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

In [2]:
```
function getPos(ped,IDs)
    posAi = Array(Int64,size(IDs,1))
    for (i,id) = enumerate(IDs[:,1])
        posAi[i] = ped.idMap[id].seqID
    end
    return posAi
end
```

Out[2]: getPos (generic function with 1 method)

In [3]:
```
; cd Data/0.5g2k/G/6
```

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/6

```
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     = 0.710
         vRes   = 0.710
         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
7076.190274 seconds (23.88 G allocations: 737.480 GB, 2.65% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          32.4682
           3.42016
```

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

```
Out[33]: 3.4201597322948767
```

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

```
Out[34]: 17.944174554772943
```

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

```
Out[35]: 2000-element Array{Float64,1}:
          0.00695496
          0.00573864
          0.012435
         -0.00366337
         -0.0089974
          0.00960843
          0.00735462
          0.00470199
         -0.00663301
          0.00604004
          0.0109965
         -0.001236
         -0.00591268
          ⋮
         -0.0198821
          0.00241207
         -0.0221701
         -0.0172054
          0.0242418
         -0.0188399
          7.93149e-6
          0.0076325
         -0.00261337
         -0.0042129
          0.0173937
         -0.00270103
```

```
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 =  0.919
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.002
```

Out[39]: 0.9191632219575988

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

Out[40]: 34.12391229166667

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

Out[41]: 1.6419342250167368

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 =  0.929
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.135
```

Out[42]: 0.928874651024181

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

Out[43]: 35.50100200000001

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

Out[44]: 2.9888388340797123

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 =  0.883
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.977
```

Out[45]: 0.8833569207864392

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

Out[46]: 33.806122358974356

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

Out[47]: 1.3311100844637427

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 =  0.708
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.868
```

Out[48]: 0.7077865112243488

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

Out[49]: 32.699646249999994

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

Out[50]: 0.13008968479849126

```
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 =  0.782
          SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV =  1.002
```

Out[51]: 0.7816685529665708

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

Out[52]: 33.23558537499999

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

Out[53]: 0.8034041956395722

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 =   0.776
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.024
```

Out[54]: 0.7762156801241396

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

Out[55]: 33.83505762499998

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

Out[56]: 1.403191153297094

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 =   0.773
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.056
```

Out[57]: 0.7733099316609019

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

Out[58]: 34.411308625000004

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

Out[59]: 1.9601985807500384

```
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 =   0.780
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.053
```

Out[60]: 0.7798921444855145

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

Out[61]: 34.995389

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

Out[62]: 2.5090863583912406

```
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 =   0.916
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.133
```

Out[63]: 0.9157893241688598

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

Out[64]: 35.566486875

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

Out[65]: 3.045635377223987

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 =  0.942
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.120
```

Out[66]: 0.9415849570089777

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

Out[67]: 33.774660000000004

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

Out[68]: 1.5359628131502854

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 =  0.940
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.088
```

Out[69]: 0.940094352311154

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

Out[70]: 34.440975

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

Out[71]: 2.0589999177102887

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 =  0.935
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.056
```

Out[72]: 0.9347590356772059

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

Out[73]: 34.990395

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

Out[74]: 2.542276318831847

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 =  0.939
SSBRJC from Gibbs – G3.Genotype.ID : regression of TBV on GEBV =  1.052
```

Out[75]: 0.9389732212517176

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

Out[76]: 35.56703

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

Out[77]: 3.029253697105119

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 =  0.867
SSBRJC from Gibbs – G4.Genotype.ID : regression of TBV on GEBV =  1.060
```

Out[78]: 0.8673978633568938

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

Out[79]: 36.112555

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

Out[80]: 3.505839697830071

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 =  0.916
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.133
```

Out[81]: 0.9157893241688598

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]: 35.566486875

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

Out[85]: 3.045635377223987

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 =  0.876
```

Out[86]: 0.6882204454331743

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

Out[87]: 32.67208179487179

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

Out[88]: 0.09404165586639397

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 =  0.763
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.004
```

Out[89]: 0.7631836316181554

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

Out[90]: 33.20467794871794

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

Out[91]: 0.7712094335351949

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 =  0.759
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.024
```

Out[92]: 0.7586935752114167

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

Out[93]: 33.805433589743586

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

Out[94]: 1.3739838413603054

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 =  0.755
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.054
```

Out[95]: 0.7553043798093625

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

Out[96]: 34.38167474358975

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

Out[97]: 1.932786911099908

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 =  0.765
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.048
```

