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/0.5g2k/G/2
```

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/2

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

Correlation.G5.G.JC.txt
Correlation.G5.G.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

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 (
          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("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                                 # wit
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)        # wit
nothing
```

In [31]:
```
vRes    = 0.806
vG      = 0.806
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
7095.927057 seconds (23.87 G allocations: 737.370 GB, 2.68% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 31.6934
  4.76313
```

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

Out[33]: 4.7631326548254505

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

Out[34]: 18.2282508670222

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

Out[35]:
```
2000-element Array{Float64,1}:
    0.0254
    0.0058882
   -0.0195324
    0.00394989
    0.0193244
    0.0080964
   -0.00782693
   -0.00681087
   -0.00377613
   -0.00501222
   -0.00373671
    0.00141458
    0.0106982
    ⋮
    0.0144245
   -0.011985
    0.0227073
    0.000932127
   -0.0017055
    0.013028
    0.010155
    0.0145408
    0.0186274
   -0.0158078
    0.0172593
    0.00734861
```

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

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 =  0.918
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.981
```

Out[39]:
```
0.9178959229980915
```

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

Out[40]: 33.45646697916667

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

Out[41]: 1.76652862010016

In [42]:
```
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 =  0.923
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.054
```

Out[42]: 0.9225097083246413

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

Out[43]: 34.82397588888889

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

Out[44]: 3.1464117944620043

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 =  0.885
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.969
```

Out[45]: 0.88494053881789

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

Out[46]: 33.140888000000004

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

Out[47]: 1.4480940414012726

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 ej
@printf("SSBRJC from Gibbs – G0.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs – G0.ID : correlation =   0.728
SSBRJC from Gibbs – G0.ID : regression of TBV on GEBV =   0.895
```

Out[48]: 0.7276454183485979

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

Out[49]: 31.9281865

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

Out[50]: 0.14297753585030804

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

```
SSBRJC from Gibbs – G1.ID : correlation =   0.783
SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV =   1.017
```

Out[51]: 0.7831202019610318

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

Out[52]: 32.629996125000005

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

Out[53]: 0.9456562814696273

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

```
SSBRJC from Gibbs - G2.ID : correlation =  0.786
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.032
```

Out[54]: 0.7855476040850654

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

Out[55]: 33.18251150000001

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

Out[56]: 1.5323665249846554

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 ep
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.763
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.013
```

Out[57]: 0.762823919983863

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

Out[58]: 33.77602525

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

Out[59]: 2.119251514309526

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

```
         SSBRJC from Gibbs - G4.ID : correlation =  0.784
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.020
```

Out[60]: 0.78449960869078

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

Out[61]: 34.339634499999995

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

Out[62]: 2.6595342349013738

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

```
         SSBRJC from Gibbs - G5.ID : correlation =  0.910
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.044
```

Out[63]: 0.9097539033734853

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

Out[64]: 34.88244799999999

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

Out[65]: 3.199385629085469

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 =  0.942
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[66]: 0.9418714747597637

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

Out[67]: 33.316475000000004

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

Out[68]: 1.7991701671183717

In [69]:
```
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 =  0.945
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.051
```

Out[69]: 0.9451226360441993

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

Out[70]: 33.738085

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

Out[71]: 2.175666152778946

In [72]:
```
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 =  0.931
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[72]: 0.9309893477765856

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

Out[73]: 34.389979999999994

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

Out[74]: 2.745826991940723

In [75]:
```
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 =  0.945
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.048
```

Out[75]: 0.9448913578010868

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

Out[76]: 34.901525

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

Out[77]: 3.1885094601157205

In [78]:
```
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 =  0.882
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.012
```

Out[78]: 0.8819375081574048

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

Out[79]: 35.43493

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

Out[80]: 3.7039328154176783

In [81]:
```
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 =  0.910
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.044
```

Out[81]: 0.9097539033734853

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]: 34.88244799999999

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

Out[85]: 3.199385629085469

```
In [86]: 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 =  0.702
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.900
```

Out[86]: 0.7021830817192037

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

Out[87]: 31.89258935897436

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

Out[88]: 0.10051105812548593

```
In [89]: 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 =  0.770
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.027
```

Out[89]: 0.769682757080612

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

Out[90]: 32.60158358974359

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

Out[91]: 0.9141175668206705

In [92]:
```
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", cor1!
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.770
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.035
```

Out[92]: 0.7702057858479429

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

Out[93]: 33.151550769230774

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

Out[94]: 1.5012521540370642

In [95]:
```
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", cor1(
@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 =  1.009
```

Out[95]: 0.7446908069101492

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

Out[96]: 33.74716628205128

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

Out[97]: 2.091834643904239

In [98]:
```
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 =  0.771
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.018
```

Out[98]: 0.7707146210031431

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

Out[99]: 34.31155

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

Out[100]: 2.6327547841189043

In [101]:
```
IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = !
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/i
o.jl:167
 in readnrows! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.j
l:222
 in readtable! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.j
l: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]: 34.31155

