```
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/0.3/G/8
```

```
/home/nicole/Jupyter/JG3/Data/0.3/G/8
```

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      = 0.831
vRes    = 1.939
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
3054.745566 seconds (23.06 G allocations: 724.240 GB, 6.80% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 10.9653
  5.33941
```

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

Out[33]: 5.3394148628293605

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

Out[34]: 8.152378192202818

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

```
Out[35]: 200-element Array{Float64,1}:
          0.142982
          0.0112911
         -0.00135372
          0.0386916
          0.0215603
          0.0417045
          0.159791
          0.158647
         -0.0120975
          0.0279607
          0.0375529
          0.0585821
         -0.0181687
          ⋮
          0.0194354
          0.0163442
         -0.0309043
          0.0119475
         -0.0256053
         -0.0146873
          0.0115287
         -0.000650724
         -0.00420629
         -0.0339584
          0.000169477
          0.146765
```

```
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 =  0.880
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.975
```

Out[39]: 0.8795158203149958

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

Out[40]: 12.5044101875

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

Out[41]: 1.558966726280974

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 =  0.975
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.037
```

Out[42]: 0.9747504996083712

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

Out[43]: 13.550216777777777

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

Out[44]: 2.6710770654686526

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 =   0.835
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.980
```

Out[45]: 0.8350066492879847

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

Out[46]: 12.263070205128205

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

Out[47]: 1.3023258787761252

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 =   0.706
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   1.177
```

Out[48]: 0.7058978099541356

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

Out[49]: 11.179765875

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

Out[50]: 0.12530320429660835

```
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 =  0.716
          SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.044
```

Out[51]: 0.7164531347125969

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

Out[52]: 11.834631500000002

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

Out[53]: 0.8709203851476135

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 =  0.697
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.014
```

Out[54]: 0.6968454137090548

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

Out[55]: 12.356289625

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

Out[56]: 1.4272337032070783

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 =  0.692
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.006
```

Out[57]: 0.6923734388796506

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

Out[58]: 12.831757875

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

Out[59]: 1.899876386790372

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 =   0.737
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.022
```

Out[60]: 0.7374623837346637

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

Out[61]: 13.233546875

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

Out[62]: 2.321197521237374

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 =   0.973
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.036
```

Out[63]: 0.9729400599007242

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

Out[64]: 13.590469375

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

Out[65]: 2.709269157006798

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 = 0.974
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.056

Out[66]: 0.9744812785441808

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

Out[67]: 12.449124999999997

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

Out[68]: 1.6293415745031308

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 =   0.974
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =   1.030
```

Out[69]: 0.9739918311808374

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

Out[70]: 12.845834999999997

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

Out[71]: 2.016546805184143

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 =   0.972
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.002
```

Out[72]: 0.972049546288055

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

Out[73]: 13.252125

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

Out[74]: 2.3804462295682565

```
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 =  0.971
         SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.054
```

Out[75]: 0.9707148160073508

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

Out[76]: 13.624974999999997

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

Out[77]: 2.7340452540172913

```
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 =  0.968
         SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.997
```

Out[78]: 0.9678254829687619

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

Out[79]: 13.968919999999999

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

Out[80]: 3.067321802544601

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 = 0.973
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.036

Out[81]: 0.9729400599007242

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]: 13.590469375

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

Out[85]: 2.709269157006798

In [86]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat1[posAi])[1,1]
reg14 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : correlation = %6.3f\n", cor14 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.689
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.267
```

Out[86]: 0.6885228328740267

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

Out[87]: 11.147218205128205

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

Out[88]: 0.08673811788105648

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 =  0.700
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.062
```

Out[89]: 0.6996214402531843

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

Out[90]: 11.808703205128204

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

Out[91]: 0.8415453487364204

```
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 = 0.681
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.020

Out[92]: 0.6811224717371493

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

Out[93]: 12.333319487179487

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

Out[94]: 1.4027923563773046

```
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 = 0.676
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.007

