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/0.5a0/M/3
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/M/3
```

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

```
Correlation.G5.M.C*.txt
Correlation.G5.M.JC*.txt
Correlation.G5.M.JC.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
MarNF.txt
MarNFCenter.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C*.txt
Regression.G5.M.JC*.txt
Regression.G5.M.JC.txt
all.ID
alphaEstimatesJC
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
epsiEstimatesJC
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

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

In [6]:
```
;awk '{print $1}' MarNF.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("MarNF.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   = 0.328
vG     = 0.328
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
2317.866472 seconds (23.02 G allocations: 723.214 GB, 7.89% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 -0.191091
 -0.90874
```

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

Out[33]:
```
-0.9087403249291615
```

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

Out[34]:
```
-0.5499155112794358
```

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

Out[35]:
```
150-element Array{Float64,1}:
 -0.0149743
 -0.113216
  0.0795814
 -0.0865454
  0.000196368
 -0.0757765
  0.0955475
 -0.0867794
  0.098515
 -0.0147227
  0.00650665
  0.100966
  0.0503531
  ⋮
  0.0703459
 -0.0695944
 -0.0420704
  0.253634
  0.0426838
  0.117185
  0.00797901
  0.0162395
 -0.00847194
 -0.0615112
 -0.000222541
 -0.0343878
```

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

In [37]:
```
epsiHat
```

Out[37]:
```
45891-element Array{Float64,1}:
 -0.565777
 -0.0896185
  0.0634141
  0.316
 -0.456268
 -0.239341
  0.132406
 -0.10262
  0.489131
 -0.0810605
 -0.106457
 -0.345062
 -0.226244
  ⋮
 -0.115096
  0.141292
 -0.117024
  0.413585
 -0.483093
  0.348182
 -0.386175
  0.0808763
  0.139675
  0.110053
 -0.151169
 -0.707102
```

In [38]:
```
writedlm("epsiEstimatesJ",epsiHat)
```

In [39]:
```
using DataFrames
```

In [40]:
```
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 [41]:
```
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 =  0.892
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.986
```

Out[41]:
```
0.8921331241759667
```

In [42]:
```
TBV = a[posAi]
mean(TBV)
```

Out[42]: 0.9415992083333332

In [43]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[43]: 1.1089526558996214

In [44]:
```
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 =  0.838
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.040
```

Out[44]: 0.8383785113931886

In [45]:
```
TBV = a[posAi]
mean(TBV)
```

Out[45]: 1.8836888888888885

In [46]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[46]: 1.9585277146408657

In [47]:
```
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 =  0.855
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.930
```

Out[47]: 0.8549444096753962

In [48]:
```
TBV = a[posAi]
mean(TBV)
```

Out[48]: 0.7241938974358975

In [49]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[49]: 0.9128968731131805

In [50]:
```
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 =  0.583
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.600
```

Out[50]: 0.5830359592008629

In [51]:
```
TBV = a[posAi]
G0TBV=mean(TBV)
```

Out[51]: 0.01346250000000001

In [52]:
```
GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

Out[52]: 0.0962910632743232

In [53]:
```
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 =  0.756
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.948
```

Out[53]: 0.7559530726699754

In [54]:
```
TBV = a[posAi]
G1TBV=mean(TBV)
```

Out[54]: 0.30798312499999997

In [55]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[55]: 0.552780700690066

In [56]:
```
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 =  1.021
```

Out[56]: 0.7601247986750822

In [57]:
```
TBV = a[posAi]
G2TBV=mean(TBV)
```

Out[57]: 0.745656375

In [58]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[58]: 0.9876473272696602

In [59]:
```
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 =  1.068
```

Out[59]: 0.7720704703846107

In [60]:
```
TBV = a[posAi]
G3TBV=mean(TBV)
```

Out[60]: 1.12481225

In [61]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[61]: 1.3427171001352887

In [62]:
```
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 =  0.764
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.085
```

Out[62]:
```
0.7641318607130243
```

In [63]:
```
TBV = a[posAi]
G4TBV=mean(TBV)
```

Out[63]:
```
1.5272693750000002
```

In [64]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[64]:
```
1.6846613047151053
```

In [65]:
```
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 =  0.817
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.990
```

Out[65]:
```
0.8168203463422052
```

In [66]:
```
TBV = a[posAi]
G5TBV=mean(TBV)
```

Out[66]:
```
1.9304116249999999
```

In [67]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[67]:
```
1.9896184393132856
```

