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/0.5/Q/3
```

```
/home/nicole/Jupyter/JG3/Data/0.5/Q/3
```

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
PedAll.txt
```

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 G
```

```
 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);                                    # 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   = 0.664
vG     = 0.664
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
3880.383819 seconds (22.96 G allocations: 722.138 GB, 7.77% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 9.66678
 7.94439
```

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

Out[33]:
```
7.944387624371022
```

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

Out[34]:
```
8.805581682456292
```

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

Out[35]:
```
50-element Array{Float64,1}:
 0.185942
 0.16499
 0.183606
 0.17287
 0.184011
 0.146793
 0.201331
 0.137813
 0.161012
 0.183228
 0.14515
 0.164898
 0.146576
 ⋮
 0.195014
 0.176494
 0.187565
 0.180867
 0.17209
 0.138984
 0.203835
 0.188193
 0.168286
 0.162684
 0.215571
 0.161038
```

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=fals
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 =  0.915
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.975
```

Out[39]:
```
0.9153723292318308
```

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

Out[40]: 11.135083416666665

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

Out[41]: 1.4754148268503444

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

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.994
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.070
```

Out[42]: 0.9941167785716042

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

Out[43]: 12.273038222222223

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

Out[44]: 2.636314310504077

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 =  0.875
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.962
```

Out[45]: 0.874897296249688

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

Out[46]: 10.872478461538462

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

Out[47]: 1.2075149460071755

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 =  0.702
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.867
```

Out[48]: 0.7023971458566146

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

Out[49]: 9.84533075

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

Out[50]: 0.1204420946748061

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 =  0.780
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.978
```

Out[51]: 0.7802895236522169

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

Out[52]: 10.40474075

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

Out[53]: 0.7553059401233458

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 =  0.760
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.990
```

Out[54]: 0.7596989771169305

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

Out[55]: 10.945704874999999

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

Out[56]: 1.2937331223278625

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 =  0.754
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.995
```

Out[57]: 0.7537707679973712

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

Out[58]: 11.422414125000001

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

Out[59]: 1.7766337664180392

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 =  0.774
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.991
```

Out[60]:
```
0.7737313423858467
```

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

Out[61]:
```
11.871169375
```

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

Out[62]:
```
2.225425067604213
```

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 =  0.993
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.069
```

Out[63]:
```
0.9934305130505364
```

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

Out[64]:
```
12.321140625
```

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

Out[65]:
```
2.6809489699538007
```

In [66]:
```
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 =  0.992
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.070
```

Out[66]:
```
0.9920218741468609
```

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

Out[67]:
```
10.961675
```

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

Out[68]:
```
1.418830088613231
```

In [69]:
```
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 =  0.992
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.077
```

Out[69]:
```
0.9919068306998468
```

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

Out[70]:
```
11.464300000000001
```

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

Out[71]:
```
1.8873594225610606
```

In [72]:
```
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 =  0.991
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.059
```

Out[72]: 0.991015664850665

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

Out[73]: 11.912560000000003

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

Out[74]: 2.297873545638345

In [75]:
```
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 =  0.991
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.059
```

Out[75]: 0.9912816145038442

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

Out[76]: 12.34098

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

Out[77]: 2.702263366710832

In [78]:
```
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 =  0.991
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.060
```

Out[78]: 0.9906826467665867

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

Out[79]: 12.761580000000002

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

Out[80]: 3.0898587510079603

In [81]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =  0.993
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[81]: 0.9934305130505364

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]: 12.321140625

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

Out[85]: 2.6809489699538007

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", cor1
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.678
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.863
```

Out[86]: 0.6781613066633814

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

Out[87]: 9.81670653846154

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

Out[88]: 0.08715009483023112

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", cor1
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.763
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.981
```

Out[89]: 0.7629060933009244

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

Out[90]: 10.377572564102563

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

Out[91]: 0.7262789277531482

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 =  0.742
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[92]: 0.7424739685566197

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

Out[93]: 10.92091371794872

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

Out[94]: 1.2679859319865683

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 =  0.736
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.994
```

Out[95]: 0.7363086557549208

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

Out[96]: 11.398861153846154

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

Out[97]: 1.7528996741028393

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 =  0.758
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.986
```

