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/0.5a0/M/8
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/8

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

```
Correlation.G5.M.C*.txt
Correlation.G5.M.J.txt
Correlation.G5.M.JC*.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
MarNFCenter.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C*.txt
Regression.G5.M.J.txt
Regression.G5.M.JC*.txt
Regression.G5.M.JC.txt
all.ID
alphaEstimatesJ
alphaEstimatesJC
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
epsiEstimatesJ
epsiEstimatesJC
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
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);                              # 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   = 0.741
vG     = 0.741
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
4693.282347 seconds (23.03 G allocations: 723.626 GB, 6.94% gc time)
```

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

Out[32]:
```
1-element Array{Float64,1}:
 2.56714
```

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

```
Out[33]: 150-element Array{Float64,1}:
          0.0201894
         -0.0443607
          0.0141232
          0.0265231
          0.276411
         -0.0352944
          0.0848698
          0.0246673
          0.000255638
          0.0145665
         -0.170047
          0.00553952
          0.0252551
          ⋮
         -0.0484504
          0.103906
          0.0542618
          0.0950992
          0.0123727
          0.0414602
          0.0692019
          0.0513145
          0.072382
          0.0124649
          0.0750803
         -0.0258059
```

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

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

```
Out[35]:  45922-element Array{Float64,1}:
            0.248574
           -0.308152
            0.401564
           -0.179886
           -0.460893
            0.207603
           -0.525579
            0.458023
            0.106477
           -0.181331
           -0.867118
            0.169129
           -0.00797246
            ⋮
           -0.0327242
           -0.144987
           -0.0808374
           -0.898057
           -0.286347
           -0.307754
           -0.543485
           -0.0463682
            0.347495
            0.18729
            0.385062
            0.816547
```

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

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

```
In [38]:  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 [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 =  0.910
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.981
```

```
Out[39]:  0.9101043471668915
```

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

Out[40]: 1.625654194153989

```
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 =   0.883
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   0.999
```

Out[41]: 0.8827359744764124

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

Out[42]: 2.8426711902038626

```
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 =   0.880
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.966
```

Out[43]: 0.8800144160119517

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

Out[44]: 1.3448041181424797

```
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", r
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G0.ID : correlation =   0.712
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   0.876
```

Out[45]: 0.7119263436881755

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

Out[46]: 0.1318585680926314

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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =   0.771
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.991
```

Out[47]: 0.7711017045047084

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

Out[48]: 0.8495772031175628

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", r
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =   0.777
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.031
```

Out[49]: 0.7766005853171749

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

Out[50]: 1.4395968875202665

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", r
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =   0.753
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.004
```

Out[51]: 0.7531080115543465

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

```
Out[52]: 1.984705927710062
```

```
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", re
         JCAll = cor7
```

```
         SSBRJC from Gibbs - G4.ID : correlation =  0.755
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.992
```

```
Out[53]: 0.7548153604126042
```

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

```
Out[54]: 2.461471981844552
```

```
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", re
         JCAll = cor8
```

```
         SSBRJC from Gibbs - G5.ID : correlation =  0.867
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.974
```

```
Out[55]: 0.8665297894164545
```

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

```
Out[56]: 2.88671459663886
```

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

```
Out[57]: 2.0371373935212973
```

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

```
Out[58]: 5-element Array{Float64,1}:
          0.849577
          1.4396
          1.98471
          2.46147
          2.88671
```

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

Out[59]:
```
2-element Array{Float64,1}:
  2.67237
  0.97359
```

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

Out[60]: `0.39191314505075486`

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

Out[61]: `0.49473813778245723`

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

Out[62]: `0.38156287070486666`

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

Out[63]: `0.9735903873687427`

In [64]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.859
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.023
```

Out[64]: `0.8585541672667919`

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

Out[65]: `1.6410243176838497`

In [66]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 )
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.893
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.000
```

Out[66]: 0.8925403270809088

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

Out[67]: 2.077561411007213

In [68]:
```
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 =  0.849
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.906
```

Out[68]: 0.8493168280939993

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

Out[69]: 2.5409558927522986

In [70]:
```
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 =  0.836
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.859
```

Out[70]: 0.8357377266811681

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

Out[71]: 2.9232922121333305

```
In [72]:  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 =   0.832
          SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.911
```

Out[72]: 0.8324267638812786

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

Out[73]: 3.2687858600427364

```
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 =   0.867
          SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   0.974
```

Out[74]: 0.8665297894164545

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

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

```
In [77]:  TBVG5Gall = a[posAi]
          TBVG5G=mean(TBVG5Gall)
```

Out[77]: 5.482843125

```
In [78]:  GEBVG5Gall = aHat1[posAi]
          GEBVG5G=mean(GEBVG5Gall)
```

Out[78]: 2.88671459663886

```
In [79]: 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 = 9
         JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.693
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.887
```

Out[79]: 0.6927361212437818

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

Out[80]: 0.09316201041080531

```
In [81]: 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 = 9
         JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.753
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.995
```

Out[81]: 0.7533896734694496

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

Out[82]: 0.81809042855629

```
In [83]: 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 = 9
         JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.762
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.036
```

Out[83]: 0.7624314506079308

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

Out[84]: 1.4113569130271373

In [85]:
```
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 =  0.739
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.003
```

Out[85]: 0.7387520121154563

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

Out[86]: 1.9606396127248502

In [87]:
```
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", cor17
@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 =  0.986
```

Out[87]: 0.7418082131390338

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

Out[88]: 2.4407716259933165

In [89]:
```
numSSBayes
```

Out[89]: SSBR.NumSSBayes(54922,45922,9000,40000,39000,1000,150)