```
In [1]:   include("/home/nicole/Jupyter/SSBRnoJ/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/0.1/G/2
```

```
/home/nicole/Jupyter/JG3/Data/0.1/G/2
```

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

```
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
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
         y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
         Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
         nothing
```

```
In [31]: vG     = 0.705
         vRes   = 6.350
         aHat3=SSBR.PBLUP(y_Vecs,Z_Mats,A_Mats,numSSBayes,vRes,vG);
```

```
In [32]: using DataFrames
```

```
In [33]: 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 [34]: IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor1 = cor(a[posAi],aHat3[posAi])[1,1]
         reg1 = linreg(aHat3[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 =  0.655
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.008
```

Out[34]: 0.6548065504419078

```
In [35]: TBV = a[posAi]
         mean(TBV)
```

Out[35]: 11.532842479166668

```
In [36]: EBV = aHat3[posAi]
         mean(EBV)
```

Out[36]: 0.7332519991184305

```
In [37]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor2 = cor(a[posAi],aHat3[posAi])[1,1]
         reg2 = linreg(aHat3[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 =  0.371
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.832
```

Out[37]: 0.370619375080398

In [38]:
```
TBV = a[posAi]
mean(TBV)
```

Out[38]: 12.12047388888889

In [39]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[39]: 1.3784610254913172

In [40]:
```
IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor3 = cor(a[posAi],aHat3[posAi])[1,1]
reg3 = linreg(aHat3[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 = 0.641
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.062

Out[40]: 0.6412559766603508

In [41]:
```
TBV = a[posAi]
mean(TBV)
```

Out[41]: 11.397235230769232

In [42]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[42]: 0.584357608416995

In [43]:
```
IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat3[posAi])[1,1]
reg4 = linreg(aHat3[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 =   0.571
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   1.781
```

Out[43]: 0.5711284508125735

In [44]:
```
TBV = a[posAi]
mean(TBV)
```

Out[44]: 10.65073

In [45]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[45]: 0.002707490636823605

In [46]:
```
IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat3[posAi])[1,1]
reg4 = linreg(aHat3[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 =   0.491
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.969
```

Out[46]: 0.4914351861057053

In [47]:
```
TBV = a[posAi]
mean(TBV)
```

Out[47]: 11.261764999999999

In [48]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[48]: 0.3460282699660859

In [49]:
```
IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor5 = cor(a[posAi],aHat3[posAi])[1,1]
reg5 = linreg(aHat3[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 =   0.527
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   0.984
```

Out[49]: 0.5270516936654034

In [50]:
```
TBV = a[posAi]
mean(TBV)
```

Out[50]: 11.491451625000002

In [51]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[51]: 0.6316576007245783

In [52]:
```
IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor6 = cor(a[posAi],aHat3[posAi])[1,1]
reg6 = linreg(aHat3[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 =   0.494
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.892
```

Out[52]: 0.493939238520827

```
In [53]: TBV = a[posAi]
         mean(TBV)
```

Out[53]: 11.69377025

```
In [54]: EBV = aHat3[posAi]
         mean(EBV)
```

Out[54]: 0.8679366035261232

```
In [55]: IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor7 = cor(a[posAi],aHat3[posAi])[1,1]
         reg7 = linreg(aHat3[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 =  0.453
         SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV =  0.840
```

Out[55]: 0.45299741185459885

```
In [56]: TBV = a[posAi]
         mean(TBV)
```

Out[56]: 11.964299125

```
In [57]: EBV = aHat3[posAi]
         mean(EBV)
```

Out[57]: 1.1446370165577775

In [58]:
```
IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat3[posAi])[1,1]
reg8 = linreg(aHat3[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 =  0.312
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.897
```

Out[58]: 0.3121476962706087

In [59]:
```
TBV = a[posAi]
mean(TBV)
```

Out[59]: 12.135038874999998

In [60]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[60]: 1.4065450132991937

In [61]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat3[posAi])[1,1]
reg9 = linreg(aHat3[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 =  0.723
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.906
```

Out[61]: 0.7234724843737522

In [62]:
```
TBV = a[posAi]
mean(TBV)
```

Out[62]: 11.856909999999997

```
In [63]: EBV = aHat3[posAi]
         mean(EBV)
```

