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/0.3/G/9
```

/home/nicole/Jupyter/JG3/Data/0.3/G/9

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

```
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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
```

In [5]:
```
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```
;awk '{print $1}' GenNF.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 G4.Genotype.ID;wc G5.Genotype
```
```
 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.ID;wc G4.noGenotype.ID;wc G
```
```
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",calculateInbreeding=false)
         nothing
         df      = read_genotypes("GenNF.txt",numSSBayes)
         M_Mats = make_MMats(df,A_Mats,ped);                           # without centering
         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 J
         nothing
```

```
In [31]: vG      = 0.746
         vRes    = 1.742
         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,nIter, outFreq=5000);
         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
2486.135195 seconds (23.05 G allocations: 723.800 GB, 7.67% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          10.0979
           5.25567
```

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

```
Out[33]: 5.255668627001173
```

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

Out[34]: 7.676776720006637

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

Out[35]: 200-element Array{Float64,1}:
           0.129562
           0.0475689
          -0.0797609
          -0.018979
           0.0789119
           0.163721
           0.00104932
           0.011233
           0.0405178
          -0.0482274
          -0.0603469
          -0.0111303
           0.148977
           ⋮
           0.11854
           0.000247569
          -0.000286619
           0.00509861
           0.137778
          -0.00169418
          -0.0759498
           0.0220426
           0.0211935
           0.015407
           0.0223334
           0.00738709

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

```
In [37]: using DataFrames
```

```
In [38]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',header=false)
         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 [39]: 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 epsilon
         @printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n", reg1)
         JCAll = cor1
```

```
         SSBRJC from Gibbs - all.ID : correlation =  0.858
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.981
```

Out[39]: 0.8581409922799871

```
In [40]: TBV = a[posAi]
         mean(TBV)
```

Out[40]: 11.418315708333331

```
In [41]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[41]: 1.3357581010859678

```
In [42]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3f\n", reg2)
         JCAll = cor2
```

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.970
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.097
```

Out[42]: 0.9698769581472021

In [43]:
```
TBV = a[posAi]
mean(TBV)
```

Out[43]: 12.31398022222222

In [44]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[44]: 2.275402827404332

In [45]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV = %6.3f\n", reg3)
JCAll = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.806
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.974
```

Out[45]: 0.8058584147263541

In [46]:
```
TBV = a[posAi]
mean(TBV)
```

Out[46]: 11.211623897435897

In [47]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[47]: 1.1189170103971147

In [48]:
```
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 epsilon
@printf("SSBRJC from Gibbs – G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs – G0.ID : correlation =   0.701
SSBRJC from Gibbs – G0.ID : regression of TBV on GEBV =   1.173
```

Out[48]: 0.7009369871870181

In [49]:
```
TBV = a[posAi]
G0TBV=mean(TBV)
```

Out[49]: 10.314537125000001

In [50]:
```
GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

Out[50]: 0.11593851243043557

In [51]:
```
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 epsilon
@printf("SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs – G1.ID : correlation =   0.688
SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV =   1.060
```

Out[51]: 0.6877837543369955

In [52]:
```
TBV = a[posAi]
G1TBV=mean(TBV)
```

Out[52]: 10.866148375

In [53]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[53]: 0.7761858279155531

In [54]:
```
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 epsilon
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.670
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.013
```

Out[54]: 0.6702239450136327

In [55]:
```
TBV = a[posAi]
G2TBV=mean(TBV)
```

Out[55]: 11.313845874999997

In [56]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[56]: 1.2556213530211613

In [57]:
```
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 epsilon
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.666
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.001
```

Out[57]: 0.6655096322109378

In [58]:
```
TBV = a[posAi]
G3TBV=mean(TBV)
```

Out[58]: 11.650402374999995

In [59]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[59]: 1.5976597529002927

In [60]:
```
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 epsilon
@printf("SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
JCAll = cor7
```

```
SSBRJC from Gibbs – G4.ID : correlation =  0.718
SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV =  1.031
```

Out[60]: 0.7177120946668146

In [61]:
```
TBV = a[posAi]
G4TBV=mean(TBV)
```

Out[61]: 12.017476874999995

In [62]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[62]: 1.9628421043745234

In [63]:
```
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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.969
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.098
```

Out[63]: 0.9685087170111214

In [64]:
```
TBV = a[posAi]
G5TBV=mean(TBV)
```

Out[64]: 12.347483624999992

In [65]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[65]: 2.3063010558738415

In [66]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.966
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.105
```

Out[66]: 0.965854376711025

In [67]:
```
TBV = a[posAi]
mean(TBV)
```

Out[67]: 11.393729999999998

In [68]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[68]: 1.4539306631049231

