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/0.5g2k/G/5
```

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/5

```
In [4]:  ;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
G5.noGenotype.ID
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.JC.txt
Regression.G5.G.PBLUP.txt
all.ID
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

```
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      = 0.704
         vRes    = 0.704
         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
7068.753053 seconds (23.84 G allocations: 736.502 GB, 2.66% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          31.7725
           3.67299
```

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

```
Out[33]: 3.6729900357540943
```

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

```
Out[34]: 17.722758009582112
```

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

```
Out[35]: 2000-element Array{Float64,1}:
          -0.00341217
          -0.00320557
          -0.00184915
           0.0106968
           0.0139124
           0.0209401
           0.0135051
           0.0104032
          -0.0123106
           0.0162602
           0.0210554
          -0.000887078
           0.0145586
           ⋮
           0.00283156
           0.0118225
           0.00570524
           0.0296561
           0.0134542
           0.0128702
           0.00237823
           6.10675e-5
          -0.00370062
          -0.000221173
           0.00229568
           0.0133134
```

```
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 =  0.916
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.991
```

Out[39]: 0.9162802565023069

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

Out[40]: 33.41670264583333

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

Out[41]: 1.6443395113197499

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 =  0.907
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.104
```

Out[42]: 0.907429830340615

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

Out[43]: 34.71152866666667

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

Out[44]: 2.917670653373607

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 =   0.884
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.969
```

Out[45]: 0.8842292060088189

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

Out[46]: 33.117896641025645

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

Out[47]: 1.3504938631534755

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 =   0.710
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   0.862
```

Out[48]: 0.7104719657121895

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

Out[49]: 31.993005999999998

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

Out[50]: 0.13379632996510174

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 =  0.786
SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV =  1.001
```

Out[51]: 0.7859171960387021

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

Out[52]: 32.57758962499999

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

Out[53]: 0.8487557852702373

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 =  0.771
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.998
```

Out[54]: 0.7706045293886239

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

Out[55]: 33.18146625

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

Out[56]: 1.4504331878866967

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 =  0.777
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.036
```

Out[57]: 0.7769646600931751

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

Out[58]: 33.7279075

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

Out[59]: 1.978445419820669

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 =   0.767
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.048
```

Out[60]: 0.7674065030845414

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

Out[61]: 34.251612

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

Out[62]: 2.488419796975335

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 =   0.890
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.095
```

Out[63]: 0.889972653981195

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

Out[64]: 34.768634500000005

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

Out[65]: 2.9661865480004606

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 =  0.943
SSBRJC from Gibbs – G0.Genotype.ID : regression of TBV on GEBV =  1.086
```

Out[66]: 0.9428977028518054

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

Out[67]: 33.146454999999996

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

Out[68]: 1.6165876993970503

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 =  0.932
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.001
```

Out[69]: 0.9324900271900417

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

Out[70]: 33.785545

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

Out[71]: 2.109653643385411

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 =  0.932
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.072
```

Out[72]: 0.9323111697270516

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

Out[73]: 34.28222000000001

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

Out[74]: 2.53575992279148

```
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 =  0.934
         SSBRJC from Gibbs – G3.Genotype.ID : regression of TBV on GEBV =  1.107
```

Out[75]: 0.9341700562257645

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

Out[76]: 34.79433

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

Out[77]: 2.995308813666946

```
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 =  0.869
         SSBRJC from Gibbs – G4.Genotype.ID : regression of TBV on GEBV =  0.993
```

Out[78]: 0.8692609295210187

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

Out[79]: 35.264860000000006

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

Out[80]: 3.390407402553012

```
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 =  0.890
         SSBRJC from Gibbs – G5.Genotype.ID : regression of TBV on GEBV =  1.095
```

Out[81]: 0.889972653981195

```
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]: 34.768634500000005

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

Out[85]: 2.9661865480004606

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 =  0.688
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.869
```

Out[86]: 0.6884036281252938

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

Out[87]: 31.963430384615382

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

Out[88]: 0.09577603844120561

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 =  0.768
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.006
```

Out[89]: 0.7681752195648107

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

Out[90]: 32.5466164102564

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

Out[91]: 0.8164250709595919

In [92]:
```julia
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 =  0.753
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.994
```

Out[92]: 0.7526253157166153

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

Out[93]: 33.15324179487179

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

Out[94]: 1.4226042972481123

In [95]:
```julia
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 =  0.761
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.033
```

Out[95]: 0.7611395043214995

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

Out[96]: 33.70056333333333

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

Out[97]: 1.952371999465636

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 =  0.753
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.044
```

Out[98]: 0.7528547862590032

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

Out[99]: 34.22563128205128

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

Out[100]: 2.465291909652831

In [101]:
```julia
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]:
```julia
TBVG5NGall = a[posAi]
TBVG5NG=mean(TBVG5NGall)
```

