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/1
```

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

In [4]: `;ls`

```
Correlation.G5.M.C*.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.JC.txt
Regression.G5.M.N.txt
all.ID
alphaEstimatesJC
alphaEstimatesLeggaraC
alphaEstimatesN
epsiEstimatesJC
epsiEstimatesLeggaraC
epsiEstimatesN
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

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

In [6]:
```
;awk '{print $1}' MarNFCenter.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("MarNFCenter.txt",numSSBayes)   # genotype file - centered already
M_Mats = make_MMats(df,A_Mats,ped);                      # M file centered already
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)        # with J
nothing
```

In [31]:
```
vRes   = 1.408
vG     = 1.408
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,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
4100.917328 seconds (23.05 G allocations: 724.027 GB, 7.05% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  0.577028
 -3.51408
```

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

```
Out[33]:  150-element Array{Float64,1}:
           0.0385779
          -0.0145098
          -0.0643831
           0.128032
           0.0100092
          -0.179515
           0.116057
          -0.0487305
          -0.036369
          -0.0429435
           0.0673132
          -0.0707248
          -0.0254926
           ⋮
           0.0276339
          -0.0786243
          -0.313737
          -0.137772
           0.0108171
           0.0613541
          -0.00310168
          -0.0215884
           0.300752
           0.10505
          -0.250671
           0.146554
```

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

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

Out[35]:
```
45950-element Array{Float64,1}:
    0.75619
   -0.12198
    0.0910298
   -0.20006
    0.232046
   -0.364023
    0.300852
   -0.275249
    0.800214
   -0.924237
    0.023814
   -0.213377
   -0.850896
    ⋮
    0.0516192
    0.192106
    0.303086
    0.252367
    1.31031
    0.423219
    0.0681592
   -0.371792
    0.335012
   -0.196193
   -0.0083293
    0.11233
```

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

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

In [38]:
```julia
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 =  0.985
```

Out[39]: 0.9031418822941625

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

Out[40]: 2.0613987345103486

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 =  0.830
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.918
```

Out[41]: 0.8300181117545601

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

Out[42]: 3.514083976819699

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]: 0.8788007571801326

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

Out[44]: 1.726163678592806

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]: 0.7932207413723649

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

Out[46]: 0.17121839239345413

```
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 =  1.007
```

Out[47]: 0.772846183829873

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

Out[48]: 1.1655646654628555

```
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 =  0.965
```

Out[49]: 0.7444562506160264

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

Out[50]: 1.886777772340337

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 =  0.964
```

Out[51]: 0.7354053618674494

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

Out[52]: 2.5212130210097

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]: 0.7401990643449503

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

Out[54]: 3.063465998281189

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 =  0.810
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.887
```

Out[55]: 0.8100336071533065

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

Out[56]: 3.560152557574556

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

Out[57]: 2.3945878921117005

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

Out[58]: 5-element Array{Float64,1}:
```
 1.16556
 1.88678
 2.52121
 3.06347
 3.56015
```

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

Out[59]: 2-element Array{Float64,1}:
```
 1.00663
 0.886717
```

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

Out[60]: 0.6016916550618194

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

Out[61]: 0.7210049007563287

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

Out[62]: 0.5335303629922916

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

Out[63]: 0.8867172388114228

In [64]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # 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 =  0.834
SSBRJC from Gibbs – G0.Genotype.ID : regression of TBV on GEBV =  0.907
```

Out[64]: 0.834017622998012

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

Out[65]: 2.2704431566949657

In [66]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # 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 =  0.875
SSBRJC from Gibbs – G1.Genotype.ID : regression of TBV on GEBV =  0.916
```

Out[66]: 0.8754735336077781

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

```
Out[67]: 2.672806794549268
```

```
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 =  0.847
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.910
```

```
Out[68]: 0.847417379076322
```

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

```
Out[69]: 3.1847348401543116
```

```
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 =  0.822
         SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.986
```

```
Out[70]: 0.8215152476899679
```

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

```
Out[71]: 3.599295716624827
```

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 =  0.713
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.712
```

Out[72]: 0.7131470919302152

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

Out[73]: 4.0003961458808455

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 =  0.810
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.887
```

Out[74]: 0.8100336071533065

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

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

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

Out[77]: 4.163481125000001

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

```
Out[78]: 3.560152557574556
```

```
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]: 0.7839827932467994
```

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

```
Out[80]: 0.11739211638572304
```

```
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 =  1.014
```

```
Out[81]: 0.7586794204174726
```

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

```
Out[82]: 1.126917431383717
```

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 =  0.965
```

Out[83]: 0.7299137721311596

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

Out[84]: 1.8534968218835686

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 =  0.957
```

Out[85]: 0.7224798177107634

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

Out[86]: 2.493569874968287

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]: 0.7303373101278331

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

Out[88]: 3.0394421483427365

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

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

```
In [90]: J1 = sortrows(J_Vecs.J1)
```

Out[90]: 45950x1 Array{Float64,2}:
$$-0.998128$$
$$-0.989112$$
$$-0.986218$$
$$-0.986069$$
$$-0.98556$$
$$-0.985539$$
$$-0.985398$$
$$-0.985287$$
$$-0.984751$$
$$-0.983664$$
$$-0.983657$$
$$-0.983607$$
$$-0.983579$$
$$\vdots$$
$$7.22383e{-}17$$
$$7.40727e{-}17$$
$$7.42191e{-}17$$
$$7.46619e{-}17$$
$$7.52197e{-}17$$
$$8.88923e{-}17$$
$$8.92435e{-}17$$
$$8.94813e{-}17$$
$$1.18284e{-}16$$
$$1.22329e{-}16$$
$$1.44477e{-}16$$
$$1.47425e{-}16$$

In [91]: J1[J1 .< 0.0,:]

Out[91]: 43902x1 Array{Float64,2}:
         -0.998128
         -0.989112
         -0.986218
         -0.986069
         -0.98556
         -0.985539
         -0.985398
         -0.985287
         -0.984751
         -0.983664
         -0.983657
         -0.983607
         -0.983579
             ⋮
         -7.21238e-36
         -7.2121e-36
         -7.20816e-36
         -7.20371e-36
         -7.18073e-36
         -2.1823e-51
         -3.19403e-65
         -2.57004e-65
         -5.46188e-67
         -2.73094e-67
         -1.79614e-67
         -1.78856e-67

In [92]: `J1[J1 .> 0.0,:]`

Out[92]: 1371x1 Array{Float64,2}:
6.06391e-83
8.05497e-52
8.08909e-52
1.60053e-51
1.60147e-51
1.60241e-51
1.60567e-51
1.60617e-51
1.60859e-51
1.61099e-51
1.61782e-51
2.21192e-51
2.45981e-51
⋮
7.22383e-17
7.40727e-17
7.42191e-17
7.46619e-17
7.52197e-17
8.88923e-17
8.92435e-17
8.94813e-17
1.18284e-16
1.22329e-16
1.44477e-16
1.47425e-16