Out[63]: 0.6530446660066612

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor9 = cor(a[posAi],aHat3[posAi])[1,1]
         reg9 = linreg(aHat3[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 =  0.774
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.003
```

Out[64]: 0.7741100661868769

```
In [65]: TBV = a[posAi]
         mean(TBV)
```

Out[65]: 11.74462

```
In [66]: EBV = aHat3[posAi]
         mean(EBV)
```

Out[66]: 0.918137962067501

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor10 = cor(a[posAi],aHat3[posAi])[1,1]
         reg10 = linreg(aHat3[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 =  0.719
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.849
```

Out[67]: 0.7185645377710624

In [68]:
```
TBV = a[posAi]
mean(TBV)
```

Out[68]: 11.890899999999998

In [69]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[69]: 1.1127177062961666

In [70]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor11 = cor(a[posAi],aHat3[posAi])[1,1]
reg11 = linreg(aHat3[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 =   0.660
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   0.824
```

Out[70]: 0.6603370356556623

In [71]:
```
TBV = a[posAi]
mean(TBV)
```

Out[71]: 12.230025000000003

In [72]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[72]: 1.425123668072474

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor12 = cor(a[posAi],aHat3[posAi])[1,1]
         reg12 = linreg(aHat3[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 =  0.426
         SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.905
```

Out[73]: 0.42556261401808154

```
In [74]: TBV = a[posAi]
         mean(TBV)
```

Out[74]: 12.297315

```
In [75]: EBV = aHat3[posAi]
         mean(EBV)
```

Out[75]: 1.6599216126987155

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor13 = cor(a[posAi],aHat3[posAi])[1,1]
         reg13 = linreg(aHat3[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 =  0.312
         SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.897
```

Out[76]: 0.3121476962706087

```
In [77]: writedlm("Correlation.G5.G.PBLUP.txt",cor13)
```

```
In [78]: writedlm("Regression.G5.G.PBLUP.txt",reg13)
```

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

Out[79]: 12.135038874999998

In [80]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[80]: 1.4065450132991937

In [81]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat3[posAi])[1,1]
reg14 = linreg(aHat3[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 =  0.543
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.893
```

Out[81]: 0.5426262567786088

In [82]:
```
TBV = a[posAi]
mean(TBV)
```

Out[82]: 10.619802307692307

In [83]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[83]: -0.013967821552146596

In [84]:
```
IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat3[posAi])[1,1]
reg14 = linreg(aHat3[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 =  0.476
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.975
```

Out[84]: 0.47566846204912144

In [85]:
```
TBV = a[posAi]
mean(TBV)
```

Out[85]: 11.249384102564102

In [86]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[86]: 0.33135879068143426

In [87]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor15 = cor(a[posAi],aHat3[posAi])[1,1]
reg15 = linreg(aHat3[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 =  0.518
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.996
```

Out[87]: 0.5183997001068605

In [88]:
```
TBV = a[posAi]
mean(TBV)
```

Out[88]: 11.48120935897436

In [89]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[89]: 0.6193227262227426

In [90]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor16 = cor(a[posAi],aHat3[posAi])[1,1]
reg16 = linreg(aHat3[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 =  0.480
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.892
```

Out[90]: 0.4803387072219058

In [91]:
```
TBV = a[posAi]
mean(TBV)
```

Out[91]: 11.680020128205127

In [92]:
```
EBV = aHat3[posAi]
mean(EBV)
```

Out[92]: 0.8536497557172424

In [93]:
```
IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor17 = cor(a[posAi],aHat3[posAi])[1,1]
reg17 = linreg(aHat3[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 =  0.450
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.847
```

Out[93]: 0.4496373477308202

```
In [94]: TBV = a[posAi]
         mean(TBV)
```

Out[94]: 11.955760256410256

```
In [95]: EBV = aHat3[posAi]
         mean(EBV)
```

Out[95]: 1.1314245910157021

```
In [96]: numSSBayes
```

Out[96]: SSBR.NumSSBayes(54914,45914,9000,40000,39000,1000,0)