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/0.5a0/M/4
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/4

```
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 (
```

```
 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   = 1.991
          vG     = 1.991
          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
          3723.860967 seconds (23.02 G allocations: 723.338 GB, 7.15% gc time)
```

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

```
Out[32]:  2-element Array{Float64,1}:
           11.2127
            0.569649
```

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

```
Out[33]:  0.5696485368813983
```

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

```
Out[34]:  5.891196713653703
```

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

```
Out[35]: 150-element Array{Float64,1}:
          0.114641
          0.031802
          0.0359461
          0.0525167
          0.201699
          0.0227949
          0.0521467
          0.162857
          0.00506218
         -0.0668264
          0.0602962
         -0.359003
         -0.0679795
          ⋮
          0.0668074
         -0.013231
         -0.187916
         -0.108912
         -0.0576619
         -0.131522
         -0.173535
         -0.270987
          0.0605901
          0.0040214
          0.220504
          0.0454203
```

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

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

```
Out[37]:  45900-element Array{Float64,1}:
           -0.0330463
           -0.0749308
           -0.950785
           -0.331875
           -1.47528
            1.04221
           -0.129797
           -0.166471
            0.671349
            0.313006
            1.02311
           -0.00277324
           -0.203727
            ⋮
            1.36316
           -0.718676
            0.11081
           -0.831241
            0.558947
            0.371858
           -0.192704
           -0.203604
            0.0789868
           -0.139509
           -0.503742
           -0.518108
```

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

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

```
In [40]:  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]:  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 =  0.919
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.012
```

```
Out[41]:  0.9194014341005281
```

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

Out[42]: 14.033610145833334

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

Out[43]: 2.805092814054402

```
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 =   0.878
          SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV =   0.993

Out[44]: 0.8782124725378398

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

Out[45]: 16.11359555555556

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

Out[46]: 4.816461755250013

```
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 =   0.894
          SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV =   1.005

Out[47]: 0.8939495133444093

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

Out[48]: 13.553613512820514

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

Out[49]: 2.340930750701568

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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.819
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.127
```

Out[50]: 0.8193281296128605

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

Out[51]: 11.54259725

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

Out[52]: 0.23917849108868514

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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.763
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.008
```

Out[53]: 0.7625439359861508

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

Out[54]: 12.770068125

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

Out[55]: 1.60432831308214

```
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 =  0.762
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.035
```

Out[56]: 0.761758801343386

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

Out[57]: 13.672560125

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

Out[58]: 2.5250007218972157

```
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 =  0.755
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.013
```

Out[59]: 0.7553895299739383

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

Out[60]: 14.580887250000002

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

Out[61]: 3.397057273227318

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", r
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.758
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.001
```

Out[62]: 0.7583005425342474

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

Out[63]: 15.439914125

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

Out[64]: 4.180551668864692

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", r
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.865
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.973
```

Out[65]: 0.8645894319981116

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

Out[66]: 16.195634

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

Out[67]: 4.884440416166361

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

Out[68]: 2-element Array{Float64,1}:
         11.4428
          0.973055

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

Out[69]: 1.134416695159818

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

Out[70]: 1.4368077632644083

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

Out[71]: 1.1037766404309384

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

Out[72]: 0.9730548300336306

In [73]:
```
IDs = readtable("G0.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 - 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 =  0.834
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.903
```

Out[73]: 0.8342155865844212

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

Out[74]: 14.014219999999998

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

Out[75]: 3.067108835729114

In [76]:
```
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 =  0.847
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.944
```

Out[76]: 0.8473836519580007

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

Out[77]: 14.530675

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

Out[78]: 3.534133726274047

In [79]:
```
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 =  0.873
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.941
```

Out[79]: 0.8729874568450562

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

Out[80]: 15.507835

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

Out[81]: 4.322143357024609

In [82]:
```
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 =  0.862
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.901
```

Out[82]: 0.8615149697323555

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

Out[83]: 16.290675000000004

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

Out[84]: 4.908612913609908

In [85]:
```
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 =  0.836
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.891
```

Out[85]: 0.8364624347699818

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

Out[86]: 16.943035000000002

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

Out[87]: 5.531163506958485

In [88]:
```
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 =  0.865
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.973
```

Out[88]: 0.8645894319981116

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]: 16.195634

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

Out[92]: 4.884440416166361

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 =  0.808
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.194
```

Out[93]: 0.8077260691151275

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

Out[94]: 11.479222307692309

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

Out[95]: 0.1666674566107254

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 =  0.748
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.020
```

