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/3
```

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

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

```
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
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.JC.txt
all.ID
alphaEstimatesJC
epsiEstimatesJC
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   = 0.664
vG     = 0.664
nIter  = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG
nothing
```

```
This is iteration 5000
This is iteration 10000
This is iteration 15000
This is iteration 20000
This is iteration 25000
This is iteration 30000
This is iteration 35000
This is iteration 40000
This is iteration 45000
This is iteration 50000
2452.872359 seconds (23.01 G allocations: 722.868 GB, 7.70% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  9.64971
 -0.680161
```

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

Out[33]: -0.6801606844970353

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

Out[34]: 4.48477702830564

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

Out[35]:
```
150-element Array{Float64,1}:
 -0.204752
  0.0846464
 -0.0829178
  0.0238987
  0.138553
 -0.195046
  0.12409
  0.0615597
 -0.0661689
 -0.021935
  0.196705
  0.146395
 -0.0403099
  ⋮
  0.0979859
  0.0785475
  0.0263092
  0.0250259
 -0.0702451
  0.126468
  0.0306198
  0.0496901
 -0.01817
 -0.0484055
 -0.0362126
 -0.0497991
```

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

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

Out[37]:
```
45866-element Array{Float64,1}:
  0.437171
  0.465249
  0.344617
  0.612772
 -0.0920398
  0.264906
 -0.509775
 -0.182248
 -0.71529
  0.410609
 -0.534741
 -0.771351
 -0.20297
  ⋮
  0.445506
  0.149641
  0.401264
  0.266705
  0.077275
  0.611508
 -0.28421
  0.825026
 -0.464581
 -0.226883
  0.222847
 -1.01549
```

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 =  0.899
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.000
```

Out[41]:
```
0.8991589819113788
```

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

Out[42]: 11.135083416666665

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

Out[43]: 1.4683845698600484

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 =  0.846
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.030
```

Out[44]: 0.8463245487363819

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

Out[45]: 12.273038222222223

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

Out[46]: 2.519237478815395

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 =  0.869
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.966
```

Out[47]: 0.8685282811104171

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

Out[48]: 10.872478461538462

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

Out[49]: 1.2258800524088143

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 =  0.698
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.855
```

Out[50]: 0.6981026508801893

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

Out[51]: 9.84533075

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

Out[52]: 0.124838751573281

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 =  0.971
```

Out[53]: 0.7651207068779271

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

Out[54]: 10.40474075

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

Out[55]: 0.7976015142593944

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 =  0.745
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.996
```

Out[56]: 0.7448395968137664

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

Out[57]: 10.945704874999999

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

Out[58]: 1.3330524115904958

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 =  0.740
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.014
```

Out[59]: 0.7396564265904514

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

Out[60]: 11.422414125000001

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

Out[61]: 1.7931295867699892

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 =  0.740
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.013
```

Out[62]:
```
0.7395577703179851
```

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

Out[63]:
```
11.871169375
```

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

Out[64]:
```
2.208362798986643
```

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 =  0.828
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.994
```

Out[65]:
```
0.8280746962388804
```

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]:
```
12.321140625
```

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

Out[69]: 2.5533223559804865

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

Out[70]:
```
2-element Array{Float64,1}:
 9.78305
 0.994036
```

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

Out[71]: 0.31114804134679996

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

Out[72]: 0.44836581732677505

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

Out[73]: 0.309292434744805

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

Out[74]: 0.9940362581298503

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 =  0.842
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.969
```

Out[75]: 0.8417307391250083

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

Out[76]: 10.961675

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

Out[77]: 1.5464764958964694

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 =  0.825
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.963
```

Out[78]: 0.8249127917184771

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

Out[79]: 11.464300000000001

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

Out[80]: 1.9462793236944986

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 =  0.850
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.978
```

Out[81]: 0.849682526361161

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

Out[82]: 11.912560000000003

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

Out[83]: 2.281753128300509

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 =  0.825
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.990
```

Out[84]: 0.8252232134285271

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

Out[85]: 12.34098

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

Out[86]: 2.6212104965115897

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 =  0.803
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.937
```

Out[87]: 0.8032132719846056

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

Out[88]: 12.761580000000002

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

Out[89]: 2.837072863070255

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 =  0.828
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.994
```

Out[90]: 0.8280746962388804

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

Out[91]: 12.321140625

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

Out[92]: 2.5533223559804865

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 =  0.677
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.862
```

Out[93]: 0.6767583254843847

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

Out[94]: 9.81670653846154

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

Out[95]: 0.08838650171884027

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 =  0.976
```

Out[96]: 0.7494105646607361

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

Out[97]: 10.377572564102563

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

Out[98]: 0.7681482370943917

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 =  0.729
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.994
```

Out[99]: 0.7287252131529885

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

Out[100]: 10.92091371794872

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

Out[101]: 1.3087267521876749

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 =  0.724
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.007
```

