In [1]:
```julia
include("/home/nicole/Jupyter/SSBRJ/src/SSBR.jl")
using SSBR
```

In [2]:
```julia
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]:
```julia
; cd Data/0.5/M/2
```

/home/nicole/Jupyter/JG3/Data/0.5/M/2

In [4]:
```julia
;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]:
```julia
;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",calculateInbreedin
nothing
df      = read_genotypes("MarNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                              # with
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)    # with
nothing
```

In [31]:
```
vRes    = 0.714
vG      = 0.714
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
2432.630285 seconds (23.04 G allocations: 723.752 GB, 7.82% gc time)
```

In [32]: `betaHat`

Out[32]:
```
2-element Array{Float64,1}:
  9.12225
 -1.14363
```

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

Out[33]: -1.1436329263975729

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

Out[34]: 3.989307829336583

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

Out[35]: 150-element Array{Float64,1}:
```
 -0.0492487
 -0.115191
  0.177183
  0.0283405
 -0.0317536
  0.0955003
 -0.0894643
  0.0452072
 -0.0767546
  0.0185004
 -0.0723027
 -0.0283663
  0.0327532
  ⋮
 -0.127895
  0.121085
 -0.111461
 -0.0677571
  0.167235
  0.0227493
 -0.150565
  0.025949
  0.038081
  0.0661365
 -0.0570323
  0.0511629
```

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

In [37]: `epsiHat`

Out[37]: 45930-element Array{Float64,1}:
```
     0.487491
     0.20198
     0.292156
     0.253993
    -0.154939
     0.299067
    -0.217182
     0.196117
    -0.210304
    -0.0322822
     0.407507
    -0.169661
    -0.369825
     ⋮
    -0.455206
    -0.0114199
    -0.789469
     0.108202
    -0.765621
    -0.599272
    -0.146671
     0.502322
     0.508228
    -0.1267
    -0.741536
     0.654292
```

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

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

In [40]:
```julia
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',heac
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]:
```julia
IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false
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 =  0.898
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.996
```

Out[41]: 0.8980421629926466

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

Out[42]: 10.6819648125

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

Out[43]: 1.5345647676748386

```
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 ) # u
         @printf("SSBRJC from Gibbs – genotype.ID  : regression of TBV on GEBV = %6.3:
         JCAll = cor2
```

```
         SSBRJC from Gibbs – genotype.ID : correlation =   0.802
         SSBRJC from Gibbs – genotype.ID  : regression of TBV on GEBV =   0.966
```

Out[44]: 0.801802333205984

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

Out[45]: 11.885646444444445

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

Out[46]: 2.6431370108175476

```
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 =   0.871
         SSBRJC from Gibbs – noGenotype.ID  : regression of TBV on GEBV =   0.966
```

Out[47]: 0.8705043332654085

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

Out[48]: 10.404192128205128

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

Out[49]: 1.2787404038726748

```
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 =  0.709
          SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.860
```

Out[50]: 0.709422164456478

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

Out[51]: 9.342736249999998

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

Out[52]: 0.1265702643241324

```
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 =  0.760
          SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.983
```

Out[53]: 0.7604952129017468

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

Out[54]: 9.906285499999997

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

Out[55]: 0.834322121598446

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 =  0.749
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.997
```

Out[56]: 0.7491274349933541

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

Out[57]: 10.46190225

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

Out[58]: 1.388063136516762

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 =  0.733
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.973
```

Out[59]: 0.733333919703709

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

Out[60]: 10.967728125

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

Out[61]: 1.857801623070438

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 ep
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =   0.741
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   0.998
```

Out[62]: 0.7409433062067501

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

Out[63]: 11.475946500000003

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

Out[64]: 2.321645276436241

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 ep
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.777
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.921
```

Out[65]: 0.7774890058140339

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]: 11.93719025

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

Out[69]: 2.6789861841030116

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

Out[70]:
```
2-element Array{Float64,1}:
  9.46909
  0.921282
```

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

Out[71]: 0.33952277666388125

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

Out[72]: 0.4767229049180523

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

Out[73]: 0.3127963833185207

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

Out[74]: 0.92128247298172

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 =  0.805
SSBRJC from Gibbs – G0.Genotype.ID : regression of TBV on GEBV =  1.005
```

Out[75]: 0.8047026332116417

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

Out[76]: 10.439739999999997

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

Out[77]: 1.6186629262156822

In [78]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 =  0.763
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.860
```

Out[78]: 0.7632029293607525

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

Out[79]: 11.023549999999998

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

Out[80]: 2.032051618537043

In [81]:
```
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 =  0.767
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.867
```

Out[81]: 0.7665311941602654

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

Out[82]: 11.504534999999999

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

Out[83]: 2.3678248851645445

In [84]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 =  0.767
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.799
```

Out[84]: 0.7665855272660841

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

Out[85]: 12.004369999999996

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

Out[86]: 2.7795938244869003

In [87]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 =  0.751
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.777
```

Out[87]: 0.7505142030180454

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

Out[88]: 12.394285

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

Out[89]: 2.9835848682649915

In [90]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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 =   0.777
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   0.921
```

