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/0.5g2k/G/10
```

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/10

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

```
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.JC.txt
Regression.G5.G.PBLUP.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}' GenNF.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("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                          # without centering
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]: vG     = 0.858
         vRes   = 0.858
         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
7134.276875 seconds (23.86 G allocations: 736.901 GB, 2.66% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          32.3899
           3.1136
```

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

```
Out[33]: 3.11359678150213
```

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

```
Out[34]: 17.751726605740842
```

In [35]: `alphaHat`

Out[35]: 2000-element Array{Float64,1}:
```
  0.0020614
  0.0146156
 -0.012226
  0.00468692
  0.00386603
  0.0081415
 -0.00908663
 -0.00547834
  0.00324635
 -0.0026534
  0.00169894
 -0.0111903
  0.00759872
  ⋮
 -0.0128452
  0.00849912
 -0.0205159
 -0.00756835
  0.00425587
  0.00299136
 -0.000883805
 -0.00841129
 -0.00194883
  0.00492376
 -0.00104616
  0.0201866
```

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

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 =  0.913
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.980
```

Out[39]: 0.9125184613002976

In [40]:
```
TBV = a[posAi]
mean(TBV)
```

Out[40]: 34.115545895833336

In [41]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[41]: 1.7172884582259764

In [42]:
```
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 =  0.917
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.076
```

Out[42]: 0.9167763212394734

In [43]:
```
TBV = a[posAi]
mean(TBV)
```

Out[43]: 35.388306

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

Out[44]: 2.995560314835624

In [45]:
```
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 =   0.881
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.965
```

Out[45]: 0.8814473264494739

In [46]:
```
TBV = a[posAi]
mean(TBV)
```

Out[46]: 33.82183202564103

In [47]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[47]: 1.422302645162211

In [48]:
```
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 =   0.750
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   0.938
```

Out[48]: 0.7498273367142502

```
In [49]: TBV = a[posAi]
         G0TBV=mean(TBV)
```

Out[49]: 32.63486125

```
In [50]: GEBV = aHat1[posAi]
         G0GEBV=mean(GEBV)
```

Out[50]: 0.1430309533648206

```
In [51]: 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 =  0.776
         SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV =  0.994
```

Out[51]: 0.7763455133487692

```
In [52]: TBV = a[posAi]
         G1TBV=mean(TBV)
```

Out[52]: 33.28914449999999

```
In [53]: GEBV = aHat1[posAi]
         G1GEBV=mean(GEBV)
```

Out[53]: 0.9046891171099463

In [54]:
```
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 =   0.764
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   0.995
```

Out[54]: 0.7641946393836294

In [55]:
```
TBV = a[posAi]
G2TBV=mean(TBV)
```

Out[55]: 33.90243849999999

In [56]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[56]: 1.5449693176207224

In [57]:
```
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 =   0.755
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.996
```

Out[57]: 0.7547871775537396

In [58]:
```
TBV = a[posAi]
G3TBV=mean(TBV)
```

Out[58]: 34.439698625

In [59]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[59]: 2.0708956616872527

In [60]:
```
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 =   0.756
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   0.986
```

Out[60]: 0.7562161489449977

In [61]:
```
TBV = a[posAi]
G4TBV=mean(TBV)
```

Out[61]: 34.985941625

In [62]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[62]: 2.5994314099679787

In [63]:
```
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 =   0.904
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.063
```

Out[63]: 0.9036375348993642

In [64]:
```
TBV = a[posAi]
G5TBV=mean(TBV)
```

Out[64]: 35.44119087500001

In [65]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[65]: 3.0407142896051362

In [66]:
```
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 =  0.925
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.064
```

Out[66]: 0.9248598716913826

In [67]:
```
TBV = a[posAi]
mean(TBV)
```

Out[67]: 33.928745000000006

In [68]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[68]: 1.734569450944706

In [69]:
```
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 =  0.938
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.084
```

Out[69]: 0.9376210821462114

In [70]:
```
TBV = a[posAi]
mean(TBV)
```

Out[70]: 34.484030000000004

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

Out[71]: 2.2230494958892204

In [72]:
```
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 =  0.929
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.062
```

Out[72]: 0.9287227272959642

In [73]:
```
TBV = a[posAi]
mean(TBV)
```

Out[73]: 34.975065

In [74]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[74]: 2.6392128778052166

