In [1]:
```julia
include("/home/nicole/Jupyter/SSBRJ/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/0.5a0/M/10
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/10

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

```
Correlation.G5.M.C*.txt
Correlation.G5.M.C.txt
Correlation.G5.M.J.txt
Correlation.G5.M.JC*.txt
Correlation.G5.M.N.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
MarNFCenter.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C*.txt
Regression.G5.M.C.txt
Regression.G5.M.J.txt
Regression.G5.M.JC*.txt
Regression.G5.M.N.txt
all.ID
alphaEstimatesC
alphaEstimatesJ
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
alphaEstimatesN
epsiEstimatesC
epsiEstimatesJ
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
epsiEstimatesN
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 (
```

```
 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)
J_Vecs = make_JVecs(numSSBayes,A_Mats)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(J_Vecs,Z_Mats,M_Mats,numSSBayes)      # wit
nothing
```

In [31]:
```
vRes   = 0.460
vG     = 0.460
nIter  = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG
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
3460.259081 seconds (23.04 G allocations: 723.737 GB, 7.38% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  4.60803
 -0.287413
```

```
In [33]: mu  = betaHat[1]
         mug = betaHat[2]
```

Out[33]: -0.2874132816364107

```
In [34]: (mu+mug)/2
```

Out[34]: 2.160309616066059

```
In [35]: alphaHat
```

Out[35]: 150-element Array{Float64,1}:
          0.0570059
         -0.0798508
         -0.00993225
          0.030548
         -0.0125479
          0.0146224
         -0.0756283
          0.239688
         -0.0170539
         -0.0226747
          0.0510622
         -0.00932946
          0.0375386
          ⋮
          0.0825392
         -0.032268
         -0.0293047
          0.0712103
         -0.0647334
          0.0187727
          0.0719713
         -0.040283
         -0.0289755
          0.0856404
          0.0317555
         -0.0225819

```
In [36]: writedlm("alphaEstimatesJC",alphaHat)
```

```
In [37]: epsiHat
```

```
Out[37]: 45929-element Array{Float64,1}:
         -0.438577
         -0.00281662
         -0.25584
          0.0562447
          0.072033
         -0.303686
         -0.269065
          0.0760219
          0.625009
         -0.111916
          0.189521
         -0.1964
         -0.298196
          ⋮
          0.389377
         -0.148043
         -0.137262
         -0.141968
          0.598403
          0.232608
         -0.316332
          0.155685
         -0.1073
         -0.325094
          0.209596
         -0.751736
```

```
In [38]: writedlm("epsiEstimatesJC",epsiHat)
```

```
In [39]: using DataFrames
```

```
In [40]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',head
         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 [41]: 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 =  0.899
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.959
```

```
Out[41]: 0.8994905691625814
```

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

Out[42]: 0.29139112348456686

In [43]:
```
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 =   0.890
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   0.975
```

Out[43]: 0.8897344772837952

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

Out[44]: 1.2547510407568032

In [45]:
```
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 =   0.862
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.938
```

Out[45]: 0.8621140781550802

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

Out[46]: 0.069077296421743

In [47]:
```
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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =   0.632
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   0.710
```

Out[47]: 0.632170475277435

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

Out[48]: -0.8333045137276006

In [49]:
```
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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.769
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.969
```

Out[49]: 0.7694537971629414

In [50]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[50]: -0.32698921643198

In [51]:
```
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", r
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.755
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.992
```

Out[51]: 0.7552961608667728

In [52]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[52]: 0.14792139156946935

In [53]:
```
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", r
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.757
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.997
```

Out[53]: 0.7569836359885453

```
In [54]:  GEBV = aHat1[posAi]
          G3GEBV=mean(GEBV)
```

Out[54]: 0.5422249704889311

```
In [55]:  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 ej
          @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
          JCAll = cor7
```

          SSBRJC from Gibbs - G4.ID : correlation =   0.757
          SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.978

Out[55]: 0.7565586631675131

```
In [56]:  GEBV = aHat1[posAi]
          G4GEBV=mean(GEBV)
```

Out[56]: 0.9273676310334424

```
In [57]:  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 ej
          @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
          JCAll = cor8
```

          SSBRJC from Gibbs - G5.ID : correlation =   0.874
          SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.948

Out[57]: 0.8740071710781963

```
In [58]:  reg8 = linreg(aHat1[posAi], a[posAi])
```

Out[58]: 2-element Array{Float64,1}:
           4.68808
           0.947922