Out[96]: 0.7480651526121702

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

Out[97]: 12.72492435897436

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

Out[98]: 1.5548461230002961

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 =  0.745
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.039
```

Out[99]: 0.7452143072087468

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

Out[100]: 13.625501794871795

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

Out[101]: 2.4789201415093336

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 =  0.740
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.007
```

Out[102]: 0.7395563433902734

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

Out[103]: 14.53704653846154

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

Out[104]: 3.358299436294431

```
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 = 0.747
           SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.997

Out[105]: 0.7465937530370872


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

Out[106]: 15.40137256410256


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

Out[107]: 4.145920596093056


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

Out[108]: SSBR.NumSSBayes(54900,45900,9000,40000,39000,1000,150)


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

Out[109]: 45900x1 Array{Float64,2}:
             3.43407e-19
            -0.00118274
             0.0
            -0.915703
            -0.504089
            -0.501463
            -0.0520833
            -0.752198
            -0.753422
            -0.772599
             1.30003e-19
            -0.834809
            -0.962637
             ⋮
            -0.943794
            -0.962573
            -0.00116242
            -0.816504
            -0.755551
            -0.753421
            -0.00117096
            -0.96261
            -0.639481
            -0.88787
            -0.502629
            -0.000586168
```

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

Out[110]: 8001x1 Array{Float64,2}:
           −0.986889
           −0.985957
           −0.985613
           −0.985433
           −0.984121
           −0.98379
           −0.983431
           −0.983277
           −0.983135
           −0.983008
           −0.981245
           −0.981129
           −0.98081
            ⋮
            5.5582e−17
            5.55843e−17
            5.56167e−17
            5.56388e−17
            5.56396e−17
            5.56412e−17
            5.5704e−17
            5.58111e−17
            5.58769e−17
            5.60402e−17
            5.84724e−17
            6.81721e−17

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

Out[111]: 45900x1 Array{Float64,2}:
          -1.00243
          -0.988969
          -0.986889
          -0.986202
          -0.985957
          -0.985613
          -0.985452
          -0.985433
          -0.985377
          -0.985375
          -0.985203
          -0.984978
          -0.984763
           ⋮
           6.48833e-17
           6.52495e-17
           6.6039e-17
           6.62586e-17
           6.66651e-17
           6.81721e-17
           7.40486e-17
           8.89238e-17
           8.91103e-17
           8.9262e-17
           9.99488e-17
           1.29767e-16

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

Out[112]: 43906x1 Array{Float64,2}:
           -1.00243
           -0.988969
           -0.986889
           -0.986202
           -0.985957
           -0.985613
           -0.985452
           -0.985433
           -0.985377
           -0.985375
           -0.985203
           -0.984978
           -0.984763
             ⋮
           -7.27634e-36
           -7.25083e-36
           -7.25083e-36
           -7.22083e-36
           -7.2166e-36
           -7.2166e-36
           -7.21128e-36
           -7.05063e-36
           -2.42284e-67
           -1.79376e-67
           -1.77772e-67
           -8.88859e-68

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

Out[113]: 1320x1 Array{Float64,2}:
8.00613e-52
8.07836e-52
1.60123e-51
1.60241e-51
1.60335e-51
1.61001e-51
1.61001e-51
1.61567e-51
1.62435e-51
2.1823e-51
2.38745e-51
4.43215e-51
4.64621e-51
⋮
6.48833e-17
6.52495e-17
6.6039e-17
6.62586e-17
6.66651e-17
6.81721e-17
7.40486e-17
8.89238e-17
8.91103e-17
8.9262e-17
9.99488e-17
1.29767e-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}:
 0.939778 1.81044 1.58522 0.520556 … 0.535 0.535333 1.19756 1.828

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

Out[116]: 1x150 Array{Float64,2}:
 0.735 1.885 1.625 0.385 0.845 1.21 … 1.22 0.635 0.635 0.965
 1.815

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

Out[117]: 1x150 Array{Float64,2}:
 0.76 1.855 1.625 0.42 0.905 1.165 … 1.105 0.59 0.595 1.11 1.7
85

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

Out[118]: 1x150 Array{Float64,2}:
 0.94 1.825 1.54 0.47 1.02 1.025 … 0.84 1.11 0.59 0.59 1.1 1.
81

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

Out[119]: 1x150 Array{Float64,2}:
 0.99 1.78 1.6 0.525 1.17 0.87 1.13 … 0.93 0.505 0.505 1.23
 1.845

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

Out[120]: 1x150 Array{Float64,2}:
 1.005 1.805 1.565 0.58 1.22 0.795 … 0.875 0.48 0.48 1.295 1.8
 3

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

Out[121]: 1x150 Array{Float64,2}:
 0.9465 1.808 1.5845 0.526125 1.13262 … 0.532125 1.20475 1.82937

```
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)
```