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/0.1/G/8
```

/home/nicole/Jupyter/JG3/Data/0.1/G/8

```
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
alphaEstimates
genotype.ID
meanOfSNPGAll
meanOfSNPGG0
meanOfSNPGG1
meanOfSNPGG2
meanOfSNPGG3
meanOfSNPGG4
meanOfSNPGG5
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     = 0.584
         vRes   = 5.259
         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
         2519.142780 seconds (23.04 G allocations: 723.675 GB, 7.56% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          9.41434
          2.08033
```

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

```
Out[33]: 2.080333478160393
```

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

Out[34]: 5.747334272474504

In [35]: `alphaHat`

Out[35]: 200-element Array{Float64,1}:
```
  0.0224651
  0.0958201
 -0.0477665
  0.0371207
 -0.00408708
 -0.0809593
  0.0495913
  0.0275222
 -0.00575706
  0.00432687
  0.0142914
  0.0313006
 -0.0372513
  ⋮
 -0.00238303
  0.0191122
 -0.0368326
 -0.00404466
  0.0409954
  0.0717337
  0.0188431
  0.0261114
  0.0299712
  0.0566676
  0.0170927
 -0.0526272
```

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 =  0.773
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.961
```

Out[39]: 0.7731789653737619

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

Out[40]: 10.476803083333333

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

Out[41]: 1.0665843261702515

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 =  0.939
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.092
```

Out[42]: 0.9385459695979601

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

Out[43]: 11.115723222222222

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

Out[44]: 1.7593861537045619

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 =  0.698
SSBRJC from Gibbs – noGenotype.ID  : regression of TBV on GEBV =  0.941
```

Out[45]: 0.6977700016985494

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

Out[46]: 10.329359974358974

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

Out[47]: 0.9067069813546412

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 =  0.528
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.251
```

Out[48]: 0.528377933308985

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

Out[49]: 9.66376525

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

Out[50]: 0.09511838454436809

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 =  0.578
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.080
```

Out[51]: 0.5776888363079306

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

Out[52]: 10.160527499999999

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

Out[53]: 0.7011383909805559

```
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 =   0.580
          SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.017
```

Out[54]: 0.5795477899871471

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

Out[55]: 10.374001375

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

Out[56]: 0.9976043712127213

```
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 =   0.632
          SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.082
```

Out[57]: 0.6322975801140839

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

Out[58]: 10.638668000000001

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

Out[59]: 1.2895035014936875

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 =  0.689
SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV =  1.080
```

Out[60]: 0.6889783105268862

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

Out[61]: 10.886312875

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

Out[62]: 1.5370174439473625

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 =  0.937
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.095
```

Out[63]: 0.936679599020056

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

Out[64]: 11.137543500000001

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

Out[65]: 1.7791238648428125

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 =  0.933
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.074
```

Out[66]: 0.9325523086316779

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

Out[67]: 10.648155

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

Out[68]: 1.3233181742336717

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 =  0.928
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.010
```

Out[69]: 0.9275752108828932

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

Out[70]: 10.596925

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

Out[71]: 1.3084325552387945

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 =  0.954
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.118
```

Out[72]: 0.9542158609854833

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

Out[73]: 10.925364999999998

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

Out[74]: 1.5948375736043028

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 =  0.949
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.065
```

Out[75]: 0.9491315519939653

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

Out[76]: 11.14334

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

Out[77]: 1.7837264262451746

```
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 =  0.941
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.070
```

Out[78]: 0.941279714595523

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

Out[79]: 11.392020000000002

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

Out[80]: 1.9971075936708222

```
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 =  0.937
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.095
```

Out[81]: 0.936679599020056

```
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]: 11.137543500000001

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

Out[85]: 1.7791238648428125

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 =  0.510
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.584
```

Out[86]: 0.5103528418213905

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

Out[87]: 9.638524487179488

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

Out[88]: 0.06362608224464238

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 =  0.565
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.108
```

Out[89]: 0.5649650857128615

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

Out[90]: 10.14933782051282

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

Out[91]: 0.6855667457431652

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 =  0.559
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.016
```

Out[92]: 0.5588072101845143

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

Out[93]: 10.35986384615385

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

Out[94]: 0.9822906993565268

```
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 = 0.616
          SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.085

Out[95]: 0.6163823457336775

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

Out[96]: 10.625727692307693

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

Out[97]: 1.276831118807752

```
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 = 0.678
          SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.080

