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/6
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/M/6
```

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

```
Correlation.G5.M.C*.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
all.ID
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
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   = 0.262
vG     = 0.262
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
3653.651201 seconds (23.03 G allocations: 723.558 GB, 7.26% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  3.13882
 -0.917678
```

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

Out[33]:
```
-0.9176784909052964
```

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

Out[34]:
```
1.110569118681747
```

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

Out[35]:
```
150-element Array{Float64,1}:
 -0.0353373
  0.0510472
 -0.0543957
  0.125093
  0.019673
  0.140986
 -0.0804191
  0.0767369
  0.0113647
  0.129193
  0.030293
 -0.0573944
  0.0185155
  ⋮
  0.0481923
 -0.0250981
  0.0140142
 -0.0552597
  0.0243971
 -0.00179322
  0.0151455
  0.00636682
  0.0101778
 -0.00790872
 -0.0680546
 -0.0103758
```

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

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

Out[37]:
```
45916-element Array{Float64,1}:
 -6.52068e-5
  0.279822
  0.118333
  0.112593
 -0.223962
 -0.668695
 -0.133309
 -0.0733476
  0.266054
  0.0196521
  0.614352
 -0.00541407
  0.0213628
  ⋮
 -0.194581
 -0.0394133
 -0.155135
  0.177933
 -0.279492
 -0.0902622
 -0.153619
  0.377844
 -0.0978863
  0.0730555
  0.495065
  0.750986
```

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 =  0.863
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.929
```

Out[41]:
```
0.8633263372752824
```

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

Out[42]: 4.017600416666667

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

Out[43]: 0.8683748999611347

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 =  0.753
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.908
```

Out[44]: 0.7525893594459028

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

Out[45]: 4.7069703333333335

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

Out[46]: 1.525911303100191

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 =  0.827
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.888
```

Out[47]: 0.8268808490419087

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

Out[48]: 3.858515051282051

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

Out[49]: 0.7166357300059679

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 =  0.541
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.526
```

Out[50]: 0.5411670077752907

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

Out[51]: 3.2996621250000002

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

Out[52]: 0.073601091987463

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 =  0.743
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.938
```

Out[53]: 0.7428852628501458

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

Out[54]: 3.54218725

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

Out[55]: 0.4437672448252809

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 =  1.005
```

Out[56]: 0.7531270351013925

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

Out[57]: 3.877764375

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

Out[58]: 0.7761351099967362

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 =  0.749
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.010
```

Out[59]: 0.7488231993613954

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

Out[60]: 4.17377175

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

Out[61]: 1.0487179462798857

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 =  0.730
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.967
```

Out[62]:
```
0.730254113310282
```

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

Out[63]:
```
4.471856625
```

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

Out[64]:
```
1.3181097462499192
```

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 =  0.715
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.841
```

Out[65]:
```
0.7146987741849735
```

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

Out[66]:
```
4.740360375
```

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

Out[67]:
```
1.5499182604275232
```

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

Out[68]:
```
2-element Array{Float64,1}:
 3.43722
 0.840781
```

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

Out[69]:
```
0.11897439720995016
```

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

Out[70]: 0.16465454857343112

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

Out[71]: 0.10003147209321461

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

Out[72]: 0.8407814995413879

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 =  0.785
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.003
```

Out[73]: 0.785126916947804

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

Out[74]: 3.7758950000000002

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

Out[75]: 0.8767734322464693

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 =  0.794
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.971
```

Out[76]: 0.7940903854459916

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

Out[77]: 4.208435

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

Out[78]: 1.1748369318374292

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 =  0.769
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.931
```

Out[79]: 0.7691201171543165

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

Out[80]: 4.4493849999999995

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

Out[81]: 1.3375621527211201

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 =  0.763
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.801
```

Out[82]: 0.7628379288071048

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

Out[83]: 4.776925

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

Out[84]: 1.5593456312129215

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 =  0.590
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.623
```

Out[85]: 0.5896869342513665

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

Out[86]: 4.9886099999999995

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

Out[87]: 1.720760074389724

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 =  0.715
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.841
```

Out[88]: 0.7146987741849735

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]: 4.740360375

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

Out[92]: 1.5499182604275232

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 =  0.523
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.516
```

Out[93]: 0.5225289220596135

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

Out[94]: 3.287451025641026

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

Out[95]: 0.05300692941671922

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 =  0.727
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.941
```

Out[96]: 0.7267000059248714

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

Out[97]: 3.5251039743589745

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

Out[98]: 0.42502186823522575

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 =  0.741
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.005
```

Out[99]: 0.7409382887549241

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

Out[100]: 3.8631074358974358

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

Out[101]: 0.7617395447986751

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 =  0.735
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.005
```

