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/7
```

```
/home/nicole/Jupyter/JG3/Data/0.5/Q/7
```

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

```
G0.Genotype.ID
G0.ID
G0.noGenotype.ID
G1.Genotype.ID
G1.ID
G1.noGenotype.ID
G2.Genotype.ID
G2.ID
G2.noGenotype.ID
G3.Genotype.ID
G3.ID
G3.noGenotype.ID
G4.Genotype.ID
G4.ID
G4.noGenotype.ID
G5.Genotype.ID
G5.ID
G5.noGenotype.ID
PedAll.txt
Phe.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   = 0.711
vG     = 0.711
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
2175.713465 seconds (22.99 G allocations: 722.842 GB, 8.58% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 9.70232
 8.0104
```

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

Out[33]:
```
8.01040134869751
```

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

Out[34]:
```
8.856361962718097
```

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

Out[35]:
```
50-element Array{Float64,1}:
  0.139141
  0.153199
  0.123026
  0.176691
  0.191763
 -0.00630941
 -0.0152649
  0.159654
  0.174405
  0.176801
  0.197957
  0.186506
  0.186672
  ⋮
  0.143985
  0.180658
  0.138001
  0.225457
  0.174085
  0.195755
  0.167637
  0.180047
  0.145591
  0.204274
  0.161044
  0.153582
```

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 =  0.918
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.972
```

Out[39]:
```
0.9177863102353448
```

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

Out[40]: 11.218311875

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

Out[41]: 1.5272481853328133

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 =  0.995
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.067
```

Out[42]: 0.9946233222430749

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

Out[43]: 12.40956711111111

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

Out[44]: 2.754901308214084

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 =  0.961
```

Out[45]: 0.8779264689003752

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

Out[46]: 10.943406820512822

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

Out[47]: 1.2439436185140587

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 =  0.713
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.887
```

Out[48]: 0.7130397567408621

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

Out[49]: 9.911972250000002

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

Out[50]: 0.12126143395814082

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 =  0.995
```

Out[51]: 0.7808967319843021

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

Out[52]: 10.446048125

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

Out[53]: 0.7570436433303684

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 =  0.782
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.017
```

Out[54]:
```
0.7823447968208248
```

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

Out[55]:
```
10.958247499999999
```

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

Out[56]:
```
1.2887680021295937
```

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 =  0.777
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.014
```

Out[57]:
```
0.7774815846395998
```

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

Out[58]:
```
11.531684875
```

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

Out[59]:
```
1.8619097002826486
```

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 =  0.787
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.015
```

Out[60]:
```
0.7873945913896442
```

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

Out[61]:
```
11.999897374999996
```

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

Out[62]:
```
2.330523373433088
```

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]:
```
0.9940254615965399
```

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

Out[64]:
```
12.462021125
```

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

Out[65]:
```
2.803982958863041
```

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 =  1.063
```

Out[66]:
```
0.9923775120985368
```

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

Out[67]:
```
10.996195
```

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

Out[68]:
```
1.4341664475706204
```

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 =  1.054
```

Out[69]:
```
0.9916582473599501
```

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

Out[70]:
```
11.449715
```

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

Out[71]:
```
1.8483455109644291
```

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 =  0.994
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.075
```

Out[72]:
```
0.9936061645637859
```

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

Out[73]:
```
12.099385
```

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

Out[74]:
```
2.469131419552749
```

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 =  0.992
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.062
```

Out[75]:
```
0.9922749097143336
```

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

Out[76]:
```
12.470485000000002
```

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

Out[77]:
```
2.8117316360384024
```

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 =  0.990
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.085
```

Out[78]: 0.9896233557422965

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

Out[79]: 12.933895000000001

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

Out[80]: 3.24786550098593

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

Out[81]: 0.9940254615965399

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]: 12.462021125

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

Out[85]: 2.803982958863041

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 =  0.692
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.889
```

Out[86]: 0.6918186718397182

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

Out[87]: 9.884171666666667

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

Out[88]: 0.08759720283987209

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 =  0.767
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.000
```

Out[89]: 0.7665376820551522

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

Out[90]: 10.420313076923078

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

Out[91]: 0.7290615441602644

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 =  0.764
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.021
```

Out[92]: 0.7638974834668986

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

Out[93]: 10.928987564102563

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

Out[94]: 1.2585022734777178

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 =  0.763
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.015
```