In [68]:
```
reg8 = linreg(aHat1[posAi], a[posAi])
```

Out[68]:
```
2-element Array{Float64,1}:
 -0.0388455
  0.989766
```

In [69]:
```
VarGEBV=var(aHat1[posAi])
```

Out[69]:
```
0.21595413580130535
```

In [70]:
```
VarTBV=var(a[posAi])
```

Out[70]: 0.31708352413037566

In [71]:
```
Cov=cov(aHat1[posAi], a[posAi])
```

Out[71]: 0.2137441061647391

In [72]:
```
b=Cov/VarGEBV
```

Out[72]: 0.989766208327681

In [73]:
```
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 =  0.840
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.005
```

Out[73]: 0.8403145394818935

In [74]:
```
TBV = a[posAi]
mean(TBV)
```

Out[74]: 0.5994250000000001

In [75]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[75]: 1.083954214553105

In [76]:
```
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 =  0.812
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.887
```

Out[76]: 0.81220568764375

In [77]:
```
TBV = a[posAi]
mean(TBV)
```

Out[77]: 1.17508

In [78]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[78]: 1.4899353506925066

In [79]:
```
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 =  0.816
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.942
```

Out[79]: 0.8163753458629919

In [80]:
```
TBV = a[posAi]
mean(TBV)
```

Out[80]: 1.5071050000000001

In [81]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[81]: 1.7110019122966706

In [82]:
```
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 =  0.785
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.871
```

Out[82]: 0.7846795933436433

In [83]:
```
TBV = a[posAi]
mean(TBV)
```

Out[83]: 1.9278850000000003

In [84]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[84]: 2.0002685116933185

In [85]:
```
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 =  0.765
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.892
```

Out[85]: 0.7651393587720348

In [86]:
```
TBV = a[posAi]
mean(TBV)
```

Out[86]: 2.34004

In [87]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[87]: 2.263849597071952

In [88]:
```
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 =  0.817
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.990
```

Out[88]: 0.8168203463422052

In [89]:
```
writedlm("Correlation.G5.M.J.txt",cor13)
```

In [90]:
```
writedlm("Regression.G5.M.J.txt",reg13)
```

In [91]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[91]: 1.9304116249999999

In [92]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[92]: 1.9896184393132856

In [93]:
```
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 =  0.562
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.593
```

Out[93]: 0.562069070752741

In [94]:
```
TBV = a[posAi]
mean(TBV)
```

Out[94]: -0.0015621794871794803

In [95]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[95]: 0.07096636708768778

In [96]:
```
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 =  0.736
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.953
```

Out[96]: 0.7363910696469411

In [97]:
```
TBV = a[posAi]
mean(TBV)
```

Out[97]: 0.2857498717948718

In [98]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[98]: 0.5287510942797471

In [99]:
```
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 =  0.744
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.020
```

Out[99]:
```
0.7443731999766454
```

In [100]:
```
TBV = a[posAi]
mean(TBV)
```

Out[100]:
```
0.7261320512820513
```

In [101]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[101]:
```
0.9690997738074291
```

In [102]:
```
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 =  0.758
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.061
```

Out[102]:
```
0.7578706999331559
```

In [103]:
```
TBV = a[posAi]
mean(TBV)
```

Out[103]:
```
1.1042206410256408
```

In [104]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[104]:
```
1.3258568075312365
```

In [105]:
```
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 =  0.751
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.071
```

Out[105]:
```
0.7505770330295077
```

In [106]:
```
TBV = a[posAi]
mean(TBV)
```

Out[106]:
```
1.506429102564103
```

In [107]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[107]:
```
1.6698103228598016
```

In [108]:
```
numSSBayes
```

Out[108]:
```
SSBR.NumSSBayes(54891,45891,9000,40000,39000,1000,150)
```

In [109]:
```
J_Vecs.J1
```

Out[109]:
```
45891x1 Array{Float64,2}:
 -0.00234278
 -0.00234124
  0.0
 -0.887719
 -0.515536
 -0.513479
 -0.00116311
 -0.752193
 -0.772986
 -0.755396
 -0.00359712
 -0.751759
 -0.962551
  ⋮
 -0.962825
  2.59929e-19
 -0.757039
 -0.752312
 -0.752467
 -0.00233845
 -0.963566
 -0.511888
 -0.887668
 -0.87918
  0.0
 -0.250329
```

In [110]:
```
sortrows(J_Vecs.J1[end-8000:end,:])
```

Out[110]:
```
8001x1 Array{Float64,2}:
 -0.988871
 -0.985631
 -0.983826
 -0.982918
 -0.982158
 -0.981862
 -0.981647
 -0.981241
 -0.981221
 -0.9812
 -0.981142
 -0.980878
 -0.980865
  ⋮
  5.55842e-17
  5.55843e-17
  5.56479e-17
  5.57301e-17
  5.58979e-17
  5.6096e-17
  5.60968e-17
  5.61815e-17
  5.71752e-17
  5.84478e-17
  5.88805e-17
  7.89541e-17
```

