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/0.5/Q/1
```

/home/nicole/Jupyter/JG3/Data/0.5/Q/1

In [4]:
```
;ls
```
```
PedAll.txt
Phe.txt
PheAll.txt
QTLNF.txt
Regression.G5.Q.J.txt
Regression.G5.Q.JC.txt
Regression.G5.Q.N.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPQAll
meanOfSNPQG0
meanOfSNPQG1
meanOfSNPQG2
meanOfSNPQG3
meanOfSNPQG4
meanOfSNPQG5
noGenotype.ID
sim.bv
sim.phenotype
```

In [5]:
```
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```
;awk '{print $1}' QTLNF.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("QTLNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                                # witl
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    = 0.668
vG      = 0.668
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
2096.857578 seconds (22.98 G allocations: 722.691 GB, 8.90% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  9.91184
  8.1946
```

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

Out[33]: 8.194604507011944

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

Out[34]: 9.053222151292564

In [35]: `alphaHat`

Out[35]: 50-element Array{Float64,1}:
  0.0321744
  0.0419024
  0.180616
  0.159661
  0.168625
  0.166364
  0.115713
  0.0734067
  0.0643975
  0.199202
  0.247673
  0.137757
  0.182508
  ⋮
  0.202992
  0.216992
  0.200406
  0.188386
  0.180687
  0.178309
  0.196391
  0.183241
  0.181067
  0.165936
  0.160537
  0.169432

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

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

In [38]:
```julia
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',head
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 = 0.917
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.964

Out[39]: 0.9167717069219157

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

Out[40]: 11.392354354166669

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

Out[41]: 1.4829045622949735

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

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.995
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.069
```

Out[42]: 0.9947283555324876

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

Out[43]: 12.525361111111112

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

Out[44]: 2.653060220613211

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 =  0.878
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.951
```

Out[45]: 0.877670090775781

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

Out[46]: 11.130891256410255

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

Out[47]: 1.212868641144611

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

```
SSBRJC from Gibbs - G0.ID : correlation =   0.710
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.856
```

Out[48]: 0.7104178502887921

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

Out[49]: 10.1364735

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

Out[50]: 0.1223532879158758

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

```
SSBRJC from Gibbs - G1.ID : correlation =   0.781
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.984
```

Out[51]: 0.7808728725293985

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

Out[52]: 10.634187875

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

Out[53]: 0.7320092064825244

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

```
         SSBRJC from Gibbs - G2.ID : correlation =  0.771
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.987
```

Out[54]: 0.7710634679322953

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

Out[55]: 11.175617749999997

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

Out[56]: 1.289891160158984

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

```
         SSBRJC from Gibbs - G3.ID : correlation =  0.772
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.993
```

Out[57]: 0.7723587294219472

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

Out[58]: 11.683383124999999

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

Out[59]: 1.796043263011165

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", re
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.793
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.004
```

Out[60]: 0.7931004509799342

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

Out[61]: 12.150585625

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

Out[62]: 2.259082142761341

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", re
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.994
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.068
```

Out[63]: 0.9941439795028852

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

Out[64]: 12.573878249999998

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

Out[65]: 2.69804831343995

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 =  0.993
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.072
```

Out[66]: 0.9927150673736566

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

Out[67]: 11.136659999999997

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

Out[68]: 1.3669517243999245

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 =  0.993
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.045
```

Out[69]: 0.9931474011728095

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

Out[70]: 11.721100000000002

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

Out[71]: 1.8991595274653361

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 =  0.992
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.059
```

Out[72]: 0.9917359782822919

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

Out[73]: 12.206114999999997

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

Out[74]: 2.3571316892567493

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 =  0.992
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.063
```

Out[75]: 0.9917598092422918

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

Out[76]: 12.621465

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

Out[77]: 2.744234199466968

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 =  0.990
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[78]: 0.9901199298381346

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

Out[79]: 13.000779999999999

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

Out[80]: 3.098300249407466

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 =  0.994
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.068
```

Out[81]: 0.9941439795028852

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

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

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

Out[84]: 12.573878249999998

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

Out[85]: 2.69804831343995

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 = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.690
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.855
```

Out[86]: 0.6902881896401257

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

Out[87]: 10.110827692307693

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

Out[88]: 0.09044050749320788

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 = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.764
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.988
```

Out[89]: 0.7636188517312671

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

Out[90]: 10.606318333333332

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

Out[91]: 0.7020822751752729

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", cor15
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.753
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.987
```

Out[92]: 0.7529382384365321

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

Out[93]: 11.14919474358974

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

Out[94]: 1.2625260183872464

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", cor16
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.756
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[95]: 0.7558053626703893

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

Out[96]: 11.659329743589744

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

Out[97]: 1.7717306748969137

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 =  0.781
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.002
```

Out[98]: 0.7811438484333142

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

Out[99]: 12.128785769230769

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

Out[100]: 2.2375637297704145

In [101]:
```
numSSBayes
```

Out[101]: SSBR.NumSSBayes(54906,45906,9000,40000,39000,1000,50)

In [102]:
```
J_Vecs.J1
```

Out[102]:
```
45906x1 Array{Float64,2}:
   9.22014e-19
  -0.00117028
  -0.887669
  -0.506888
  -0.501171
  -0.0122736
  -0.752051
  -0.771989
  -0.752044
  -0.971901
  -0.501765
  -0.959207
  -0.513216
   ⋮
  -0.961393
  -0.963504
  -2.89386e-35
  -0.838608
  -0.752192
  -0.751756
   1.2987e-19
  -0.962573
  -0.638225
  -0.91827
  -0.878362
  -0.00156891
```