Out[102]: 34.22563128205128

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

Out[103]: 2.465291909652831

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

Out[104]: SSBR.NumSSBayes(54875,45875,9000,40000,39000,1000,2000)

In [105]: J_Vecs.J1

Out[105]: 45875x1 Array{Float64,2}:
           0.0
          -0.16719
          -0.00117165
          -0.887669
          -0.536842
          -0.512643
          -0.00117096
          -0.752194
          -0.850056
          -0.169042
          -0.75187
          -0.962624
          -0.501463
           ⋮
          -0.972081
           1.33335e-19
          -0.756444
          -0.768563
          -0.757909
          -0.00117096
          -0.962588
          -0.50382
          -0.890361
          -0.886087
           1.30001e-19
           0.0

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

Out[106]: 8001x1 Array{Float64,2}:
   -0.989406
   -0.988687
   -0.98529
   -0.984261
   -0.984123
   -0.984032
   -0.983764
   -0.983685
   -0.983122
   -0.981267
   -0.981231
   -0.980886
   -0.980804
    ⋮
    5.56412e-17
    5.56574e-17
    5.57142e-17
    5.57466e-17
    5.57937e-17
    5.58668e-17
    5.6026e-17
    5.70573e-17
    5.83323e-17
    6.10083e-17
    6.10569e-17
    8.99651e-17

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

Out[107]: 45875x1 Array{Float64,2}:
          -1.00013
          -0.989406
          -0.989104
          -0.988687
          -0.986955
          -0.986772
          -0.98594
          -0.985627
          -0.985612
          -0.985601
          -0.985574
          -0.985536
          -0.985534
           ⋮
           6.10569e-17
           6.32562e-17
           6.62234e-17
           6.63866e-17
           6.66704e-17
           7.02019e-17
           7.43747e-17
           7.69405e-17
           8.8762e-17
           8.89062e-17
           8.99651e-17
           1.07791e-16

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

Out[108]: 43858x1 Array{Float64,2}:
　　　　　-1.00013
　　　　　-0.989406
　　　　　-0.989104
　　　　　-0.988687
　　　　　-0.986955
　　　　　-0.986772
　　　　　-0.98594
　　　　　-0.985627
　　　　　-0.985612
　　　　　-0.985601
　　　　　-0.985574
　　　　　-0.985536
　　　　　-0.985534
　　　　　　⋮
　　　　　-7.21236e-36
　　　　　-7.20815e-36
　　　　　-7.20799e-36
　　　　　-7.19558e-36
　　　　　-7.17281e-36
　　　　　-7.16503e-36
　　　　　-5.41067e-36
　　　　　-7.17032e-66
　　　　　-3.55806e-67
　　　　　-1.78322e-67
　　　　　-1.78322e-67
　　　　　-1.78112e-67

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

Out[109]: 1354x1 Array{Float64,2}:
    8.02145e-52
    8.03092e-52
    8.03092e-52
    1.20141e-51
    1.59268e-51
    1.59774e-51
    1.60146e-51
    1.60148e-51
    1.60241e-51
    1.60241e-51
    1.60352e-51
    1.60352e-51
    1.60429e-51
    ⋮
    6.10569e-17
    6.32562e-17
    6.62234e-17
    6.63866e-17
    6.66704e-17
    7.02019e-17
    7.43747e-17
    7.69405e-17
    8.8762e-17
    8.89062e-17
    8.99651e-17
    1.07791e-16

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

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

Out[111]: 1x2000 Array{Float64,2}:
    0.223 1.45111 0.726333 1.94711 1.77222 … 0.693889 1.02056 0.681667

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

Out[112]: 1x2000 Array{Float64,2}:
    0.15 1.665 0.585 1.935 1.695 0.35 … 1.26 0.45 0.745 0.915 0.52

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

Out[113]: 1x2000 Array{Float64,2}:
  0.205 1.555 0.615 1.91 1.75 0.44 … 1.34 1.33 0.5 0.69 0.97 0.67

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

Out[114]: 1x2000 Array{Float64,2}:
  0.26 1.485 0.665 1.945 1.795 … 1.295 1.29 0.42 0.71 0.99 0.67

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

Out[115]: 1x2000 Array{Float64,2}:
  0.225 1.435 0.77 1.92 1.7 0.535 … 1.325 0.43 0.705 1.01 0.71

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

Out[116]: 1x2000 Array{Float64,2}:
  0.245 1.435 0.745 1.97 1.8 0.58 … 1.315 0.355 0.695 1.065 0.725

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

Out[117]: 1x2000 Array{Float64,2}:
  0.22375 1.44312 0.732625 1.9485 … 0.4095 0.692 1.02438 0.6845

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)`