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/8
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/M/8
```

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

```
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   = 0.741
vG     = 0.741
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
3474.742358 seconds (23.03 G allocations: 723.641 GB, 7.22% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
  2.56502
 -1.50697
```

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

Out[33]:
```
-1.506970839900363
```

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

Out[34]:
```
0.5290269234437619
```

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

Out[35]:
```
150-element Array{Float64,1}:
  0.021041
 -0.0600779
  0.0100726
  0.0265608
  0.266531
 -0.0695508
  0.059055
  0.0209715
 -0.00879924
  0.00746458
 -0.173733
  0.00293164
  0.0256312
  ⋮
 -0.0587001
  0.0940221
  0.0445802
  0.0910923
 -0.00780692
  0.0370375
  0.0541196
  0.0401799
  0.0542105
  0.00277239
  0.0643831
 -0.0364954
```

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

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

Out[37]:
```
45922-element Array{Float64,1}:
  0.264124
 -0.318466
  0.4038
 -0.1752
 -0.462835
  0.210432
 -0.523685
  0.455477
  0.112434
 -0.181591
 -0.862904
  0.181902
 -0.00555183
  ⋮
 -0.0382325
 -0.143383
 -0.0786818
 -0.906978
 -0.283655
 -0.301503
 -0.536173
 -0.0481624
  0.337449
  0.191381
  0.3951
  0.821082
```

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 =  0.910
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.980
```

Out[41]:
```
0.9100674942182678
```

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

Out[42]: 4.199781354166666

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

Out[43]: 1.6279271599642042

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 =  0.882
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.000
```

Out[44]: 0.8824364611370743

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

Out[45]: 5.430348888888889

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

Out[46]: 2.8456599933947375

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 =  0.880
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.966
```

Out[47]: 0.879986634359013

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

Out[48]: 3.9158042307692305

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

Out[49]: 1.3469118907110045

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 =  0.712
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.875
```

Out[50]: 0.7118381724380834

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

Out[51]: 2.8020739999999997

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

Out[52]: 0.133126064130343

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 =  0.771
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.991
```

Out[53]: 0.7710561468313961

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

Out[54]: 3.3759308749999994

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

Out[55]: 0.8524112686098433

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 =  0.776
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.031
```

Out[56]:
```
0.7764610265035168
```

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

Out[57]:
```
3.9699628750000002
```

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

Out[58]:
```
1.4422142526786743
```

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 =  0.753
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.003
```

Out[59]:
```
0.7531384637351652
```

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

Out[60]:
```
4.535933375
```

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

Out[61]:
```
1.9865888695975604
```

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 =  0.755
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.992
```

Out[62]:
```
0.7550035030132739
```

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

Out[63]:
```
5.0319438750000005
```

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

Out[64]:
```
2.463466093201565
```

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 =  0.866
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.974
```

Out[65]:
```
0.8662020674131058
```

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

Out[66]:
```
5.482843125
```

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

Out[67]:
```
2.8897564115672396
```

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

Out[68]:
```
2-element Array{Float64,1}:
 2.66714
 0.974375
```

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

Out[69]:
```
0.3909863174083998
```

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

Out[70]: 0.49473813778245723

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

Out[71]: 0.3809672918690532

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

Out[72]: 0.974374997043998

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 =  0.858
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.026
```

Out[73]: 0.8581023857779165

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

Out[74]: 3.963215000000001

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

Out[75]: 1.64642030510634

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 =  0.891
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.001
```

Out[76]: 0.8909309492165929

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

Out[77]: 4.539180000000001

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

Out[78]: 2.0802400487214543

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 =  0.851
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.905
```

Out[79]: 0.850528739724963

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

Out[80]: 5.082269999999999

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

Out[81]: 2.5415516745216893

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 =  0.836
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.859
```

Out[82]: 0.8363354890894502

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

Out[83]: 5.5289

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

Out[84]: 2.924495210135894

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 =  0.831
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.909
```

Out[85]: 0.8308941216996814

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

Out[86]: 5.938410000000001

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

Out[87]: 3.271736001588228

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 =  0.866
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.974
```

Out[88]: 0.8662020674131058

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]: 5.482843125

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

Out[92]: 2.8897564115672396

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 =  0.693
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.887
```

Out[93]:
```
0.6926832429034665
```

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

Out[94]:
```
2.7723011538461537
```

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

Out[95]:
```
0.094323647695061
```

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 =  0.753
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.996
```

Out[96]:
```
0.7533755260036383
```

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

Out[97]:
```
3.3461039743589738
```

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

Out[98]:
```
0.8209284793762123
```

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 =  0.762
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.036
```

Out[99]:
```
0.7622615405809187
```

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

Out[100]:
```
3.941442179487179
```

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

Out[101]:
```
1.4140261136570589
```

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 =  0.739
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.002
```