Out[98]: 0.6781409830949097

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

Out[99]: 10.873346025641025

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

Out[100]: 1.5252202606211205

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]: 10.873346025641025

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

Out[103]: 1.5252202606211205

In [104]: `numSSBayes`

Out[104]: SSBR.NumSSBayes(54898,45898,9000,40000,39000,1000,200)

In [105]: `J_Vecs.J1`

Out[105]: 45898x1 Array{Float64,2}:
     -0.0471947
     -0.0347176
     -0.00117302
     -0.887595
     -0.504397
     -0.501755
      0.0
     -0.751903
     -0.752203
     -0.752041
     -0.00204742
     -0.751756
     -0.962624
      ⋮
     -0.962551
     -0.00117268
     -0.817443
     -0.751759
     -0.752496
     -0.00233505
     -0.971262
     -0.515266
     -0.938361
     -0.878433
      2.60463e-19
     -0.000585166

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

Out[106]: 8001x1 Array{Float64,2}:
           −0.987317
           −0.985478
           −0.983768
           −0.982376
           −0.981743
           −0.981648
           −0.98128
           −0.98124
           −0.981162
           −0.981091
           −0.98087
           −0.980862
           −0.980803
            ⋮
            5.556e−17
            5.56168e−17
            5.56409e−17
            5.56572e−17
            5.56574e−17
            5.56575e−17
            5.5676e−17
            5.84031e−17
            5.98911e−17
            6.61437e−17
            7.42424e−17
            1.12735e−16

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

Out[107]: 45898x1 Array{Float64,2}:
    -0.999677
    -0.988268
    -0.987495
    -0.987317
    -0.985555
    -0.985552
    -0.985548
    -0.985478
    -0.985337
    -0.985319
    -0.985304
    -0.985265
    -0.985234
     ⋮
     7.42531e-17
     7.43058e-17
     7.45843e-17
     7.8553e-17
     7.87587e-17
     7.91296e-17
     8.99596e-17
     9.59437e-17
     1.05193e-16
     1.11265e-16
     1.12735e-16
     1.13945e-16

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

Out[108]: 43887x1 Array{Float64,2}:
          -0.999677
          -0.988268
          -0.987495
          -0.987317
          -0.985555
          -0.985552
          -0.985548
          -0.985478
          -0.985337
          -0.985319
          -0.985304
          -0.985265
          -0.985234
             ⋮
          -1.08202e-35
          -7.22083e-36
          -7.21698e-36
          -7.2166e-36
          -7.21238e-36
          -7.20814e-36
          -7.20807e-36
          -7.20352e-36
          -7.19941e-36
          -4.36461e-51
          -4.36461e-51
          -2.52441e-65

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

Out[109]: 1278x1 Array{Float64,2}:
```
 1.5995e-51
 1.60051e-51
 1.60147e-51
 1.60241e-51
 1.60249e-51
 2.56194e-51
 3.202e-51
 3.20435e-51
 3.2086e-51
 4.81768e-51
 7.6617e-51
 1.79756e-50
 3.23271e-50
 ⋮
 7.42531e-17
 7.43058e-17
 7.45843e-17
 7.8553e-17
 7.87587e-17
 7.91296e-17
 8.99596e-17
 9.59437e-17
 1.05193e-16
 1.11265e-16
 1.12735e-16
 1.13945e-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}:
```
 0.204333  1.82311  0.364222  1.95711  …  0.774667  1.80022  0.900333
```

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

Out[112]: 1x200 Array{Float64,2}:
```
 0.145  1.815  0.37  1.945  1.76  0.275  …  0.835  0.825  0.79  1.83  0.965
```

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

```
Out[113]: 1x200 Array{Float64,2}:
           0.155  1.78  0.48  1.945  1.71  0.265  …  0.805  0.805  0.805  1.83  0.99
```

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

```
Out[114]: 1x200 Array{Float64,2}:
           0.18  1.76  0.425  1.95  1.765  0.25  …  0.4  0.875  0.87  0.765  1.8  0.915
```

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

```
Out[115]: 1x200 Array{Float64,2}:
           0.18  1.805  0.38  1.94  1.755  0.185  …  0.39  0.91  0.905  0.77  1.8  0.87
```

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

```
Out[116]: 1x200 Array{Float64,2}:
           0.255  1.855  0.315  1.975  1.81  …  0.41  0.885  0.87  0.78  1.79  0.89
```

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

```
Out[117]: 1x200 Array{Float64,2}:
           0.207  1.82563  0.3605  1.95788  …  0.87625  0.77375  1.799  0.897125
```

```
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)
```