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/9
```

/home/nicole/Jupyter/JG3/Data/0.1/G/9

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

```
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.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      = 1.027
         vRes    = 9.251
         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
         2530.858409 seconds (23.04 G allocations: 723.689 GB, 7.59% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          10.8627
           3.56406
```

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

```
Out[33]: 3.5640606748882706
```

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

```
Out[34]: 7.213361943289827
```

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

```
Out[35]: 200-element Array{Float64,1}:
          -0.00864553
           0.0305794
           0.05325
           0.0626444
          -0.0419287
           0.0423973
           0.08259
           0.094932
          -0.00779665
           0.000326203
          -0.00261247
           0.126389
           0.0814335
           ⋮
           0.0564518
           0.0306266
          -0.000297119
           0.0264147
           0.124442
           0.0706786
          -0.0227194
          -0.0121777
          -0.0114169
           0.0281632
           0.00848515
           0.0347472
```

```
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 =  0.775
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.979
```

Out[39]: 0.7746374270928363

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

Out[40]: 12.248163125000001

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

Out[41]: 1.4058894359462641

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 =  1.138
```

Out[42]: 0.9389126616147441

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

Out[43]: 13.001277777777778

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

```
Out[44]: 2.227473616033014
```

```
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 =  0.710
         SSBRJC from Gibbs – noGenotype.ID  : regression of TBV on GEBV =  0.965
```

```
Out[45]: 0.7102950846028255
```

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

```
Out[46]: 12.074367435897438
```

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

```
Out[47]: 1.216293086695475
```

```
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 =  0.552
         SSBRJC from Gibbs – G0.ID : regression of TBV on GEBV =  1.308
```

```
Out[48]: 0.5522222678685083
```

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

Out[49]: 11.138523375000002

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

Out[50]: 0.13020863836157612

```
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 = 0.543
          SSBRJC from Gibbs – G1.ID : regression of TBV on GEBV = 1.071

Out[51]: 0.5432424816319715

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

Out[52]: 11.911574250000003

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

Out[53]: 1.0183958457456586

```
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 =   0.606
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.080
```

Out[54]: 0.6058953890481905

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

Out[55]: 12.185726250000004

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

Out[56]: 1.383266268349218

```
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 =   0.635
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.087
```

Out[57]: 0.6346922740971209

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

Out[58]: 12.490748875000003

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

Out[59]: 1.7014632076840062

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 =   0.685
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.113
```

Out[60]: 0.6853927998223465

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

Out[61]: 12.740078500000003

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

Out[62]: 1.9562969019932994

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 =   0.938
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.139
```

Out[63]: 0.9378387002467194

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

Out[64]: 13.022327500000003

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

Out[65]: 2.245705753543826

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 =  0.925
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.096
```

Out[66]: 0.9248364023511406

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

Out[67]: 12.65842

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

Out[68]: 1.9299283151737143

```
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 =  0.941
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.121
```

Out[69]: 0.9409570897899954

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

Out[70]: 12.442825000000003

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

Out[71]: 1.747466576189878

```
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 =  0.944
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.131
```

Out[72]: 0.9444698927638486

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

Out[73]: 12.764944999999996

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

Out[74]: 2.014277817808212

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 =  0.937
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.135
```

Out[75]: 0.9365853886734369

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

Out[76]: 12.96761

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

Out[77]: 2.21811253118973

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 =  0.940
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.128
```

Out[78]: 0.9399524492190146

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

Out[79]: 13.330599999999999

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

Out[80]: 2.498297339371069

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 = 0.938
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.139

Out[81]: 0.9378387002467194

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]: 13.022327500000003

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

Out[85]: 2.245705753543826

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 =  0.540
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.757
```

Out[86]: 0.540346867302086

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

Out[87]: 11.099551666666668

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

Out[88]: 0.0840619799817777

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 =  0.525
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.091
```

Out[89]: 0.5246937155132113

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

Out[90]: 11.89795243589744

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

Out[91]: 0.9997017244522169

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 =  0.591
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.083
```

Out[92]: 0.5905476569783948

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

Out[93]: 12.170874487179487

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

Out[94]: 1.3670864850297566

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 =  0.623
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.089
```

Out[95]: 0.6234800820040464

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

Out[96]: 12.478521666666667

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

Out[97]: 1.6882157891325775

In [98]:
```julia
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 =  0.673
SSBRJC from Gibbs – G4.noGenotype.ID : regression of TBV on GEBV =  1.113
```