Out[95]: 0.6763425301079323

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

Out[96]: 12.811418974358974

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

Out[97]: 1.8784874414768613

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 =  0.726
SSBRJC from Gibbs – G4.noGenotype.ID : regression of TBV on GEBV =  1.024
```

Out[98]: 0.726151210867036

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

Out[99]: 13.214691153846154

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

Out[100]: 2.302066129408984

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]: 13.214691153846154

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

Out[103]: 2.302066129408984

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

Out[104]: SSBR.NumSSBayes(54939,45939,9000,40000,39000,1000,200)

In [105]: `J_Vecs.J1`

Out[105]: 45939x1 Array{Float64,2}:
           0.0
          -0.168179
          -0.897101
          -0.504094
          -0.512646
          -0.00117028
          -0.752193
          -0.752188
          -0.773032
          -0.00117376
          -0.752338
          -0.971289
          -0.512564
           ⋮
          -0.943794
          -0.972728
           0.0
          -0.791711
          -0.876229
           1.29707e-19
          -0.972832
          -0.609982
          -0.918231
          -0.878224
          -0.00233813
          -0.00159851

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

Out[106]: 8001x1 Array{Float64,2}:
            -0.985093
            -0.984565
            -0.984457
            -0.981384
            -0.981162
            -0.98101
            -0.980927
            -0.980883
            -0.980872
            -0.98085
            -0.979256
            -0.979238
            -0.97911
             ⋮
             5.54868e-17
             5.55599e-17
             5.55844e-17
             5.56411e-17
             5.57545e-17
             5.68523e-17
             6.40869e-17
             6.53653e-17
             6.61749e-17
             8.52751e-17
             8.87762e-17
             8.88231e-17

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

Out[107]: 45939x1 Array{Float64,2}:
          −0.988939
          −0.986116
          −0.985709
          −0.98564
          −0.985614
          −0.985479
          −0.985305
          −0.985093
          −0.984565
          −0.984457
          −0.984177
          −0.983774
          −0.983486
             ⋮
           7.41214e−17
           7.41582e−17
           7.42759e−17
           7.43696e−17
           7.44926e−17
           7.55633e−17
           8.52751e−17
           8.87762e−17
           8.88231e−17
           9.4e−17
           1.11122e−16
           1.11218e−16

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

Out[108]: 43943x1 Array{Float64,2}:
 -0.988939
 -0.986116
 -0.985709
 -0.98564
 -0.985614
 -0.985479
 -0.985305
 -0.985093
 -0.984565
 -0.984457
 -0.984177
 -0.983774
 -0.983486
  ⋮
 -1.42797e-35
 -1.41009e-35
 -1.38405e-35
 -1.38134e-35
 -1.35569e-35
 -1.15249e-35
 -7.22508e-36
 -7.22508e-36
 -7.20806e-36
 -7.17913e-36
 -6.77843e-36
 -1.74584e-50

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

```
Out[109]: 1290x1 Array{Float64,2}:
          1.50511e-51
          1.59409e-51
          1.60051e-51
          1.60429e-51
          1.60429e-51
          3.0672e-51
          4.80442e-51
          6.27295e-51
          9.93799e-51
          1.51194e-50
          1.68059e-50
          1.68067e-50
          1.82755e-50
          ⋮
          7.41214e-17
          7.41582e-17
          7.42759e-17
          7.43696e-17
          7.44926e-17
          7.55633e-17
          8.52751e-17
          8.87762e-17
          8.88231e-17
          9.4e-17
          1.11122e-16
          1.11218e-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}:
          0.256111  1.47967  0.657111  1.91844  1.77333  …  0.620778  1.82278  1.01733
```

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

```
Out[112]: 1x200 Array{Float64,2}:
          0.165  1.55  0.615  1.89  1.72  0.42  …  0.895  0.895  0.7  1.795  1.04
```

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

```
Out[113]: 1x200 Array{Float64,2}:
          0.205  1.55  0.65  1.935  1.735  0.515  …  0.89  0.895  0.645  1.82  1.055
```

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

```
Out[114]: 1x200 Array{Float64,2}:
          0.27  1.5  0.675  1.935  1.76  0.535  …  0.965  0.965  0.65  1.845  1.035
```

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

```
Out[115]: 1x200 Array{Float64,2}:
          0.29  1.47  0.63  1.925  1.795  0.635  …  0.39  0.95  0.95  0.615  1.8  1.04
```

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

```
Out[116]: 1x200 Array{Float64,2}:
          0.275  1.46  0.665  1.92  1.78  0.715  …  0.97  0.97  0.605  1.84  1.015
```

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

```
Out[117]: 1x200 Array{Float64,2}:
          0.258  1.47637  0.658375  1.91813  …  0.956  0.618  1.82313  1.01487
```

```
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)
```