In [69]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.969
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.089
```

Out[69]: 0.9688379696409265

In [70]:
```
TBV = a[posAi]
mean(TBV)
```

Out[70]: 11.78747

In [71]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[71]: 1.7714614013169805

In [72]:
```
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg10)
JCAll = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.961
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.058
```

Out[72]: 0.9614848577741789

In [73]:
```
TBV = a[posAi]
mean(TBV)
```

Out[73]: 11.98991

In [74]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[74]: 1.9793930851983643

In [75]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg11)
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.961
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[75]: 0.9611039974574664

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

Out[76]: 12.374974999999997

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

Out[77]: 2.3332909221634437

In [78]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg12)
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =  0.961
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.072
```

Out[78]: 0.9606765116460092

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

Out[79]: 12.683680000000003

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

Out[80]: 2.6030089264575635

In [81]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg13)
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =  0.969
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.098
```

Out[81]: 0.9685087170111214

In [82]:
```
writedlm("Correlation.G5.G.J.txt",cor13)
```

In [83]:
```
writedlm("Regression.G5.G.J.txt",reg13)
```

In [84]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[84]: 12.347483624999992

In [85]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[85]: 2.3063010558738415

In [86]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs – G0.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCAll = cor14
```

```
SSBRJC from Gibbs – G0.noGenotype.ID : correlation =  0.689
SSBRJC from Gibbs – G0.noGenotype.ID : regression of TBV on GEBV =  1.254
```

Out[86]: 0.6887047013365187

In [87]:
```
TBV = a[posAi]
mean(TBV)
```

Out[87]: 10.286865512820512

In [88]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[88]: 0.08163102138749997

```
In [89]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
         JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.669
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.073
```

Out[89]: 0.6692843384689082

```
In [90]: TBV = a[posAi]
         mean(TBV)
```

Out[90]: 10.842524743589742

```
In [91]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[91]: 0.7506659414180806

```
In [92]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg15)
         JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.657
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.016
```

Out[92]: 0.6571259155454734

```
In [93]: TBV = a[posAi]
         mean(TBV)
```

Out[93]: 11.296510897435894

In [94]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[94]: 1.2370631034781563

In [95]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg16)
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.649
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.000
```

Out[95]: 0.6488250281908677

In [96]:
```
TBV = a[posAi]
mean(TBV)
```

Out[96]: 11.631823589743584

In [97]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[97]: 1.5787974152268787

In [98]:
```
IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg17)
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.704
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.029
```

Out[98]: 0.7038279945242699

In [99]:
```
TBV = a[posAi]
mean(TBV)
```

Out[99]: 12.00039474358974

In [100]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[100]: 1.946427570474958

In [101]:
```
IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor18 = cor(a[posAi],aHat1[posAi])[1,1]
reg18 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : correlation = %6.3f\n", cor18 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg18)
JCAll = cor17
```

```
LoadError: BoundsError: attempt to access 0-element Array{UInt8,1}
  at index [1]
while loading In[101], in expression starting on line 1

 [inlined code] from /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:167
 in readnrows! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:222
 in readtable! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:774
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:862
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:956
```

In [102]:
```
TBVG5NGall = a[posAi]
TBVG5NG=mean(TBVG5NGall)
```

Out[102]: 12.00039474358974

In [103]:
```
GEBVG5NGall = aHat1[posAi]
GEBVG5NG=mean(GEBVG5NGall)
```

Out[103]: 1.946427570474958

```
In [104]: numSSBayes
```

```
Out[104]: SSBR.NumSSBayes(54907,45907,9000,40000,39000,1000,200)
```

```
In [105]: J_Vecs.J1
```

```
Out[105]: 45907x1 Array{Float64,2}:
          -0.0122807
          -0.00224068
          -0.00119661
          -0.890239
          -0.550245
          -0.501751
          -0.0122766
          -0.751889
          -0.752193
          -0.81379
          -0.00119904
          -0.752192
          -0.962551
              ⋮
          -0.943831
          -0.962803
          -0.757015
          -0.752192
          -0.751901
          -0.00233166
          -0.965804
          -0.504306
          -0.887654
          -0.91875
          -0.00117096
          -0.00353859
```

In [106]: `sortrows(J_Vecs.J1[end-8000:end,:])`

Out[106]: 8001x1 Array{Float64,2}:
           −0.987731
           −0.986989
           −0.985997
           −0.985621
           −0.984063
           −0.982663
           −0.981263
           −0.981259
           −0.981248
           −0.981169
           −0.981142
           −0.981136
           −0.980874
            ⋮
            5.56513e−17
            5.56887e−17
            5.57063e−17
            5.57143e−17
            5.57144e−17
            5.57145e−17
            5.57221e−17
            5.58196e−17
            5.595e−17
            6.61923e−17
            8.89478e−17
            1.15514e−16

