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]:
```
; cd Data/0.5a0/M/3
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/3

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

```
Correlation.G5.M.C*.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
all.ID
alphaEstimatesLeggaraC
epsiEstimatesLeggaraC
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 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,center=true);                    # with
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
nothing
```

In [31]:
```
vRes   = 0.328
vG     = 0.328
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
4633.360234 seconds (23.02 G allocations: 723.213 GB, 7.08% gc time)
```

In [32]: `betaHat`

Out[32]:
```
2-element Array{Float64,1}:
  0.236099
 -0.931998
```

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

Out[33]: -0.9319984557280269

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

Out[34]: -0.34794992252058

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

Out[35]: 150-element Array{Float64,1}:
          -0.0151666
          -0.11197
           0.0732471
          -0.084686
           0.00161656
          -0.0766918
           0.0949154
          -0.0858252
           0.100499
          -0.0148254
           0.00762634
           0.0988418
           0.0480567
           ⋮
           0.0702816
          -0.0692549
          -0.0416334
           0.254128
           0.0413478
           0.117531
           0.00870113
           0.0152946
          -0.00879811
          -0.0612699
          -0.000310354
          -0.0345762

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

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

Out[37]:
```
45891-element Array{Float64,1}:
 -0.563398
 -0.0926436
  0.0605697
  0.313083
 -0.459815
 -0.236077
  0.130277
 -0.103264
  0.487928
 -0.0770951
 -0.101874
 -0.348547
 -0.22413
  ⋮
 -0.118442
  0.143254
 -0.116725
  0.413919
 -0.486477
  0.349642
 -0.386621
  0.0826786
  0.139986
  0.105128
 -0.151867
 -0.709968
```

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

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

In [40]:
```
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 [41]:
```
IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=fals
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 =  0.892
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.986
```

Out[41]:
```
0.8921198488590892
```

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

Out[42]: 0.68169979294243

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 ) # u
@printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3:
JCAll = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.838
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.041
```

Out[43]: 0.8384747317788175

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

Out[44]: 1.5310738188720137

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 =  0.855
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.930
```

Out[45]: 0.8549286007028678

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

Out[46]: 0.48569040234329525

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", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.583
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.600
```

Out[47]: 0.5829877109738009

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

Out[48]: -0.3310274047782723

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 =   0.756
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.948
```

Out[49]: 0.7559163712090684

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

Out[50]: 0.12564144566757654

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 =   0.760
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.021
```

Out[51]: 0.7600569988083551

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

Out[52]: 0.560509817670648

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 =   0.772
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.068
```

Out[53]: 0.7720894936869034

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

Out[54]: 0.915601149251713

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

```
         SSBRJC from Gibbs - G4.ID : correlation =   0.764
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.085
```

Out[55]: 0.7641551421766215

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

Out[56]: 1.257333922128415

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

```
         SSBRJC from Gibbs - G5.ID : correlation =   0.817
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.991
```

Out[57]: 0.8169539278704727

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

```
Out[58]: 2-element Array{Float64,1}:
          0.382671
          0.990782
```

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

Out[59]: 0.21558191166159313

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

Out[60]: 0.31708352413037566

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

Out[61]: 0.21359474452286883

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

Out[62]: 0.9907823104294408

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

Out[63]: 1.5621398277145

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

Out[64]: 1.4364983820469235

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

Out[65]: 5-element Array{Float64,1}:
```
 0.125641
 0.56051
 0.915601
 1.25733
 1.56214
```

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 =  0.840
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.006
```

Out[66]: 0.8402714349548558

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

Out[67]: 0.6571039914229665

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 =  0.812
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.887
```

Out[68]: 0.8122291688030318

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

Out[69]: 1.0629383534462742

In [70]:
```
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =   0.817
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   0.943
```

Out[70]: 0.8166679552296533

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

Out[71]: 1.2838925137755337

In [72]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =   0.784
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   0.869
```

Out[72]: 0.7839882324026242

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

Out[73]: 1.5726630931737242

In [74]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =   0.765
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.892
```

Out[74]: 0.7649332697852264

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

Out[75]: 1.8361307888421265

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 =  0.817
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.991
```

Out[76]: 0.8169539278704727

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]: 1.9304116249999999

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

Out[80]: 1.5621398277145

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 =  0.562
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.593
```

Out[81]: 0.5620259416517054

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

Out[82]: -0.35636410724497075

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", cor1
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.736
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.953
```

Out[83]: 0.7363499342193582

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

Out[84]: 0.10160819162196888

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 =  0.744
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.020
```

Out[85]: 0.7442921770135073

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

Out[86]: 0.5419615434115485

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 =  0.758
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.061
```

Out[87]: 0.7579125437734807

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

Out[88]: 0.8987534070998665

In [89]:
```
IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',h
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 =  0.751
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.071
```

Out[89]: 0.7506153606082214

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

Out[90]: 1.2424929768280633

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

Out[91]: SSBR.NumSSBayes(54891,45891,9000,40000,39000,1000,150)

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

Out[92]: 45891x1 Array{Float64,2}:
 −0.988871
 −0.988537
 −0.986445
 −0.986275
 −0.98594
 −0.985938
 −0.985646
 −0.985631
 −0.985575
 −0.985565
 −0.985309
 −0.983826
 −0.983599
     ⋮
  6.18017e-17
  6.3726e-17
  6.63379e-17
  6.63385e-17
  6.68956e-17
  7.40627e-17
  7.55288e-17
  7.57539e-17
  7.89541e-17
  8.8821e-17
  1.11064e-16
  1.11418e-16

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

Out[93]: 43894x1 Array{Float64,2}:
         −0.988871
         −0.988537
         −0.986445
         −0.986275
         −0.98594
         −0.985938
         −0.985646
         −0.985631
         −0.985575
         −0.985565
         −0.985309
         −0.983826
         −0.983599
            ⋮
         −1.41032e−35
         −1.12728e−35
         −1.08265e−35
         −7.2166e−36
         −7.2166e−36
         −7.2166e−36
         −7.21238e−36
         −7.21238e−36
         −7.20816e−36
         −2.1823e−51
         −5.33216e−67
         −2.66608e−67

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

```
Out[94]: 1293x1 Array{Float64,2}:
         2.95994e-83
         5.91989e-83
         1.60147e-51
         1.60241e-51
         1.60717e-51
         2.40139e-51
         3.202e-51
         3.21433e-51
         4.80278e-51
         1.59813e-50
         6.84829e-49
         1.37333e-48
         4.91411e-36
         ⋮
         6.18017e-17
         6.3726e-17
         6.63379e-17
         6.63385e-17
         6.68956e-17
         7.40627e-17
         7.55288e-17
         7.57539e-17
         7.89541e-17
         8.8821e-17
         1.11064e-16
         1.11418e-16
```