In [75]:
```
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 =  0.932
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.094
```

Out[75]: 0.9317077187803272

In [76]:
```
TBV = a[posAi]
mean(TBV)
```

Out[76]: 35.536075000000004

In [77]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[77]: 3.1373306936800707

In [78]:
```
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 =  0.863
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.035
```

Out[78]: 0.8634995882339408

```
In [79]: TBV = a[posAi]
         mean(TBV)
```

```
Out[79]: 35.90222
```

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

```
Out[80]: 3.4374800650784136
```

```
In [81]: 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 =  0.904
         SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.063
```

```
Out[81]: 0.9036375348993642
```

```
In [82]: writedlm("Correlation.G5.G.J.txt",cor13)
```

```
In [83]: writedlm("Regression.G5.G.J.txt",reg13)
```

```
In [84]: TBVG5Gall = a[posAi]
         TBVG5G=mean(TBVG5Gall)
```

```
Out[84]: 35.44119087500001
```

```
In [85]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[85]: 3.0407142896051362
```

In [86]:
```
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 =  0.732
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.952
```

Out[86]: 0.7323383127500533

In [87]:
```
TBV = a[posAi]
mean(TBV)
```

Out[87]: 32.60168474358974

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

Out[88]: 0.10222227393969532

In [89]:
```
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 =  0.760
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.002
```

Out[89]: 0.7601317290761455

In [90]:
```
TBV = a[posAi]
mean(TBV)
```

Out[90]: 33.25850641025641

In [91]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[91]: 0.8708850048335544

In [92]:
```
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 =  0.749
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.995
```

Out[92]: 0.748975460246022

In [93]:
```
TBV = a[posAi]
mean(TBV)
```

Out[93]: 33.87493525641025

In [94]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[94]: 1.5169117904365046

In [95]:
```
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 =  0.738
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[95]: 0.7375020868255808

In [96]:
```
TBV = a[posAi]
mean(TBV)
```

Out[96]: 34.411586410256405

In [97]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[97]: 2.043551173687437

In [98]:
```
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 =  0.744
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.979
```

Out[98]: 0.7439774229107254

In [99]:
```
TBV = a[posAi]
mean(TBV)
```

Out[99]: 34.962447307692315

In [100]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[100]: 2.5779429829138647

In [101]:
```
IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor18 = cor(a[posAi],aHat1[posAi])[1,1]
reg18 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : correlation = %6.3f\n", cor18 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg18)
JCAll = cor17
```

```
LoadError: BoundsError: attempt to access 0-element Array{UInt8,1}
  at index [1]
while loading In[101], in expression starting on line 1

 [inlined code] from /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:167
 in readnrows! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:222
 in readtable! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:774
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:862
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:956
```

In [102]:
```
TBVG5NGall = a[posAi]
TBVG5NG=mean(TBVG5NGall)
```

Out[102]: 34.962447307692315

In [103]:
```
GEBVG5NGall = aHat1[posAi]
GEBVG5NG=mean(GEBVG5NGall)
```

Out[103]: 2.5779429829138647

In [104]:
```
numSSBayes
```

Out[104]: SSBR.NumSSBayes(54904,45904,9000,40000,39000,1000,2000)

```
In [105]: J_Vecs.J1
```

```
Out[105]: 45904x1 Array{Float64,2}:
          -0.00116985
          -0.88772
          -0.536844
          -0.50481
          -0.751759
          -0.752193
          -0.768557
           0.0
          -0.752053
          -0.962602
          -0.504807
          -0.94389
          -0.501171
            ⋮
          -0.962883
           1.30003e-19
          -0.756585
          -0.813766
          -0.752058
          -5.81375e-34
          -0.962551
          -0.504388
          -0.887749
          -0.885169
          -0.00233475
          -0.000585138
```

In [106]: `sortrows(J_Vecs.J1[end-8000:end,:])`

Out[106]: 8001x1 Array{Float64,2}:
```
 -0.98694
 -0.984724
 -0.982593
 -0.981394
 -0.981345
 -0.98129
 -0.981255
 -0.981254
 -0.981231
 -0.981149
 -0.980921
 -0.980872
 -0.980843
  ⋮
  5.55842e-17
  5.56158e-17
  5.5617e-17
  5.56899e-17
  5.5768e-17
  5.57895e-17
  5.59006e-17
  5.62308e-17
  5.62995e-17
  5.67726e-17
  6.09002e-17
  7.41359e-17
```