```
In [59]:  VarGEBV=var(aHat1[posAi])
```

Out[59]: 0.2607610930387981

```
In [60]:  VarTBV=var(a[posAi])
```

Out[60]: 0.30673105008526064

```
In [61]:  Cov=cov(aHat1[posAi], a[posAi])
```

Out[61]: 0.24718110141255473

In [62]: `b=Cov/VarGEBV`

Out[62]: 0.94792171075835

In [63]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[63]: 1.2911264779751388

In [64]: `GEBVG5G1=G5GEBV-G1GEBV`

Out[64]: 1.6181156944071189

In [65]: `GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]`

Out[65]:
```
5-element Array{Float64,1}:
 -0.326989
  0.147921
  0.542225
  0.927368
  1.29113
```

In [66]:
```
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 =  0.887
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.969
```

Out[66]: 0.8869612569971398

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

Out[67]: 0.2433992298696931

In [68]:
```
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 =  0.876
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.960
```

Out[68]: 0.8764394619855546

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

Out[69]: 0.6927065039169393

```
In [70]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         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 =  0.864
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.923
```

Out[70]: 0.8641937623592659

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

Out[71]: 0.9619383699369749

```
In [72]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         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 =  0.835
         SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.828
```

Out[72]: 0.8346849699246215

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

Out[73]: 1.2966114360243597

```
In [74]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         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 =  0.849
         SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.845
```

Out[74]: 0.8489067846415042

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

Out[75]: 1.624082175302635

In [76]:
```
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 =  0.874
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.948
```

Out[76]: 0.8740071710781963

In [77]:
```
writedlm("Correlation.G5.M.JC.txt",cor13)
```

In [78]:
```
writedlm("Regression.G5.M.JC.txt",reg13)
```

In [79]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[79]: 5.911964

In [80]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[80]: 1.2911264779751388

In [81]:
```
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 =  0.609
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.703
```

Out[81]: 0.60948257105179

In [82]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[82]: -0.860912302024967

In [83]:
```
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 =  0.752
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.973
```

Out[83]: 0.7516286687094066

In [84]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[84]: -0.35313526054349065

In [85]:
```
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 =  0.740
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.994
```

Out[85]: 0.740146201690496

In [86]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[86]: 0.12704916135491795

In [87]:
```
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 =  0.742
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.995
```

Out[87]: 0.7422054628359827

In [88]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[88]: 0.5228817277828944

```
In [89]: 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 =  0.742
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.973
```

Out[89]: 0.7418579545965994

```
In [90]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[90]: 0.9095031555393605

```
In [91]: numSSBayes
```

Out[91]: SSBR.NumSSBayes(54929,45929,9000,40000,39000,1000,150)

```
In [92]: J1 = sortrows(J_Vecs.J1)
```

Out[92]: 45929x1 Array{Float64,2}:
         -0.999204
         -0.99309
         -0.989635
         -0.989354
         -0.986951
         -0.985619
         -0.985586
         -0.985568
         -0.98548
         -0.985301
         -0.984423
         -0.98427
         -0.98317
           ⋮
          7.41993e-17
          7.42088e-17
          7.65502e-17
          7.85836e-17
          8.88438e-17
          8.88468e-17
          8.90394e-17
          8.90569e-17
          1.10945e-16
          1.11217e-16
          1.21753e-16
          1.2328e-16

```
In [93]: J1[J1 .< 0.0,:]
```

Out[93]: 43854x1 Array{Float64,2}:
          -0.999204
          -0.99309
          -0.989635
          -0.989354
          -0.986951
          -0.985619
          -0.985586
          -0.985568
          -0.98548
          -0.985301
          -0.984423
          -0.98427
          -0.98317
           ⋮
          -1.12625e-35
          -1.10536e-35
          -7.23354e-36
          -7.22508e-36
          -7.2166e-36
          -7.19638e-36
          -7.19638e-36
          -4.91411e-36
          -7.61803e-65
          -2.53068e-66
          -1.43549e-66
          -8.89359e-67

```
In [94]: J1[J1 .> 0.0,:]
```

Out[94]: 1344x1 Array{Float64,2}:
          1.59792e-51
          1.60429e-51
          1.60574e-51
          1.60617e-51
          2.45438e-51
          3.20065e-51
          3.20071e-51
          3.21147e-51
          4.00532e-51
          6.46485e-51
          8.01063e-51
          1.09353e-50
          1.13972e-50
          ⋮
          7.41993e-17
          7.42088e-17
          7.65502e-17
          7.85836e-17
          8.88438e-17
          8.88468e-17
          8.90394e-17
          8.90569e-17
          1.10945e-16
          1.11217e-16
          1.21753e-16
          1.2328e-16