In [107]: `J1 = sortrows(J_Vecs.J1)`

Out[107]: 45907x1 Array{Float64,2}:
          −0.987731
          −0.987296
          −0.986989
          −0.985997
          −0.985966
          −0.985621
          −0.985559
          −0.985451
          −0.98528
          −0.984272
          −0.984141
          −0.984133
          −0.984109
           ⋮
           6.63613e−17
           6.65015e−17
           6.6618e−17
           6.98076e−17
           7.14802e−17
           7.63585e−17
           7.9197e−17
           8.89478e−17
           1.10977e−16
           1.11504e−16
           1.15514e−16
           1.46297e−16

In [108]: `J1[J1 .< 0.0,:]`

Out[108]: 43846x1 Array{Float64,2}:
```
 -0.987731
 -0.987296
 -0.986989
 -0.985997
 -0.985966
 -0.985621
 -0.985559
 -0.985451
 -0.98528
 -0.984272
 -0.984141
 -0.984133
 -0.984109
   ⋮
 -7.2166e-36
 -7.21448e-36
 -7.21238e-36
 -7.21237e-36
 -7.20922e-36
 -7.20815e-36
 -7.10566e-36
 -6.61399e-36
 -2.59857e-65
 -1.29929e-65
 -3.43441e-67
 -1.63047e-67
```

```
In [109]:  J1[J1 .> 0.0,:]
```

```
Out[109]:  1331x1 Array{Float64,2}:
            2.88499e-81
            7.343e-52
            8.01203e-52
            1.4686e-51
            1.54672e-51
            1.57777e-51
            1.60053e-51
            1.60077e-51
            1.60147e-51
            1.60241e-51
            1.60288e-51
            1.60288e-51
            1.60358e-51
            ⋮
            6.63613e-17
            6.65015e-17
            6.6618e-17
            6.98076e-17
            7.14802e-17
            7.63585e-17
            7.9197e-17
            8.89478e-17
            1.10977e-16
            1.11504e-16
            1.15514e-16
            1.46297e-16
```

```
In [110]:  G = convert(Array,readtable("GenNF.txt", separator = ' ',header=false));
```

```
In [111]:  GAll=mean(G[:,2:end],1)
```

```
Out[111]:  1x200 Array{Float64,2}:
            0.192  1.78  0.357  1.93722  1.81611  …  0.551778  1.82522  0.776778
```

```
In [112]:  GG0=mean(G[1:200,2:end],1)
```

```
Out[112]:  1x200 Array{Float64,2}:
            0.175  1.735  0.475  1.92  1.72  …  0.33  0.91  0.905  0.715  1.79  0.9
```

```
In [113]: GG1=mean(G[201:400,2:end],1)
```

```
Out[113]: 1x200 Array{Float64,2}:
           0.225  1.7  0.46  1.925  1.78  0.355  …  1.005  1.005  0.64  1.83  0.79
```

```
In [114]: GG2=mean(G[401:600,2:end],1)
```

```
Out[114]: 1x200 Array{Float64,2}:
           0.16  1.76  0.405  1.915  1.76  0.33  …  0.26  1.06  1.06  0.585  1.81  0.77
```

```
In [115]: GG3=mean(G[601:800,2:end],1)
```

```
Out[115]: 1x200 Array{Float64,2}:
           0.16  1.795  0.345  1.965  1.83  0.37  …  1.035  1.04  0.585  1.84  0.75
```

```
In [116]: GG4=mean(G[801:1000,2:end],1)
```

```
Out[116]: 1x200 Array{Float64,2}:
           0.225  1.79  0.315  1.935  1.855  0.44  …  1.115  1.125  0.495  1.825  0.77
```

```
In [117]: GG5=mean(G[1001:9000,2:end],1)
```

```
Out[117]: 1x200 Array{Float64,2}:
           0.192375  1.783  0.351625  1.93788  …  1.07212  0.54525  1.826  0.774375
```

```
In [118]: writedlm("meanOfSNPGAll",GAll)
```

```
In [119]: writedlm("meanOfSNPGG0",GG0)
```

```
In [120]: writedlm("meanOfSNPGG1",GG1)
```

```
In [121]: writedlm("meanOfSNPGG2",GG2)
```

```
In [122]: writedlm("meanOfSNPGG3",GG3)
```

```
In [123]: writedlm("meanOfSNPGG4",GG4)
```

```
In [124]: writedlm("meanOfSNPGG5",GG5)
```