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/M/1
```

```
/home/nicole/Jupyter/JG3/Data/0.5/M/1
```

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

```
Correlation.G5.M.C*.txt
Correlation.G5.M.JC*.txt
Correlation.G5.M.JC.txt
Correlation.G5.M.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
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
Regression.G5.M.N.txt
all.ID
alphaEstimatesJC
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
alphaEstimatesN
epsiEstimatesJC
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
epsiEstimatesN
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   = 0.668
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
2399.167472 seconds (23.03 G allocations: 723.421 GB, 8.11% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  9.88006
 -1.17925
```

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

Out[33]:
```
-1.1792516597273632
```

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

Out[34]:
```
4.350405351461203
```

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

Out[35]:
```
150-element Array{Float64,1}:
 -0.0743309
  0.0612122
 -0.00429009
 -0.105428
 -0.0325895
  0.0522857
  0.0252937
 -0.00606044
  0.0724257
  0.060029
 -0.029289
  0.0344942
 -0.0284581
  ⋮
  0.0822378
  0.00924866
  0.121778
  0.0334424
  0.0126739
 -0.0789064
 -0.0554321
 -0.18663
  0.0319198
 -0.0205963
  0.0778522
 -0.0225416
```

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

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

Out[37]:
```
45906-element Array{Float64,1}:
  0.396977
 -0.403664
  0.179495
 -1.00154
  0.0959709
 -0.0342631
 -0.134194
  0.625879
 -0.981655
 -0.000102299
 -0.858489
  0.0882536
 -0.133046
  ⋮
 -0.168079
  0.368186
  0.330258
 -0.17885
  0.608638
 -0.666914
 -0.302288
  0.0088426
  0.160584
 -0.376198
  0.085846
 -1.40685
```

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 =  0.895
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.988
```

Out[41]:
```
0.8945966319165612
```

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

Out[42]: 11.392354354166669

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

Out[43]: 1.4906581584245102

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 =  0.798
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.996
```

Out[44]: 0.79826003945036

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

Out[45]: 12.525361111111112

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

Out[46]: 2.551549359308963

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 =  0.868
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.958
```

Out[47]: 0.8679150232760645

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

Out[48]: 11.130891256410255

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

Out[49]: 1.2458371120665594

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 =  0.703
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.836
```

Out[50]: 0.7031188889232887

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

Out[51]: 10.1364735

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

Out[52]: 0.13070926186274068

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 =  0.765
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.997
```

Out[53]: 0.7647058582463974

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

Out[54]: 10.634187875

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

Out[55]: 0.8114200217913485

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 =  0.753
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.995
```

Out[56]:
```
0.7526536589357578
```

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

Out[57]:
```
11.175617749999997
```

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

Out[58]:
```
1.3528440771413497
```

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 =  0.748
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.001
```

Out[59]:
```
0.7477229482893151
```

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

Out[60]:
```
11.683383124999999
```

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

Out[61]:
```
1.8298070938668045
```

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 =  0.749
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.017
```

Out[62]:
```
0.7492099094530342
```

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

Out[63]:
```
12.150585625
```

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

Out[64]:
```
2.2335402727335243
```

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 =  0.774
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.953
```

Out[65]:
```
0.7739574424418546
```

In [66]:
```
writedlm("Correlation.G5.M.J.txt",cor13)
```

```
LoadError: UndefVarError: cor13 not defined
while loading In[66], in expression starting on line 1
```

In [67]:
```
writedlm("Regression.G5.M.J.txt",reg13)
```

```
LoadError: UndefVarError: reg13 not defined
while loading In[67], in expression starting on line 1
```

In [68]:
```
TBV = a[posAi]
G5TBV=mean(TBV)
```

Out[68]:
```
12.573878249999998
```

In [69]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[69]: 2.585628223151294

In [70]:
```
reg8 = linreg(aHat1[posAi], a[posAi])
```

Out[70]:
```
2-element Array{Float64,1}:
 10.109
  0.953288
```

In [71]:
```
VarGEBV=var(aHat1[posAi])
```

Out[71]: 0.3109978631167181

In [72]:
```
VarTBV=var(a[posAi])
```

Out[72]: 0.4718144954888738

In [73]:
```
Cov=cov(aHat1[posAi], a[posAi])
```

Out[73]: 0.2964704571616585

In [74]:
```
b=Cov/VarGEBV
```

Out[74]: 0.9532877627856643

In [75]:
```
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 =  0.798
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.018
```