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

Out[103]: 2.6327547841189043

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

Out[104]: SSBR.NumSSBayes(54938,45938,9000,40000,39000,1000,2000)

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

Out[105]: 45938x1 Array{Float64,2}:
           -0.00117302
            0.0
            0.0
           -0.887734
           -0.503513
           -0.501173
           -0.167187
           -0.751773
           -0.816466
           -0.751888
           -0.00234051
           -0.751902
           -0.97124
            ⋮
           -0.962594
            1.85615e-17
           -0.848113
           -0.758342
           -0.768436
           -0.00117096
           -0.962551
           -0.503807
           -0.887654
           -0.878357
           -0.00233845
           -0.272998

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

```
Out[106]:  8001x1 Array{Float64,2}:
           -1.04929
           -0.989361
           -0.987291
           -0.984226
           -0.981563
           -0.981317
           -0.981276
           -0.981272
           -0.981173
           -0.981162
           -0.980936
           -0.980865
           -0.98085
            ⋮
            5.56412e-17
            5.56557e-17
            5.56899e-17
            5.57876e-17
            5.58033e-17
            5.58262e-17
            5.59034e-17
            5.59142e-17
            5.62437e-17
            5.85579e-17
            5.89033e-17
            1.15321e-16
```

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

Out[107]: 45938x1 Array{Float64,2}:
          -1.04929
          -0.992412
          -0.991604
          -0.990203
          -0.989361
          -0.989207
          -0.988073
          -0.987735
          -0.987396
          -0.987291
          -0.986093
          -0.985642
          -0.985634
           ⋮
           6.38313e-17
           6.63856e-17
           6.66828e-17
           7.93088e-17
           7.93813e-17
           8.87674e-17
           8.89335e-17
           1.10998e-16
           1.11053e-16
           1.12008e-16
           1.1205e-16
           1.15321e-16

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

Out[108]: 43914x1 Array{Float64,2}:
           -1.04929
           -0.992412
           -0.991604
           -0.990203
           -0.989361
           -0.989207
           -0.988073
           -0.987735
           -0.987396
           -0.987291
           -0.986093
           -0.985642
           -0.985634
            ⋮
           -7.2166e-36
           -7.2166e-36
           -7.21238e-36
           -7.21238e-36
           -7.20817e-36
           -5.39146e-36
           -4.91411e-36
           -2.1823e-51
           -1.86734e-66
           -3.56554e-67
           -3.55965e-67
           -1.77955e-67

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

```
Out[109]:  1337x1 Array{Float64,2}:
           8.00735e-52
           8.01438e-52
           1.60147e-51
           1.60147e-51
           1.60288e-51
           1.60312e-51
           1.60577e-51
           3.07026e-51
           3.17857e-51
           3.20625e-51
           3.21155e-51
           3.21235e-51
           4.0047e-51
           ⋮
           6.38313e-17
           6.63856e-17
           6.66828e-17
           7.93088e-17
           7.93813e-17
           8.87674e-17
           8.89335e-17
           1.10998e-16
           1.11053e-16
           1.12008e-16
           1.1205e-16
           1.15321e-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}:
            0.230667  1.70822  0.502889  1.93389  1.749  …  0.511444  0.948778  0.56
           5778
```

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

```
Out[112]:  1x2000 Array{Float64,2}:
            0.175  1.705  0.53  1.92  1.7  0.29  0.78  …  1.4  0.66  0.615  0.91  0.
           545
```

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

```
Out[113]:  1x2000 Array{Float64,2}:
            0.14  1.695  0.57  1.9  1.665  0.325  …  1.405  0.66  0.595  0.93  0.58
```

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

```
Out[114]:  1x2000 Array{Float64,2}:
            0.18  1.695  0.505  1.915  1.75  0.35  …  1.485  0.735  0.515  0.98  0.6
           6
```

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

Out[115]: 1x2000 Array{Float64,2}:
 0.2 1.72 0.51 1.95 1.73 0.335 0.75 … 1.56 0.745 0.445 1.01
 0.585

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

Out[116]: 1x2000 Array{Float64,2}:
 0.275 1.705 0.47 1.93 1.79 0.38 … 1.5 1.52 0.8 0.495 0.93 0.
 545

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

Out[117]: 1x2000 Array{Float64,2}:
 0.23525 1.70875 0.501125 1.93525 … 0.752 0.50875 0.948375 0.5636
 25

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)`