In [111]:
```
J1 = sortrows(J_Vecs.J1)
```

Out[111]:
```
45891x1 Array{Float64,2}:
 -0.988871
 -0.988537
 -0.986445
 -0.986275
 -0.98594
 -0.985938
 -0.985646
 -0.985631
 -0.985575
 -0.985565
 -0.985309
 -0.983826
 -0.983599
  ⋮
  6.18017e-17
  6.3726e-17
  6.63379e-17
  6.63385e-17
  6.68956e-17
  7.40627e-17
  7.55288e-17
  7.57539e-17
  7.89541e-17
  8.8821e-17
  1.11064e-16
  1.11418e-16
```

In [112]:
```
J1[J1 .< 0.0,:]
```

Out[112]:
```
43894x1 Array{Float64,2}:
 -0.988871
 -0.988537
 -0.986445
 -0.986275
 -0.98594
 -0.985938
 -0.985646
 -0.985631
 -0.985575
 -0.985565
 -0.985309
 -0.983826
 -0.983599
  ⋮
 -1.41032e-35
 -1.12728e-35
 -1.08265e-35
 -7.2166e-36
 -7.2166e-36
 -7.2166e-36
 -7.21238e-36
 -7.21238e-36
 -7.20816e-36
 -2.1823e-51
 -5.33216e-67
 -2.66608e-67
```

In [113]:
```
J1[J1 .> 0.0,:]
```

Out[113]:
```
1293x1 Array{Float64,2}:
 2.95994e-83
 5.91989e-83
 1.60147e-51
 1.60241e-51
 1.60717e-51
 2.40139e-51
 3.202e-51
 3.21433e-51
 4.80278e-51
 1.59813e-50
 6.84829e-49
 1.37333e-48
 4.91411e-36
 ⋮
 6.18017e-17
 6.3726e-17
 6.63379e-17
 6.63385e-17
 6.68956e-17
 7.40627e-17
 7.55288e-17
 7.57539e-17
 7.89541e-17
 8.8821e-17
 1.11064e-16
 1.11418e-16
```

In [114]:
```
G = convert(Array,readtable("MarNF.txt", separator = ' ',header=false));
```

In [115]:
```
GAll=mean(G[:,2:end],1)
```

Out[115]:
```
1x150 Array{Float64,2}:
 0.046  1.771  1.93111  1.42378  …  0.272556  0.377889  0.388222  1.321
```

In [116]:
```
GG0=mean(G[1:200,2:end],1)
```

Out[116]:
```
1x150 Array{Float64,2}:
 0.065  1.715  1.93  1.54  0.19  0.445  …  1.54  0.425  0.615  0.615  1.1
45
```

In [117]:
```
GG1=mean(G[201:400,2:end],1)
```

Out[117]:
```
1x150 Array{Float64,2}:
 0.055  1.795  1.93  1.535  0.12  0.295  …  1.595  0.345  0.52  0.525  1.
225
```

In [118]:
```
GG2=mean(G[401:600,2:end],1)
```

Out[118]:
```
1x150 Array{Float64,2}:
 0.055  1.79  1.91  1.505  0.11  0.235  …  1.63  0.305  0.525  0.53  1.17
```

In [119]:
```
GG3=mean(G[601:800,2:end],1)
```

Out[119]:
```
1x150 Array{Float64,2}:
 0.04  1.815  1.97  1.44  0.115  0.235  …  1.675  0.26  0.365  0.375  1.3
05
```

In [120]:
```
GG4=mean(G[801:1000,2:end],1)
```

Out[120]:
```
1x150 Array{Float64,2}:
 0.04  1.745  1.92  1.35  0.15  0.18  …  1.705  0.215  0.27  0.285  1.42
```

In [121]:
```
GG5=mean(G[1001:9000,2:end],1)
```

Out[121]:
```
1x150 Array{Float64,2}:
 0.045375  1.77087  1.931  1.4175  …  0.267875  0.36775  0.3785  1.3295
```

In [122]:
```
writedlm("meanOfSNPMAll",GAll)
```

In [123]:
```
writedlm("meanOfSNPMG0",GG0)
```

In [124]:
```
writedlm("meanOfSNPMG1",GG1)
```

In [125]:
```
writedlm("meanOfSNPMG2",GG2)
```

In [126]:
```
writedlm("meanOfSNPMG3",GG3)
```

In [127]:
```
writedlm("meanOfSNPMG4",GG4)
```

In [128]:
```
writedlm("meanOfSNPMG5",GG5)
```