Out[98]: 0.6733049357553925

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

Out[99]: 12.724936923076926

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

Out[100]: 1.9423994548810486

```
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]: 12.724936923076926

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

Out[103]: 1.9423994548810486

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

Out[104]: SSBR.NumSSBayes(54899,45899,9000,40000,39000,1000,200)

In [105]:   J_Vecs.J1

Out[105]: 45899x1 Array{Float64,2}:
            0.0
           -0.00117165
           -0.0435078
           -0.887988
           -0.503797
           -0.512924
           -0.188558
           -0.751902
           -0.751756
           -0.752038
           -0.00231423
           -0.753277
           -0.971223
            ⋮
           -0.878366
           -0.943867
           -0.962551
           -0.00117062
           -0.76992
           -0.751756
            1.30308e-19
           -0.962731
           -0.627419
           -0.898257
           -0.9232
           -0.00175748

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

Out[106]: 8001x1 Array{Float64,2}:
```
-0.986955
-0.986628
-0.985916
-0.985607
-0.984934
-0.981489
-0.9813
-0.981167
-0.980825
-0.97942
-0.979419
-0.979315
-0.979065
   ⋮
 4.46601e-17
 5.46502e-17
 5.55603e-17
 5.55626e-17
 5.55824e-17
 5.58089e-17
 5.63398e-17
 5.84496e-17
 6.09891e-17
 7.27244e-17
 8.87431e-17
 1.11022e-16
```

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

Out[107]: 45899x1 Array{Float64,2}:
          -1.04142
          -0.986977
          -0.986955
          -0.986628
          -0.985959
          -0.985916
          -0.985701
          -0.985696
          -0.985696
          -0.985607
          -0.985574
          -0.985554
          -0.985534
           ⋮
           8.86227e-17
           8.87431e-17
           8.88647e-17
           8.8963e-17
           9.96573e-17
           1.11022e-16
           1.11153e-16
           1.11157e-16
           1.1232e-16
           1.2086e-16
           1.44088e-16
           1.44428e-16

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

Out[108]: 43931x1 Array{Float64,2}:
    -1.04142
    -0.986977
    -0.986955
    -0.986628
    -0.985959
    -0.985916
    -0.985701
    -0.985696
    -0.985696
    -0.985607
    -0.985574
    -0.985554
    -0.985534
    ⋮
    -7.21238e-36
    -7.21238e-36
    -7.21238e-36
    -7.18419e-36
    -7.16814e-36
    -6.60363e-36
    -5.41483e-36
    -7.33705e-66
    -3.66852e-66
    -5.36633e-67
    -1.77851e-67
    -1.62792e-67

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

Out[109]: 1349x1 Array{Float64,2}:
```
 8.14576e-82
 7.3315e-52
 8.00969e-52
 1.20233e-51
 1.4663e-51
 1.59165e-51
 1.59521e-51
 1.60147e-51
 1.60147e-51
 1.60194e-51
 1.60429e-51
 2.41678e-51
 4.47899e-51
 ⋮
 8.86227e-17
 8.87431e-17
 8.88647e-17
 8.8963e-17
 9.96573e-17
 1.11022e-16
 1.11153e-16
 1.11157e-16
 1.1232e-16
 1.2086e-16
 1.44088e-16
 1.44428e-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}:
```
 0.0897778  1.59578  0.730222  1.91289  …  0.832  0.586667  1.79678  0.979556
```

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

Out[112]: 1x200 Array{Float64,2}:
```
 0.075  1.57  0.755  1.875  1.545  0.29  …  0.835  0.83  0.67  1.83  0.97
```

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

```
Out[113]: 1x200 Array{Float64,2}:
           0.085  1.575  0.73  1.87  1.56  0.29  …  0.32  0.86  0.845  0.59  1.84  0.99
```

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

```
Out[114]: 1x200 Array{Float64,2}:
           0.105  1.63  0.655  1.875  1.555  0.285  …  0.86  0.85  0.59  1.825  0.985
```

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

```
Out[115]: 1x200 Array{Float64,2}:
           0.055  1.585  0.755  1.91  1.555  0.305  …  0.825  0.815  0.61  1.78  1.005
```

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

```
Out[116]: 1x200 Array{Float64,2}:
           0.105  1.6  0.74  1.935  1.56  0.37  …  0.865  0.86  0.545  1.795  0.96
```

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

```
Out[117]: 1x200 Array{Float64,2}:
           0.090375  1.59625  0.730625  1.91538  …  0.831  0.584875  1.79463  0.97925
```

```
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)
```