Out[102]: 0.7354040122681442

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

Out[103]: 4.158306282051282

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

Out[104]: 1.0356249287175

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 =  0.722
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.962
```

Out[105]:
```
0.7219752912416713
```

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

Out[106]:
```
4.458606538461539
```

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

Out[107]:
```
1.307785378861719
```

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

Out[108]:
```
SSBR.NumSSBayes(54916,45916,9000,40000,39000,1000,150)
```

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

Out[109]:
```
45916x1 Array{Float64,2}:
  0.0
 -0.00117028
 -0.0023385
 -0.88846
 -0.516681
 -0.501759
  1.30079e-19
 -0.752161
 -0.797068
 -0.751759
 -0.00117372
 -0.752051
 -0.962559
  ⋮
 -0.962619
  1.59463e-18
 -0.758099
 -0.758366
 -0.751903
 -0.0457756
 -0.974882
 -0.51785
 -0.890304
 -0.894478
 -0.0134387
  1.30311e-19
```

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

Out[110]:
```
8001x1 Array{Float64,2}:
 -0.986553
 -0.985416
 -0.984239
 -0.981694
 -0.981395
 -0.981335
 -0.981231
 -0.981177
 -0.980851
 -0.98073
 -0.980514
 -0.979571
 -0.97947
  ⋮
  5.56813e-17
  5.57143e-17
  5.57143e-17
  5.61345e-17
  5.65405e-17
  5.72102e-17
  6.06575e-17
  6.31852e-17
  6.66038e-17
  6.95754e-17
  7.11282e-17
  1.11714e-16
```

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

Out[111]:
```
45916x1 Array{Float64,2}:
 -0.988548
 -0.986981
 -0.986553
 -0.985968
 -0.98556
 -0.985416
 -0.985321
 -0.985276
 -0.984341
 -0.984239
 -0.983132
 -0.982628
 -0.981694
  ⋮
  6.66038e-17
  6.95754e-17
  7.11282e-17
  7.11548e-17
  7.17203e-17
  7.29782e-17
  7.43911e-17
  7.92991e-17
  8.60319e-17
  8.91038e-17
  1.11144e-16
  1.11714e-16
```

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

Out[112]:
```
43939x1 Array{Float64,2}:
 -0.988548
 -0.986981
 -0.986553
 -0.985968
 -0.98556
 -0.985416
 -0.985321
 -0.985276
 -0.984341
 -0.984239
 -0.983132
 -0.982628
 -0.981694
  ⋮
 -7.31545e-36
 -7.24235e-36
 -7.22085e-36
 -7.2166e-36
 -7.21449e-36
 -7.21238e-36
 -7.20815e-36
 -5.41087e-36
 -7.16595e-66
 -2.03618e-66
 -3.51359e-67
 -1.77903e-67
```

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

Out[113]:
```
1304x1 Array{Float64,2}:
 8.01203e-52
 8.12178e-52
 1.20145e-51
 1.58238e-51
 1.60053e-51
 1.60194e-51
 1.60241e-51
 1.60812e-51
 1.62436e-51
 1.6311e-51
 2.41071e-51
 3.16476e-51
 3.20194e-51
 ⋮
 6.66038e-17
 6.95754e-17
 7.11282e-17
 7.11548e-17
 7.17203e-17
 7.29782e-17
 7.43911e-17
 7.92991e-17
 8.60319e-17
 8.91038e-17
 1.11144e-16
 1.11714e-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}:
 0.130111  1.72833  0.365556  1.96944  …  0.902556  0.501333  1.83967
```

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

Out[116]:
```
1x150 Array{Float64,2}:
 0.155  1.735  0.465  1.93  1.725  0.69  …  1.115  1.445  0.8  0.665  1.8
4
```

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

Out[117]:
```
1x150 Array{Float64,2}:
 0.115  1.725  0.465  1.92  1.75  0.835  …  1.18  1.53  0.795  0.625  1.7
9
```

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

Out[118]:
```
1x150 Array{Float64,2}:
 0.14  1.775  0.35  1.96  1.855  0.845  …  1.15  1.475  0.87  0.59  1.815
```

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

Out[119]:
```
1x150 Array{Float64,2}:
 0.13  1.795  0.28  1.98  1.895  0.99  …  1.245  1.545  0.845  0.555  1.8
2
```

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

Out[120]:
```
1x150 Array{Float64,2}:
 0.12  1.705  0.365  1.98  1.845  …  0.985  1.32  1.65  0.995  0.4  1.85
```

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

Out[121]:
```
1x150 Array{Float64,2}:
 0.129875  1.726  0.363125  1.97138  …  1.5775  0.90775  0.493125  1.8417
5
```

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)
```