```
In [107]: J1 = sortrows(J_Vecs.J1)
```

Out[107]: 45904x1 Array{Float64,2}:
    -0.989598
    -0.98694
    -0.986794
    -0.985679
    -0.985611
    -0.985572
    -0.985511
    -0.985379
    -0.985308
    -0.985286
    -0.985255
    -0.984879
    -0.984724
     ⋮
     6.21143e-17
     6.29141e-17
     6.3084e-17
     6.31154e-17
     6.59642e-17
     6.61671e-17
     7.41359e-17
     7.82785e-17
     8.88245e-17
     9.73674e-17
     1.10202e-16
     1.11218e-16

In [108]: `J1[J1 .< 0.0,:]`

Out[108]: 43837x1 Array{Float64,2}:
    -0.989598
    -0.98694
    -0.986794
    -0.985679
    -0.985611
    -0.985572
    -0.985511
    -0.985379
    -0.985308
    -0.985286
    -0.985255
    -0.984879
    -0.984724
     ⋮
    -7.24659e-36
    -7.23354e-36
    -7.21667e-36
    -7.2166e-36
    -7.21273e-36
    -7.21238e-36
    -7.19923e-36
    -7.07921e-36
    -7.0126e-66
    -3.5063e-66
    -8.6437e-98
    -4.32185e-98

```
In [109]: J1[J1 .> 0.0,:]
```

```
Out[109]: 1322x1 Array{Float64,2}:
          9.59643e-114
          3.89278e-82
          7.78555e-82
          1.59855e-51
          1.60241e-51
          1.60907e-51
          2.80217e-51
          3.17361e-51
          3.19876e-51
          3.202e-51
          4.7946e-51
          4.9225e-51
          6.51627e-51
          ⋮
          6.21143e-17
          6.29141e-17
          6.3084e-17
          6.31154e-17
          6.59642e-17
          6.61671e-17
          7.41359e-17
          7.82785e-17
          8.88245e-17
          9.73674e-17
          1.10202e-16
          1.11218e-16
```

```
In [110]: G = convert(Array,readtable("GenNF.txt", separator = ' ',header=false));
```

```
In [111]: GAll=mean(G[:,2:end],1)
```

```
Out[111]: 1x2000 Array{Float64,2}:
          0.142111  1.57078  0.644444  1.93133  …  0.760778  0.988778  0.739778
```

```
In [112]: GG0=mean(G[1:200,2:end],1)
```

```
Out[112]: 1x2000 Array{Float64,2}:
          0.135  1.63  0.625  1.935  1.685  0.28  …  1.185  0.555  0.85  0.905  0.64
```

In [113]: `GG1=mean(G[201:400,2:end],1)`

Out[113]: 1x2000 Array{Float64,2}:
 0.165 1.645 0.575 1.93 1.71 0.325 … 1.305 0.565 0.725 0.965 0.7

In [114]: `GG2=mean(G[401:600,2:end],1)`

Out[114]: 1x2000 Array{Float64,2}:
 0.155 1.595 0.615 1.93 1.72 0.35 … 1.245 0.5 0.775 0.985 0.72

In [115]: `GG3=mean(G[601:800,2:end],1)`

Out[115]: 1x2000 Array{Float64,2}:
 0.12 1.535 0.715 1.91 1.68 0.425 … 1.29 0.605 0.72 0.995 0.765

In [116]: `GG4=mean(G[801:1000,2:end],1)`

Out[116]: 1x2000 Array{Float64,2}:
 0.145 1.54 0.645 1.945 1.76 0.435 … 1.255 0.535 0.765 1.01 0.775

In [117]: `GG5=mean(G[1001:9000,2:end],1)`

Out[117]: 1x2000 Array{Float64,2}:
 0.141875 1.5685 0.645625 1.9315 … 0.538875 0.76 0.990875 0.74225

In [118]: `writedlm("meanOfSNPGAll",GAll)`

In [119]: `writedlm("meanOfSNPGG0",GG0)`

In [120]: `writedlm("meanOfSNPGG1",GG1)`

In [121]: `writedlm("meanOfSNPGG2",GG2)`

In [122]: `writedlm("meanOfSNPGG3",GG3)`

In [123]: `writedlm("meanOfSNPGG4",GG4)`

In [124]: `writedlm("meanOfSNPGG5",GG5)`