Out[75]: 0.7977055753519683

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

Out[76]: 11.136659999999997

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

Out[77]: 1.5998753488854922

In [78]:
```
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 =  0.819
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.930
```

Out[78]:
```
0.8188786973875645
```

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

Out[79]:
```
11.721100000000002
```

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

Out[80]:
```
1.97219191153943
```

In [81]:
```
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 =  0.773
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.845
```

Out[81]:
```
0.7732097883207902
```

In [82]:
```
TBV = a[posAi]
mean(TBV)
```

Out[82]:
```
12.206114999999997
```

In [83]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[83]:
```
2.3459883045490173
```

In [84]:
```
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 =  0.811
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.921
```

Out[84]: 0.8105315152922808

In [85]:
```
TBV = a[posAi]
mean(TBV)
```

Out[85]: 12.621465

In [86]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[86]: 2.597741922691752

In [87]:
```
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 =  0.693
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.762
```

Out[87]: 0.6925937366883752

In [88]:
```
TBV = a[posAi]
mean(TBV)
```

Out[88]: 13.000779999999999

In [89]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[89]: 2.87879475518589

In [90]:
```
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 =  0.774
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.953
```

Out[90]: 0.7739574424418546

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

Out[91]: 12.573878249999998

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

Out[92]: 2.585628223151294

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 =  0.688
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.854
```

Out[93]: 0.68838509210188

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

Out[94]: 10.110827692307693

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

Out[95]: 0.093038336554465

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 =  0.749
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.005
```

Out[96]: 0.7493146486503101

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

Out[97]: 10.606318333333332

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

Out[98]: 0.7816566400029361

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 =  0.737
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.995
```

Out[99]: 0.7370395956750945

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

Out[100]: 11.14919474358974

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

Out[101]: 1.327378840541153

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 =  0.734
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.990
```

Out[102]:
```
0.733953423438511
```

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

Out[103]:
```
11.659329743589744
```

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

Out[104]:
```
1.8101164572302677
```

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 =  0.740
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.009
```

Out[105]:
```
0.7404536100035662
```

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

Out[106]:
```
12.128785769230769
```

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

Out[107]:
```
2.2169952860039768
```

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

Out[108]:
```
SSBR.NumSSBayes(54906,45906,9000,40000,39000,1000,150)
```

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

Out[109]:
```
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 [110]:
```
sortrows(J_Vecs.J1[end-8000:end,:])
```

Out[110]:
```
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 [111]:
```
J1 = sortrows(J_Vecs.J1)
```

Out[111]:
```
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 [112]:
```
J1[J1 .< 0.0,:]
```

Out[112]:
```
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 [113]:
```
J1[J1 .> 0.0,:]
```

Out[113]:
```
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 [114]:
```
G = convert(Array,readtable("MarNF.txt", separator = ' ',header=false));
```

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

Out[115]:
```
1x150 Array{Float64,2}:
 0.124111  1.60911  0.649  1.86378  1.61022  …  0.953222  0.537444  1.816
89
```

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

Out[116]:
```
1x150 Array{Float64,2}:
 0.09  1.665  0.58  1.88  1.63  0.305  …  1.115  0.3  0.885  0.885  0.63
1.8
```

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

Out[117]:
```
1x150 Array{Float64,2}:
 0.125  1.665  0.575  1.885  1.65  …  0.99  0.17  0.96  0.96  0.53  1.79
```

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

Out[118]:
```
1x150 Array{Float64,2}:
 0.14  1.535  0.71  1.84  1.59  0.37  …  0.13  0.985  0.985  0.525  1.805
```

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

Out[119]:
```
1x150 Array{Float64,2}:
 0.125  1.575  0.72  1.87  1.585  0.375  …  0.15  0.93  0.93  0.575  1.80
5
```

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

Out[120]:
```
1x150 Array{Float64,2}:
 0.125  1.63  0.61  1.86  1.62  0.44  …  0.085  0.97  0.975  0.505  1.83
```

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

Out[121]:
```
1x150 Array{Float64,2}:
 0.1245  1.6085  0.65025  1.86338  …  0.95175  0.954  0.5355  1.81825
```

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)
```