Out[102]:
```
0.7387788697044233
```

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

Out[103]:
```
4.510472692307693
```

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

Out[104]:
```
1.9625399890709367
```

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 =  0.742
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.986
```

Out[105]:
```
0.7420335595078851
```

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

Out[106]:
```
5.008701153846155
```

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

Out[107]:
```
2.4427412237557524
```

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

Out[108]:
```
SSBR.NumSSBayes(54922,45922,9000,40000,39000,1000,150)
```

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

Out[109]:
```
45922x1 Array{Float64,2}:
 -0.49978
 -0.00117096
 -0.491837
 -0.887603
 -0.545001
 -0.503598
  0.0
 -0.757608
 -0.751899
 -0.751756
 -0.0023364
 -0.752046
 -0.962571
  ⋮
 -0.943798
 -0.962551
 -0.00116961
 -0.777271
 -0.83546
 -0.752337
 -0.00114469
 -0.962549
 -0.504092
 -0.915773
 -0.888455
 -0.00175387
```

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

Out[110]:
```
8001x1 Array{Float64,2}:
 -0.986886
 -0.985547
 -0.98549
 -0.981241
 -0.981221
 -0.981201
 -0.981088
 -0.980847
 -0.980821
 -0.980528
 -0.980309
 -0.980157
 -0.979688
  ⋮
  5.55844e-17
  5.56086e-17
  5.57302e-17
  5.60264e-17
  5.61608e-17
  5.62219e-17
  5.62407e-17
  5.71251e-17
  5.73554e-17
  6.62311e-17
  7.35847e-17
  8.88706e-17
```

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

Out[111]:
```
45922x1 Array{Float64,2}:
 -0.986886
 -0.98681
 -0.986652
 -0.986167
 -0.985627
 -0.985584
 -0.985549
 -0.985547
 -0.98549
 -0.98527
 -0.985215
 -0.984637
 -0.984623
  ⋮
  7.0587e-17
  7.35847e-17
  7.43413e-17
  7.45955e-17
  8.59149e-17
  8.86198e-17
  8.88706e-17
  8.9519e-17
  9.67177e-17
  1.07311e-16
  1.22139e-16
  1.40744e-16
```

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

Out[112]:
```
43953x1 Array{Float64,2}:
 -0.986886
 -0.98681
 -0.986652
 -0.986167
 -0.985627
 -0.985584
 -0.985549
 -0.985547
 -0.98549
 -0.98527
 -0.985215
 -0.984637
 -0.984623
  ⋮
 -7.2166e-36
 -7.2166e-36
 -7.2092e-36
 -6.60657e-36
 -6.60657e-36
 -2.1823e-51
 -5.19078e-65
 -2.70994e-65
 -2.58495e-65
 -1.29248e-65
 -1.62865e-67
 -1.62865e-67
```

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

Out[113]:
```
1271x1 Array{Float64,2}:
 2.86987e-81
 7.33477e-52
 7.33477e-52
 1.46695e-51
 1.60076e-51
 1.60241e-51
 1.60241e-51
 2.1823e-51
 2.1823e-51
 2.3838e-51
 3.20013e-51
 3.20294e-51
 3.20397e-51
 ⋮
 7.0587e-17
 7.35847e-17
 7.43413e-17
 7.45955e-17
 8.59149e-17
 8.86198e-17
 8.88706e-17
 8.9519e-17
 9.67177e-17
 1.07311e-16
 1.22139e-16
 1.40744e-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}:
 0.292222  1.89067  1.77333  0.411778  …  1.42078  0.359778  1.881  0.424
444
```

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

Out[116]:
```
1x150 Array{Float64,2}:
 0.18  1.905  1.725  0.335  0.915  1.205  …  0.335  1.06  0.545  1.875
 0.77
```

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

Out[117]:
```
1x150 Array{Float64,2}:
 0.245  1.88  1.755  0.415  1.09  1.035  …  0.285  1.22  0.53  1.88  0.57
5
```

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

Out[118]:
```
1x150 Array{Float64,2}:
 0.23  1.87  1.73  0.46  1.305  0.865  …  0.22  1.32  0.415  1.865  0.495
```

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

Out[119]:
```
1x150 Array{Float64,2}:
 0.315  1.885  1.765  0.405  1.4  0.74  …  0.11  1.49  0.315  1.89  0.335
```

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

Out[120]:
```
1x150 Array{Float64,2}:
 0.315  1.89  1.8  0.41  1.485  0.67  …  1.88  0.11  1.55  0.27  1.895
 0.34
```

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

Out[121]:
```
1x150 Array{Float64,2}:
 0.296625  1.89125  1.77563  0.412625  …  1.43237  0.352875  1.881  0.414
625
```

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)
```