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/1
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/1

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

```
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
all.ID
genotype.ID
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 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("MarNF.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]:  vRes    = 1.408
          vG      = 1.408
          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
          4774.177838 seconds (23.05 G allocations: 724.012 GB, 6.80% gc time)
```

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

```
Out[32]:  1-element Array{Float64,1}:
           0.581058
```

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

```
Out[33]: 150-element Array{Float64,1}:
          0.0450976
          0.00649591
         -0.0391901
          0.186162
          0.0035803
         -0.139886
          0.210863
          0.012557
         -0.0440867
         -0.0148991
          0.097907
         -0.0687499
         -0.0133963
          ⋮
          0.0600793
         -0.0835222
         -0.291572
         -0.126077
          0.00553735
          0.11423
         -0.00317697
         -0.0197596
          0.347267
          0.114608
         -0.241843
          0.162234
```

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

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

```
Out[35]:  45950-element Array{Float64,1}:
           0.756602
          -0.127293
           0.107458
          -0.223964
           0.249437
          -0.371336
           0.294034
          -0.280149
           0.792976
          -0.899288
           0.0153121
          -0.238349
          -0.85103
           ⋮
           0.0572903
           0.173197
           0.306563
           0.260004
           1.28723
           0.431307
           0.0730604
          -0.352056
           0.34435
          -0.19057
          -0.0188053
           0.103989
```

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

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

```
In [38]:  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 [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 epsilon
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n", reg1)
JCAll = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.903
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.986
```

Out[39]: 0.9028931549366657

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

Out[40]: 2.0565342793905446

In [41]:
```
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 =  0.827
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.916
```

Out[41]: 0.827063887689994

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

Out[42]: 3.505477522542709

In [43]:
```
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 =  0.879
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.983
```

Out[43]: 0.878725845827762

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

Out[44]: 1.7221627617400455

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 epsilon
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.793
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.084
```

Out[45]: 0.7932370807182478

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

Out[46]: 0.1686030736005844

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 epsilon
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.773
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.006
```

Out[47]: 0.7729652830577491

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

Out[48]: 1.1613344552734706

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 epsilon
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.744
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.964
```

Out[49]: 0.7441275906388729

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

Out[50]: 1.8833962744688826

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 epsilon
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.735
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.963
```

Out[51]: 0.7348769760336258

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

Out[52]: 2.517003933909608

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 epsilon
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.740
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.954
```

Out[53]: 0.7396245969964932

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

Out[54]: 3.057628364506465

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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.807
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.885
```

Out[55]: 0.8066971160320201

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

Out[56]: 3.5512395745842578

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

Out[57]: 2.389905119310787

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

Out[58]: 5-element Array{Float64,1}:
 1.16133
 1.8834
 2.517
 3.05763
 3.55124

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

Out[59]: 2-element Array{Float64,1}:
 1.02159
 0.884731

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

Out[60]: 0.5994277364759081

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

Out[61]: 0.7210049007563287

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

Out[62]: 0.5303322404510973

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

Out[63]: 0.8847308994558215

In [64]:
```
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 =  0.835
SSBRJC from Gibbs – G0.Genotype.ID : regression of TBV on GEBV =  0.902
```

Out[64]: 0.8353044919317983

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

Out[65]: 2.263616336296544

In [66]:
```
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 =  0.873
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.908
```

Out[66]: 0.8734442227197008

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

Out[67]: 2.67172988374707

In [68]:
```
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 =  0.843
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.899
```

Out[68]: 0.8430221657819023

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

Out[69]: 3.179078399346494

In [70]:
```
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 =  0.823
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.988
```

Out[70]: 0.822981424538246

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

Out[71]: 3.5903775335447183

In [72]:
```
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 =  0.703
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.702
```

Out[72]: 0.703329362682948

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

Out[73]: 3.9921033781167785

```
In [74]: 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 =  0.807
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.885
```

Out[74]: 0.8066971160320201

```
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]: 4.163481125000001

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

Out[78]: 3.5512395745842578

```
In [79]: 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 =  0.784
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.135
```

Out[79]: 0.7839326975393701

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

Out[80]: 0.11488478481350853

In [81]:
```
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 =   0.759
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   1.013
```

Out[81]: 0.7588591679921649

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

Out[82]: 1.122606367363891

In [83]:
```
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 =   0.730
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   0.964
```

Out[83]: 0.7296481470261627

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

Out[84]: 1.850173655882277

```
In [85]: 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 =  0.722
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.956
```

Out[85]: 0.7219146121257298

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

Out[86]: 2.489481533918964

```
In [87]: 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 =  0.730
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.950
```

Out[87]: 0.7299045872046862

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

Out[88]: 3.0336674667215853

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

Out[89]: SSBR.NumSSBayes(54950,45950,9000,40000,39000,1000,150)