In [1]:
```
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/7
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/7

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 alr
         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)        # witl
         nothing
```

```
In [31]: vRes    = 0.738
         vG      = 0.738
         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
        3676.674278 seconds (23.01 G allocations: 723.132 GB, 7.43% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
            1.00305
           -2.76301
```

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

```
Out[33]: 150-element Array{Float64,1}:
          0.0157717
          0.0756223
         -0.117183
          0.00336481
          0.0438372
         -0.202481
         -0.0172156
          0.0144092
          0.0648119
          0.133406
         -0.0646764
         -0.159109
          0.105842
          ⋮
          0.0895759
          0.0295807
         -0.117306
          0.0198256
          0.0258394
         -0.0068585
          0.060779
          0.0321913
          0.0150344
         -0.0648659
          0.0648771
          0.116919
```

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

In [35]: `epsiHat`

Out[35]: 45885-element Array{Float64,1}:
         -0.582555
         -0.330915
          0.310186
          0.383455
         -0.467154
          0.601823
         -0.809419
         -0.274005
         -0.262379
         -0.281979
         -0.405287
         -0.0839759
         -0.82952
          ⋮
          0.250157
         -0.208485
          0.222444
          0.299228
          0.0657388
         -0.693018
         -0.275312
          0.0302035
         -0.533467
         -0.240071
          0.196072
          0.513018

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

In [37]:
```julia
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 = 0.901
         SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.002

Out[39]: 0.9008552308180721

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

Out[40]: 1.6003036459248103

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 =  0.810
SSBRJC from Gibbs – genotype.ID  : regression of TBV on GEBV =  0.997
```

Out[41]: 0.8096257061566148

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

Out[42]: 2.7630099615799772

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 =  0.873
SSBRJC from Gibbs – noGenotype.ID  : regression of TBV on GEBV =  0.967
```

Out[43]: 0.8731642875791128

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

Out[44]: 1.3319868038505407

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 =  0.714
SSBRJC from Gibbs – G0.ID : regression of TBV on GEBV =  0.862
```

Out[45]: 0.7144766401079451

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

Out[46]: 0.13281621054582388

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

```
         SSBRJC from Gibbs - G1.ID : correlation =   0.758
         SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.970
```

Out[47]: 0.757833994089983

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

Out[48]: 0.8618453594316047

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

```
         SSBRJC from Gibbs - G2.ID : correlation =   0.757
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.017
```

Out[49]: 0.7571274258115752

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

Out[50]: 1.4339006579011488

```
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 ej
         @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 =  1.013
```

Out[51]: 0.7568253241218127

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

Out[52]: 1.9591722429801164

```
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", r_
         JCAll = cor7
```

```
         SSBRJC from Gibbs - G4.ID : correlation =   0.726
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.006
```

Out[53]: 0.726127202884884

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

Out[54]: 2.412311838652496

```
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", r_
         JCAll = cor8
```

```
         SSBRJC from Gibbs - G5.ID : correlation =   0.786
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.951
```

Out[55]: 0.7862637679763668

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

Out[56]: 2.8017755660376715

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

Out[57]: 1.9399302066060669

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

Out[58]: 5-element Array{Float64,1}:
          0.861845
          1.4339
          1.95917
          2.41231
          2.80178

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

```
Out[59]: 2-element Array{Float64,1}:
          1.29101
          0.951216
```

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

```
Out[60]: 0.3689286940925807
```

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

```
Out[61]: 0.5399637294086136
```

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

```
Out[62]: 0.3509310329374613
```

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

```
Out[63]: 0.9512164235438868
```

```
In [64]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
         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 =  0.826
         SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.954
```

```
Out[64]: 0.8258592754162714
```

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

```
Out[65]: 1.7108054417392484
```

```
In [66]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
         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 =  0.758
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.901
```

```
Out[66]: 0.7579511046305256
```

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

Out[67]: 2.0943734531789984

In [68]:
```
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 =  0.816
SSBRJC from Gibbs – G2.Genotype.ID : regression of TBV on GEBV =  0.843
```

Out[68]: 0.8159346057523839

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

Out[69]: 2.5032802749768237

In [70]:
```
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 =  0.707
SSBRJC from Gibbs – G3.Genotype.ID : regression of TBV on GEBV =  0.751
```

Out[70]: 0.7070501641995497

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

Out[71]: 2.811474497118721

In [72]:
```
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 =  0.754
SSBRJC from Gibbs – G4.Genotype.ID : regression of TBV on GEBV =  0.866
```

Out[72]: 0.7538211574640202

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

Out[73]: 3.1444919625783405

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 =  0.786
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.951
```

Out[74]: 0.7862637679763668

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]: 3.9561027499999994

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

Out[78]: 2.8017755660376715

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 =  0.699
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.883
```

Out[79]: 0.6986377878029955

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

Out[80]: 0.09235494820753092

```
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 =  0.743
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.978
```

Out[81]: 0.7430843267927831

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

Out[82]: 0.8302420749765435

```
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 =  0.740
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.017
```

Out[83]: 0.7400849130773576

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

Out[84]: 1.4064806677197212

```
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 =  0.745
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.006
```

Out[85]: 0.7450521419326923

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

Out[86]: 1.9373183390278443

```
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", cor1'
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = '
         JCAll = cor17
```

```
         SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.712
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[87]: 0.7118942072944184

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

Out[88]: 2.3935379893210635

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

Out[89]: SSBR.NumSSBayes(54885,45885,9000,40000,39000,1000,150)

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

Out[90]: 45885x1 Array{Float64,2}:
         -0.990515
         -0.988862
         -0.986904
         -0.985937
         -0.985772
         -0.98563
         -0.985588
         -0.985585
         -0.985577
         -0.985568
         -0.985522
         -0.985411
         -0.985291
          ⋮
          6.28015e-17
          6.28015e-17
          6.66725e-17
          7.05189e-17
          7.40958e-17
          7.41458e-17
          7.43712e-17
          7.70326e-17
          8.89475e-17
          1.001e-16
          1.0697e-16
          1.11088e-16

```

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

Out[91]: 43889x1 Array{Float64,2}:
          -0.990515
          -0.988862
          -0.986904
          -0.985937
          -0.985772
          -0.98563
          -0.985588
          -0.985585
          -0.985577
          -0.985568
          -0.985522
          -0.985411
          -0.985291
            ⋮
          -1.25934e-35
          -1.15288e-35
          -7.22719e-36
          -7.21871e-36
          -7.2166e-36
          -7.2166e-36
          -2.59644e-65
          -7.1781e-66
          -2.56107e-66
          -3.40781e-67
          -1.77903e-67
          -8.89515e-68

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

Out[92]: 1241x1 Array{Float64,2}:
         1.97512e-83
         8.01203e-52
         1.53474e-51
         1.60241e-51
         1.60288e-51
         1.60476e-51
         2.5599e-51
         3.06949e-51
         3.20571e-51
         4.91957e-51
         9.69951e-51
         1.1534e-50
         2.30681e-50
         ⋮
         6.28015e-17
         6.28015e-17
         6.66725e-17
         7.05189e-17
         7.40958e-17
         7.41458e-17
         7.43712e-17
         7.70326e-17
         8.89475e-17
         1.001e-16
         1.0697e-16
         1.11088e-16