Out[90]: 0.7774890058140339

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

Out[91]: 11.93719025

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

Out[92]: 2.6789861841030116

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", cor14
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =   0.693
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.874
```

Out[93]: 0.6926079336108749

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

Out[94]: 9.31460794871795

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

Out[95]: 0.08831147812178497

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", cor14
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.745
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.991
```

Out[96]: 0.7454223184730672

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

Out[97]: 9.877637692307692

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

Out[98]: 0.8036111088564305

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", cor15
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.734
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.994
```

Out[99]: 0.7338448979616031

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

Out[100]: 10.435168076923075

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

Out[101]: 1.362941040397588

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", cor16
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.716
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.966
```

Out[102]: 0.7162486550805385

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

Out[103]: 10.941147564102565

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

Out[104]: 1.8341659255982212

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", cor17
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.730
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.988
```

Out[105]: 0.7300905614892059

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

Out[106]: 11.452399358974363

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

Out[107]: 2.3046724663893503

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

Out[108]: SSBR.NumSSBayes(54930,45930,9000,40000,39000,1000,150)

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

Out[109]: 45930x1 Array{Float64,2}:
           1.42087e-17
          -0.00116959
          -0.00117062
          -0.887647
          -0.504384
          -0.538863
           0.0
          -0.751902
          -0.787879
          -0.752155
          -0.0122672
          -0.751756
          -0.971282
            ⋮
          -0.962529
          -0.00117165
          -0.756884
          -0.751896
          -0.752213
           6.10158e-17
          -0.962529
          -0.518561
          -0.887929
          -0.937853
          -0.500658
           1.2985e-19

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

Out[110]: 8001x1 Array{Float64,2}:
           −0.986842
           −0.985605
           −0.985237
           −0.985237
           −0.983768
           −0.983498
           −0.982039
           −0.981231
           −0.981231
           −0.980863
           −0.980769
           −0.979643
           −0.979574
            ⋮
            5.55112e−17
            5.55112e−17
            5.55363e−17
            5.55842e−17
            5.5658e−17
            5.56861e−17
            5.57111e−17
            5.57358e−17
            5.57798e−17
            5.58446e−17
            5.59818e−17
            6.10158e−17

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

Out[111]: 45930x1 Array{Float64,2}:
           −0.990158
           −0.987733
           −0.986842
           −0.985656
           −0.985605
           −0.985577
           −0.985391
           −0.985278
           −0.985237
           −0.985237
           −0.984445
           −0.984331
           −0.98427
            ⋮
            6.10158e−17
            6.6476e−17
            6.95133e−17
            7.39894e−17
            7.40868e−17
            8.14434e−17
            8.86519e−17
            1.00099e−16
            1.11372e−16
            1.16871e−16
            1.22182e−16
            1.4449e−16

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

```
Out[112]:  43908x1 Array{Float64,2}:
            -0.990158
            -0.987733
            -0.986842
            -0.985656
            -0.985605
            -0.985577
            -0.985391
            -0.985278
            -0.985237
            -0.985237
            -0.984445
            -0.984331
            -0.98427
             ⋮
            -1.26861e-35
            -1.0855e-35
            -7.35892e-36
            -7.24634e-36
            -7.24206e-36
            -7.24206e-36
            -7.22509e-36
            -7.22509e-36
            -7.21237e-36
            -7.20816e-36
            -5.42752e-36
            -1.78112e-67
```

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

Out[113]: 1260x1 Array{Float64,2}:
   8.02146e-52
   1.60429e-51
   1.60429e-51
   1.60806e-51
   1.60806e-51
   1.60901e-51
   1.63401e-51
   2.81688e-51
   3.20481e-51
   3.20904e-51
   3.20953e-51
   4.76425e-51
   4.8278e-51
   ⋮
   6.10158e-17
   6.6476e-17
   6.95133e-17
   7.39894e-17
   7.40868e-17
   8.14434e-17
   8.86519e-17
   1.00099e-16
   1.11372e-16
   1.16871e-16
   1.22182e-16
   1.4449e-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}:
  0.0788889 1.31689 1.95211 0.990778 … 1.06111 0.528111 1.82033 0.
777

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

Out[116]: 1x150 Array{Float64,2}:
  0.105 1.605 1.925 0.76 0.765 0.685 … 0.92 0.915 0.66 1.805 0.
955

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

Out[117]: 1x150 Array{Float64,2}:
  0.13 1.535 1.925 0.86 0.87 0.78 … 0.915 0.915 0.58 1.8 0.935

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

Out[118]: 1x150 Array{Float64,2}:
  0.085 1.425 1.945 0.88 0.89 0.815 … 0.975 0.975 0.58 1.82 0.8
6

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

Out[119]: 1x150 Array{Float64,2}:
           0.075 1.295 1.955 1.02 1.015 … 0.165 1.08 1.08 0.51 1.8 0.76

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

Out[120]: 1x150 Array{Float64,2}:
           0.06 1.185 1.965 1.1 1.095 1.06 … 1.11 1.11 0.515 1.835 0.71

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

Out[121]: 1x150 Array{Float64,2}:
           0.077375 1.30537 1.95325 0.999125 … 1.06888 0.523 1.82137 0.7686
           25

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)`