Out[98]:
```
0.757723178037754
```

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

Out[99]:
```
11.848338333333334
```

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

Out[100]:
```
2.203260101363091
```

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

Out[101]:
```
SSBR.NumSSBayes(54866,45866,9000,40000,39000,1000,50)
```

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

Out[102]:
```
45866x1 Array{Float64,2}:
  0.0
 -0.00117302
 -0.887723
 -0.504384
 -0.501755
 -1.21757e-64
 -0.757182
 -0.752189
 -0.752047
 -0.00117102
 -0.972845
 -0.501755
 -0.945121
  ⋮
 -0.957917
 -0.962595
 -0.777018
 -0.802518
 -0.81379
 -0.00117302
 -0.962551
 -0.504094
 -0.887588
 -0.913356
 -0.00117096
 -0.00058548
```

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

Out[103]:
```
8001x1 Array{Float64,2}:
 -0.984926
 -0.983886
 -0.982583
 -0.981896
 -0.981718
 -0.981265
 -0.98111
 -0.981026
 -0.98102
 -0.980888
 -0.980687
 -0.980459
 -0.979645
  ⋮
  5.56333e-17
  5.56717e-17
  5.58164e-17
  5.58897e-17
  5.59488e-17
  5.60308e-17
  5.68502e-17
  5.86245e-17
  5.8916e-17
  6.66984e-17
  9.72087e-17
  1.07645e-16
```

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

Out[104]:
```
45866x1 Array{Float64,2}:
 -0.999514
 -0.989317
 -0.98626
 -0.985919
 -0.985309
 -0.985285
 -0.984926
 -0.984854
 -0.984306
 -0.984196
 -0.984131
 -0.983886
 -0.983656
  ⋮
  7.07401e-17
  7.2845e-17
  7.33351e-17
  8.29252e-17
  8.89268e-17
  8.89663e-17
  8.89737e-17
  9.40272e-17
  9.72087e-17
  9.73518e-17
  1.07645e-16
  1.17135e-16
```

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

Out[105]:
```
43894x1 Array{Float64,2}:
 -0.999514
 -0.989317
 -0.98626
 -0.985919
 -0.985309
 -0.985285
 -0.984926
 -0.984854
 -0.984306
 -0.984196
 -0.984131
 -0.983886
 -0.983656
  ⋮
 -1.26309e-35
 -1.25967e-35
 -1.08297e-35
 -7.2166e-36
 -7.21238e-36
 -7.20818e-36
 -7.20816e-36
 -4.91411e-36
 -1.21757e-64
 -7.63876e-65
 -6.08783e-65
 -7.00015e-66
```

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

Out[106]:
```
1293x1 Array{Float64,2}:
 1.60053e-51
 1.60241e-51
 2.1823e-51
 2.79703e-51
 2.80462e-51
 3.17934e-51
 3.20482e-51
 4.80488e-51
 9.97839e-51
 1.99568e-50
 3.15259e-50
 6.30517e-50
 6.63481e-50
 ⋮
 7.07401e-17
 7.2845e-17
 7.33351e-17
 8.29252e-17
 8.89268e-17
 8.89663e-17
 8.89737e-17
 9.40272e-17
 9.72087e-17
 9.73518e-17
 1.07645e-16
 1.17135e-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}:
 0.478667  1.53011  1.41056  1.32089  …  0.467111  1.38089  1.54844  1.96
233
```

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

Out[109]:
```
1x50 Array{Float64,2}:
 0.23  1.59  0.925  0.85  0.1  1.47  1.04  …  1.875  0.45  1.13  1.305
 1.905
```

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

Out[110]:
```
1x50 Array{Float64,2}:
 0.315  1.55  1.115  1.03  0.165  1.595  …  1.855  0.525  1.195  1.385
 1.9
```

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

Out[111]:
```
1x50 Array{Float64,2}:
 0.375  1.535  1.315  1.195  0.22  1.63  …  1.89  0.51  1.37  1.48  1.945
```

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

Out[112]:
```
1x50 Array{Float64,2}:
 0.47  1.56  1.395  1.31  0.275  1.615  …  0.9  1.89  0.52  1.385  1.57
 1.97
```

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

Out[113]:
```
1x50 Array{Float64,2}:
 0.59  1.5  1.59  1.5  0.39  1.73  1.525  …  1.93  0.385  1.48  1.65  1.9
95
```

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

Out[114]:
```
1x50 Array{Float64,2}:
 0.489  1.528  1.42837  1.33888  0.314  …  0.46575  1.3895  1.55725  1.96
475
```

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)
```