Out[95]: 0.7631896784115693

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

Out[96]: 11.507613076923077

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

Out[97]: 1.8375552916735265

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 =  0.774
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.013
```

Out[98]:
```
0.7741322169804535
```

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

Out[99]:
```
11.975948717948715
```

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

Out[100]:
```
2.3070017804189122
```

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

Out[101]:
```
SSBR.NumSSBayes(54917,45917,9000,40000,39000,1000,50)
```

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

Out[102]:
```
45917x1 Array{Float64,2}:
 -0.168084
 -0.00350809
  3.90161e-19
 -0.887661
 -0.503514
 -0.502671
  0.0
 -0.752156
 -0.752184
 -0.753424
 -0.00231388
 -0.815662
 -0.962573
  ⋮
 -0.971951
 -0.00117033
 -0.854178
 -0.753751
 -0.752204
 -0.00231016
 -0.962551
 -0.503514
 -0.890363
 -0.87827
 -0.00117165
 -0.25701
```

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

Out[103]:
```
8001x1 Array{Float64,2}:
 -0.981325
 -0.981294
 -0.981267
 -0.981241
 -0.981173
 -0.981142
 -0.980858
 -0.980804
 -0.980797
 -0.979775
 -0.979548
 -0.979536
 -0.979227
  ⋮
  5.56159e-17
  5.58444e-17
  5.5891e-17
  5.59013e-17
  5.59142e-17
  5.61862e-17
  5.62307e-17
  5.65449e-17
  5.86647e-17
  6.10506e-17
  8.51031e-17
  8.89559e-17
```

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

Out[104]:
```
45917x1 Array{Float64,2}:
 -0.986868
 -0.985718
 -0.985549
 -0.985507
 -0.985337
 -0.98531
 -0.98449
 -0.983869
 -0.983768
 -0.983758
 -0.983587
 -0.983232
 -0.982671
  ⋮
  7.40483e-17
  7.42043e-17
  7.42098e-17
  7.4361e-17
  8.51031e-17
  8.51031e-17
  8.61278e-17
  8.89559e-17
  1.02969e-16
  1.11022e-16
  1.11095e-16
  1.11274e-16
```

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

Out[105]:
```
43998x1 Array{Float64,2}:
 -0.986868
 -0.985718
 -0.985549
 -0.985507
 -0.985337
 -0.98531
 -0.98449
 -0.983869
 -0.983768
 -0.983758
 -0.983587
 -0.983232
 -0.982671
  ⋮
 -7.34107e-36
 -7.23782e-36
 -7.2166e-36
 -7.2166e-36
 -7.21449e-36
 -7.00015e-66
 -3.56334e-67
 -3.55597e-67
 -1.78167e-67
 -1.77903e-67
 -1.77799e-67
 -8.89515e-68
```

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

Out[106]:
```
1315x1 Array{Float64,2}:
 1.97512e-83
 3.94792e-83
 3.9561e-83
 3.87655e-66
 8.01203e-52
 8.01203e-52
 8.03559e-52
 8.03559e-52
 1.60147e-51
 1.60194e-51
 1.60241e-51
 1.60241e-51
 1.60479e-51
 ⋮
 7.40483e-17
 7.42043e-17
 7.42098e-17
 7.4361e-17
 8.51031e-17
 8.51031e-17
 8.61278e-17
 8.89559e-17
 1.02969e-16
 1.11022e-16
 1.11095e-16
 1.11274e-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}:
 1.773  0.631778  1.15422  0.671667  …  1.88789  1.58778  0.802333  1.085
56
```

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

Out[109]:
```
1x50 Array{Float64,2}:
 1.69  0.605  1.145  0.695  1.2  0.815  …  0.715  1.72  1.315  0.805  1.0
35
```

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

Out[110]:
```
1x50 Array{Float64,2}:
 1.705  0.595  1.16  0.71  1.215  1.03  …  0.865  1.795  1.415  0.775  1.
095
```

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

Out[111]:
```
1x50 Array{Float64,2}:
 1.76  0.64  1.115  0.685  1.37  0.925  …  0.985  1.885  1.55  0.835  1.0
2
```

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

Out[112]:
```
1x50 Array{Float64,2}:
 1.805  0.625  1.085  0.715  1.415  …  1.465  1.005  1.89  1.6  0.77  1.1
```

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

Out[113]:
```
1x50 Array{Float64,2}:
 1.805  0.635  1.175  0.655  1.525  0.96  …  1.125  1.935  1.68  0.835
 1.095
```

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

Out[114]:
```
1x50 Array{Float64,2}:
 1.7755  0.63325  1.1565  0.669125  …  1.89325  1.59725  0.802125  1.0876
3
```

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)
```