```
In [103]: sortrows(J_Vecs.J1[end-8000:end,:])
```

Out[103]: 8001x1 Array{Float64,2}:
          -0.999676
          -0.983545
          -0.981624
          -0.981231
          -0.981231
          -0.980891
          -0.980888
          -0.980879
          -0.980864
          -0.980808
          -0.980732
          -0.979785
          -0.979419
           ⋮
           5.56413e-17
           5.56418e-17
           5.57142e-17
           5.574e-17
           5.59134e-17
           5.62542e-17
           5.7199e-17
           5.76026e-17
           5.90253e-17
           6.67238e-17
           1.10761e-16
           1.10949e-16

```
In [104]:  J1 = sortrows(J_Vecs.J1)
```

Out[104]: 45906x1 Array{Float64,2}:
           −0.999676
           −0.997643
           −0.988757
           −0.987284
           −0.985823
           −0.985587
           −0.985551
           −0.985066
           −0.984633
           −0.984498
           −0.984346
           −0.984273
           −0.984156
            ⋮
            6.08279e−17
            6.14904e−17
            6.60531e−17
            6.67238e−17
            6.67549e−17
            7.5108e−17
            8.07893e−17
            8.88438e−17
            9.974e−17
            1.0006e−16
            1.10761e−16
            1.10949e−16

```
In [105]: J1[J1 .< 0.0,:]
```

Out[105]: 43936x1 Array{Float64,2}:
 -0.999676
 -0.997643
 -0.988757
 -0.987284
 -0.985823
 -0.985587
 -0.985551
 -0.985066
 -0.984633
 -0.984498
 -0.984346
 -0.984273
 -0.984156
  ⋮
 -7.21871e-36
 -7.20816e-36
 -7.20816e-36
 -7.20812e-36
 -7.20812e-36
 -7.20395e-36
 -7.05053e-36
 -4.91411e-36
 -2.5921e-65
 -5.33294e-67
 -2.66647e-67
 -1.78216e-67

In [106]: `J1[J1 .> 0.0,:]`

Out[106]: 1264x1 Array{Float64,2}:
 8.00262e-52
 8.02614e-52
 1.60052e-51
 1.60476e-51
 1.60523e-51
 1.60523e-51
 2.40174e-51
 3.19885e-51
 3.20388e-51
 3.20953e-51
 4.53675e-51
 4.80349e-51
 6.42512e-51
 ⋮
 6.08279e-17
 6.14904e-17
 6.60531e-17
 6.67238e-17
 6.67549e-17
 7.5108e-17
 8.07893e-17
 8.88438e-17
 9.974e-17
 1.0006e-16
 1.10761e-16
 1.10949e-16

In [107]: `G = convert(Array,readtable("QTLNF.txt", separator = ' ',header=false));`

In [108]: `GAll=mean(G[:,2:end],1)`

Out[108]: 1x50 Array{Float64,2}:
 1.249 0.753333 1.22478 1.24344 … 1.46811 1.69378 1.88756 0.915889

In [109]: `GG0=mean(G[1:200,2:end],1)`

Out[109]: 1x50 Array{Float64,2}:
 1.425 0.575 1.125 1.19 1.22 1.555 … 1.79 1.205 1.46 1.695 0.96

In [110]: `GG1=mean(G[201:400,2:end],1)`

Out[110]: 1x50 Array{Float64,2}:
 1.395 0.605 1.155 1.235 1.23 1.655 … 1.91 1.355 1.605 1.835 0.915

In [111]: `GG2=mean(G[401:600,2:end],1)`

Out[111]: 1x50 Array{Float64,2}:
 1.24 0.76 1.195 1.245 1.25 1.63 … 1.935 1.41 1.68 1.895 0.885

```
In [112]: GG3=mean(G[601:800,2:end],1)
```

```
Out[112]: 1x50 Array{Float64,2}:
           1.27  0.735  1.23  1.235  1.29  1.645  …  1.945  1.49  1.68  1.865  0.91
          5
```

```
In [113]: GG4=mean(G[801:1000,2:end],1)
```

```
Out[113]: 1x50 Array{Float64,2}:
           1.21  0.79  1.26  1.255  1.295  …  1.77  1.995  1.54  1.77  1.94  0.93
```

```
In [114]: GG5=mean(G[1001:9000,2:end],1)
```

```
Out[114]: 1x50 Array{Float64,2}:
           1.24162  0.760875  1.22875  1.24487  …  1.47663  1.70063  1.89275  0.915
          25
```

```
In [115]: writedlm("meanOfSNPQAll",GAll)
```

```
In [116]: writedlm("meanOfSNPQG0",GG0)
```

```
In [117]: writedlm("meanOfSNPQG1",GG1)
```

```
In [118]: writedlm("meanOfSNPQG2",GG2)
```

```
In [119]: writedlm("meanOfSNPQG3",GG3)
```

```
In [120]: writedlm("meanOfSNPQG4",GG4)
```

```
In [121]: writedlm("meanOfSNPQG5",GG5)
```