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/0.5a0/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
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
all.ID
alphaEstimatesC
alphaEstimatesJ
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
epsiEstimatesC
epsiEstimatesJ
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 (
```

```
         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",calculateInbreedir
         nothing
         df      = read_genotypes("MarNF.txt",numSSBayes)
         M_Mats = make_MMats(df,A_Mats,ped);                                # witl
         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   = 0.460
         vG     = 0.460
         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
        2612.895633 seconds (23.04 G allocations: 723.723 GB, 7.06% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
          3.67631
```

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

```
Out[33]: 150-element Array{Float64,1}:
          0.0570648
         -0.0764777
         -0.00656222
          0.0289168
         -0.00928152
          0.0177129
         -0.0789507
          0.240513
         -0.017681
         -0.0217598
          0.0501537
         -0.00680608
          0.0389882
          ⋮
          0.0848923
         -0.0287735
         -0.0279479
          0.0744424
         -0.061992
          0.0222619
          0.0694173
         -0.0374101
         -0.0258157
          0.0896902
          0.0336096
         -0.020744
```

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

In [35]: `epsiHat`

Out[35]: 45929-element Array{Float64,1}:
```
 -0.438308
 -0.0104917
 -0.254357
  0.0551436
  0.0759085
 -0.29872
 -0.268355
  0.0755305
  0.623331
 -0.115393
  0.188938
 -0.193369
 -0.295534
  ⋮
  0.388973
 -0.150603
 -0.140508
 -0.14318
  0.595437
  0.23259
 -0.313904
  0.160202
 -0.109229
 -0.323435
  0.205753
 -0.751074
```

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

In [37]: **using** DataFrames

In [38]:
```julia
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]:
```julia
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 =  0.900
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.958
```

Out[39]: 0.899515192560375

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

Out[40]: 1.2231363266829676

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

Out[41]: 0.8899471317040069

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

Out[42]: 2.1864654969641464

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

Out[43]: 0.8621263335250294

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

Out[44]: 1.0008295950796189

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 =  0.632
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.711
```

Out[45]: 0.6322538886009661

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

Out[46]: 0.09871391843993374

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

Out[47]: 0.7694304849778759

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

Out[48]: 0.6044822893779189

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

Out[49]: 0.7552308944095173

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

Out[50]: 1.0796695481310026

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 =   0.757
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.996
```

Out[51]: 0.7568773800465484

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

Out[52]: 1.4739364218309643

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 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[53]: 0.7566724312416426

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

Out[54]: 1.8591591754742598

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 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 =  0.947
```

Out[55]: 0.8742752636226016

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

Out[56]: 2.2228566068437274

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

Out[57]: 1.6183743174658085

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

Out[58]: 5-element Array{Float64,1}:
```
 0.604482
 1.07967
 1.47394
 1.85916
 2.22286
```

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

```
Out[59]:  2-element Array{Float64,1}:
           3.80674
           0.947081
```

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

```
Out[60]:  0.26138471101649613
```

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

```
Out[61]:  0.30673105008526064
```

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

```
Out[62]:  0.24755240623987945
```

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

```
Out[63]:  0.9470806661842448
```

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

```
Out[64]:  0.8870484880150665
```

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

```
Out[65]:  1.1739766572879753
```

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

Out[66]: 0.876276523962038

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

Out[67]: 1.6247219325338649

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 =  0.864
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.923
```

Out[68]: 0.863996085897805

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

Out[69]: 1.8935002523265811

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 =  0.835
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.828
```

Out[70]: 0.8351746715802785

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

Out[71]: 2.228534926425855

```
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 =  0.849
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.845
```

Out[72]: 0.8494651802765703

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

Out[73]: 2.5559493210632103

```
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 =  0.874
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.947
```

Out[74]: 0.8742752636226016

```
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]: 5.911964

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

Out[78]: 2.2228566068437274

```
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 =   0.610
         SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.703
```

Out[79]: 0.6095722081298681

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

Out[80]: 0.07114307898229165

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

Out[81]: 0.7516072437014867

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

Out[82]: 0.5783222985277665

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

Out[83]: 0.7400793710823901

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

Out[84]: 1.0588020941772693

```
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 = 9
         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[85]: 0.7420820856834377

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

Out[86]: 1.454587742225967

```
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 = 9
         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[87]: 0.7419743934174854

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

Out[88]: 1.8412927614847994

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

Out[89]: SSBR.NumSSBayes(54929,45929,9000,40000,39000,1000,150)