.977
```

Out[86]: 0.7328161165545378

```
In [87]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[87]: 0.9996333717268189

```
In [88]:  numSSBayes
```

Out[88]: SSBR.NumSSBayes(54914,45914,9000,40000,39000,1000,150)