Out[102]:
```
0.7244362274311138
```

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

Out[103]:
```
11.398861153846154
```

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

Out[104]:
```
1.7718967429304613
```

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 =  0.727
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.998
```

Out[105]:
```
0.7270567802507709
```

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

Out[106]:
```
11.848338333333334
```

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

Out[107]:
```
2.1922420281127044
```

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

Out[108]:
```
SSBR.NumSSBayes(54866,45866,9000,40000,39000,1000,150)
```

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

Out[109]:
```
45866x1 Array{Float64,2}:
  0.0
 -0.00117302
 -0.887723
 -0.504384
 -0.501755
 -1.21757e-64
 -0.757182
 -0.752189
 -0.752047
 -0.00117102
 -0.972845
 -0.501755
 -0.945121
  ⋮
 -0.957917
 -0.962595
 -0.777018
 -0.802518
 -0.81379
 -0.00117302
 -0.962551
 -0.504094
 -0.887588
 -0.913356
 -0.00117096
 -0.00058548
```

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

Out[110]:
```
8001x1 Array{Float64,2}:
 -0.984926
 -0.983886
 -0.982583
 -0.981896
 -0.981718
 -0.981265
 -0.98111
 -0.981026
 -0.98102
 -0.980888
 -0.980687
 -0.980459
 -0.979645
  ⋮
  5.56333e-17
  5.56717e-17
  5.58164e-17
  5.58897e-17
  5.59488e-17
  5.60308e-17
  5.68502e-17
  5.86245e-17
  5.8916e-17
  6.66984e-17
  9.72087e-17
  1.07645e-16
```

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

Out[111]:
```
45866x1 Array{Float64,2}:
 -0.999514
 -0.989317
 -0.98626
 -0.985919
 -0.985309
 -0.985285
 -0.984926
 -0.984854
 -0.984306
 -0.984196
 -0.984131
 -0.983886
 -0.983656
  ⋮
  7.07401e-17
  7.2845e-17
  7.33351e-17
  8.29252e-17
  8.89268e-17
  8.89663e-17
  8.89737e-17
  9.40272e-17
  9.72087e-17
  9.73518e-17
  1.07645e-16
  1.17135e-16
```

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

Out[112]:
```
43894x1 Array{Float64,2}:
 -0.999514
 -0.989317
 -0.98626
 -0.985919
 -0.985309
 -0.985285
 -0.984926
 -0.984854
 -0.984306
 -0.984196
 -0.984131
 -0.983886
 -0.983656
  ⋮
 -1.26309e-35
 -1.25967e-35
 -1.08297e-35
 -7.2166e-36
 -7.21238e-36
 -7.20818e-36
 -7.20816e-36
 -4.91411e-36
 -1.21757e-64
 -7.63876e-65
 -6.08783e-65
 -7.00015e-66
```

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

Out[113]:
```
1293x1 Array{Float64,2}:
 1.60053e-51
 1.60241e-51
 2.1823e-51
 2.79703e-51
 2.80462e-51
 3.17934e-51
 3.20482e-51
 4.80488e-51
 9.97839e-51
 1.99568e-50
 3.15259e-50
 6.30517e-50
 6.63481e-50
 ⋮
 7.07401e-17
 7.2845e-17
 7.33351e-17
 8.29252e-17
 8.89268e-17
 8.89663e-17
 8.89737e-17
 9.40272e-17
 9.72087e-17
 9.73518e-17
 1.07645e-16
 1.17135e-16
```

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

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

Out[115]:
```
1x150 Array{Float64,2}:
 0.622889  1.861  1.64889  0.577222  1.37967  …  1.23622  0.455444  0.618
556
```

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

Out[116]:
```
1x150 Array{Float64,2}:
 0.62  1.855  1.625  0.365  0.92  1.15  …  1.62  0.34  0.99  0.99  0.57
 0.86
```

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

Out[117]:
```
1x150 Array{Float64,2}:
 0.635  1.86  1.645  0.465  1.1  0.97  …  0.305  1.08  1.08  0.525  0.78
```

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

Out[118]:
```
1x150 Array{Float64,2}:
 0.625  1.885  1.66  0.55  1.28  …  1.66  0.34  1.22  1.22  0.51  0.635
```

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

Out[119]:
```
1x150 Array{Float64,2}:
 0.595  1.89  1.675  0.595  1.36  0.69  …  0.215  1.275  1.265  0.41  0.5
9
```

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

Out[120]:
```
1x150 Array{Float64,2}:
 0.635  1.84  1.65  0.635  1.555  0.5  …  0.22  1.335  1.335  0.4  0.535
```

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

Out[121]:
```
1x150 Array{Float64,2}:
 0.623  1.86038  1.64863  0.584125  …  1.246  1.2435  0.452  0.610875
```

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)
```