In [1]:
```
include("/home/nicole/Jupyter/SSBRJ/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/8
```

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

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
MarNFCenter.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}' 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 (
```

```
 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("MarNFCenter.txt",numSSBayes)  # genotype file - cen
M_Mats = make_MMats(df,A_Mats,ped);                    # M file centered alre
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   = 0.741
vG     = 0.741
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
2400.620501 seconds (23.03 G allocations: 723.640 GB, 7.72% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  2.56546
 -2.84517
```

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

```
Out[33]: 150-element Array{Float64,1}:
          0.0206446
         -0.0576277
          0.00956102
          0.026468
          0.267723
         -0.0698461
          0.0567077
          0.0197038
         -0.00822948
          0.00806435
         -0.174697
          0.00224031
          0.0251699
          ⋮
         -0.0578916
          0.0921704
          0.047118
          0.0919291
         -0.00420788
          0.0347679
          0.0564126
          0.0423154
          0.0553967
          0.00403897
          0.0672013
         -0.0385823
```

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

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

```
Out[35]: 45922-element Array{Float64,1}:
            0.262724
           -0.3267
            0.396397
           -0.175396
           -0.466188
            0.210406
           -0.528345
            0.449072
            0.112549
           -0.180749
           -0.868534
            0.180405
           -0.00739324
            ⋮
           -0.0370565
           -0.141164
           -0.0933464
           -0.910881
           -0.28559
           -0.304869
           -0.538472
           -0.0510051
            0.339869
            0.185026
            0.390784
            0.822403
```

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

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

```
In [38]: 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]: 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 =  0.980
```

```
Out[39]: 0.9100666221329701
```

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

Out[40]: 1.6274671990268925

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

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.882
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.000
```

Out[41]: 0.8824703362197117

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

Out[42]: 2.8451692881936417

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]: 0.87998196685487

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

Out[44]: 1.3464590246037964

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 =  0.712
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.875
```

Out[45]: 0.7118666694047132

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

Out[46]: 0.13282630805043072

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

Out[47]: 0.7710547409581873

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

Out[48]: 0.85175270684589

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 =  0.776
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.031
```

Out[49]: 0.7764691679123311

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

Out[50]: 1.441666520117917

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 =  0.753
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.003
```

Out[51]: 0.7530756185474616

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

Out[52]: 1.9861795435333038

```
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]: 0.7549052445447134

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

Out[54]: 2.463111340360666

```
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 =   0.866
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.974
```

Out[55]: 0.8662274519484835

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

Out[56]: 2.889266775253148

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

Out[57]: 2.037514068407258

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

```
Out[58]: 5-element Array{Float64,1}:
          0.851753
          1.44167
          1.98618
          2.46311
          2.88927
```

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

Out[59]: 2-element Array{Float64,1}:
  2.66779
  0.974316

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

Out[60]: 0.3910569797406603

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

Out[61]: 0.49473813778245723

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

Out[62]: 0.3810128815867415

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

Out[63]: 0.9743155123824161

In [64]:
```
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 = 0.858
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.026

Out[64]: 0.8581047994194432

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

Out[65]: 1.645306663795712

In [66]:
```
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 = 0.891
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.000

Out[66]: 0.8909917391380713

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

Out[67]: 2.079778983372257

```
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 =  0.851
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.907
```

Out[68]: 0.8506454570316262

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

Out[69]: 2.5412926785058945

```
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]: 0.8363599847881019

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

Out[71]: 2.924466787888294

```
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 =  0.831
         SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.909
```

Out[72]: 0.8311553771026318

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

Out[73]: 3.2711018450258114

```
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 =  0.866
         SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.974
```

Out[74]: 0.8662274519484835

```
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]: 5.482843125

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

Out[78]: 2.889266775253148

```
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 = %
         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]: 0.6927076506532129

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

Out[80]: 0.09404476046721838

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 = ¦
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]: 0.7533729730473585

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

Out[82]: 0.820264853601624

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 = ¦
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]: 0.7622662229770367

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

Out[84]: 1.4134709775951482

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 =  1.002
```

Out[85]: 0.7387081211829564

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

Out[86]: 1.9621208962421504

```
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]: 0.7419245390194513

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

Out[88]: 2.442393635112841

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

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

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

Out[90]: 45922x1 Array{Float64,2}:
         -0.986886
         -0.98681
         -0.986652
         -0.986167
         -0.985627
         -0.985584
         -0.985549
         -0.985547
         -0.98549
         -0.98527
         -0.985215
         -0.984637
         -0.984623
          ⋮
          7.0587e-17
          7.35847e-17
          7.43413e-17
          7.45955e-17
          8.59149e-17
          8.86198e-17
          8.88706e-17
          8.9519e-17
          9.67177e-17
          1.07311e-16
          1.22139e-16
          1.40744e-16

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

Out[91]: 43953x1 Array{Float64,2}:
          -0.986886
          -0.98681
          -0.986652
          -0.986167
          -0.985627
          -0.985584
          -0.985549
          -0.985547
          -0.98549
          -0.98527
          -0.985215
          -0.984637
          -0.984623
           ⋮
          -7.2166e-36
          -7.2166e-36
          -7.2092e-36
          -6.60657e-36
          -6.60657e-36
          -2.1823e-51
          -5.19078e-65
          -2.70994e-65
          -2.58495e-65
          -1.29248e-65
          -1.62865e-67
          -1.62865e-67

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

```
Out[92]: 1271x1 Array{Float64,2}:
         2.86987e-81
         7.33477e-52
         7.33477e-52
         1.46695e-51
         1.60076e-51
         1.60241e-51
         1.60241e-51
         2.1823e-51
         2.1823e-51
         2.3838e-51
         3.20013e-51
         3.20294e-51
         3.20397e-51
         ⋮
         7.0587e-17
         7.35847e-17
         7.43413e-17
         7.45955e-17
         8.59149e-17
         8.86198e-17
         8.88706e-17
         8.9519e-17
         9.67177e-17
         1.07311e-16
         1.22139e-16
         1.40744e-16
```