Out[98]: 0.7649371376484314

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

Out[99]: 34.966743717948724

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

Out[100]: 2.483528580456911

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]: 34.966743717948724

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

Out[103]: 2.483528580456911

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

Out[104]: SSBR.NumSSBayes(54946,45946,9000,40000,39000,1000,2000)

In [105]: `J_Vecs.J1`

Out[105]: 45946x1 Array{Float64,2}:
          -0.00469658
          -0.00117165
          -0.887967
          -0.503803
           1.51592e-18
          -0.752193
          -0.75218
          -0.751904
           0.0
          -0.753423
          -0.962529
          -0.501462
          -0.943928
           ⋮
          -0.975799
          -0.506908
          -0.85003
          -0.814722
          -0.772643
           0.0
          -0.962529
          -0.504387
          -0.887654
          -0.878363
          -0.49978
          -0.00058548

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

Out[106]: 8001x1 Array{Float64,2}:
 -0.985828
 -0.985708
 -0.984119
 -0.982082
 -0.981262
 -0.981205
 -0.981171
 -0.981152
 -0.980868
 -0.980861
 -0.980821
 -0.980789
 -0.980689
    ⋮
  5.55655e-17
  5.56382e-17
  5.57061e-17
  5.57302e-17
  5.64118e-17
  5.98597e-17
  6.35214e-17
  6.5812e-17
  6.61749e-17
  6.6208e-17
  8.8709e-17
  1.1126e-16

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

Out[107]: 45946x1 Array{Float64,2}:
           -0.985828
           -0.985708
           -0.985612
           -0.985512
           -0.985284
           -0.984711
           -0.984187
           -0.984149
           -0.984119
           -0.984071
           -0.98377
           -0.98369
           -0.983599
              ⋮
            7.41365e-17
            7.41367e-17
            7.45212e-17
            8.8709e-17
            8.91041e-17
            8.91276e-17
            9.66885e-17
            1.1126e-16
            1.11863e-16
            1.1205e-16
            1.14303e-16
            1.44555e-16

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

Out[108]: 43884x1 Array{Float64,2}:
```
-0.985828
-0.985708
-0.985612
-0.985512
-0.985284
-0.984711
-0.984187
-0.984149
-0.984119
-0.984071
-0.98377
-0.98369
-0.983599
   ⋮
-7.23354e-36
-7.22931e-36
-7.2166e-36
-7.2166e-36
-7.21441e-36
-7.21238e-36
-7.21238e-36
-7.20807e-36
-7.20807e-36
-7.15497e-36
-1.72239e-66
-1.72239e-66
```

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

```
Out[109]: 1362x1 Array{Float64,2}:
          8.0096e-52
          1.55445e-51
          1.60051e-51
          1.60051e-51
          1.60147e-51
          1.60192e-51
          1.60241e-51
          1.60241e-51
          1.60523e-51
          1.60617e-51
          1.61289e-51
          1.61756e-51
          1.64882e-51
          ⋮
          7.41365e-17
          7.41367e-17
          7.45212e-17
          8.8709e-17
          8.91041e-17
          8.91276e-17
          9.66885e-17
          1.1126e-16
          1.11863e-16
          1.1205e-16
          1.14303e-16
          1.44555e-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}:
          0.166222  1.642  0.666556  1.84944  …  0.576  0.539222  1.06822  0.675556
```

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

```
Out[112]: 1x2000 Array{Float64,2}:
          0.125  1.635  0.685  1.87  1.57  0.31  …  1.41  0.555  0.59  1.025  0.685
```

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

Out[113]: 1x2000 Array{Float64,2}:
  0.145 1.625 0.66 1.84 1.6 0.255 … 1.365 0.555 0.64 1.02 0.715

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

Out[114]: 1x2000 Array{Float64,2}:
  0.175 1.61 0.625 1.82 1.605 … 1.42 1.43 0.54 0.59 1.005 0.61

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

Out[115]: 1x2000 Array{Float64,2}:
  0.145 1.675 0.605 1.885 1.63 0.33 … 1.495 0.58 0.545 1.08 0.625

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

Out[116]: 1x2000 Array{Float64,2}:
  0.185 1.635 0.695 1.83 1.585 0.345 … 1.56 0.595 0.48 1.105 0.71

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

Out[117]: 1x2000 Array{Float64,2}:
  0.167625 1.64275 0.668125 1.8495 … 0.577375 0.5355 1.07088 0.676375

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)`