```
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/5
```

```
/home/nicole/Jupyter/JG3/Data/0.1/G/5
```

```
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     = 0.872
         vRes   = 7.848
         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 =  0.665
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.026
```

Out[34]: 0.6654131323778678

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

Out[35]: 12.021351125

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

Out[36]: 0.7944545858306331

```
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 =  0.417
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.900
```

Out[37]: 0.4169044505538227

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

Out[38]: 12.704885333333333

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

Out[39]: 1.5266133932071357

```
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 =  0.648
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.076
```

Out[40]: 0.6475004113445585

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

Out[41]: 11.863612461538462

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

Out[42]: 0.6254948610514403

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 =   0.577
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   1.858
```

Out[43]: 0.576826728243708

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

Out[44]: 11.057711750000003

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

Out[45]: 0.0003567903096852009

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 =   0.487
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.948
```

Out[46]: 0.4869908445585463

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

Out[47]: 11.6935705

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

Out[48]: 0.34827929725787454

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 =   0.507
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   0.939
```

Out[49]: 0.5068493590490303

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

Out[50]: 11.94432025

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

Out[51]: 0.6622469387544497

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 =   0.557
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.006
```

Out[52]: 0.5565291563692225

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

Out[53]: 12.217771250000002

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

Out[54]: 0.9476413202945403

```
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 = 0.524
          SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV = 0.950

Out[55]: 0.5243128639419062

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

Out[56]: 12.489685875

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

Out[57]: 1.2480996088331544

```
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 =  0.350
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.959
```

Out[58]: 0.3496945738390492

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

Out[59]: 12.725047124999998

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

Out[60]: 1.560103559534095

```
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 =  0.715
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.831
```

Out[61]: 0.7154509721404695

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

Out[62]: 12.315005000000001

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

Out[63]: 0.6700022432108531

```
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 =  0.752
          SSBRJC from Gibbs – G1.Genotype.ID : regression of TBV on GEBV =  0.944
```

Out[64]: 0.7519224386971107

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

Out[65]: 12.191195000000002

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

Out[66]: 0.962924452630234

```
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 =  0.810
          SSBRJC from Gibbs – G2.Genotype.ID : regression of TBV on GEBV =  1.060
```

Out[67]: 0.809995572879607

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

Out[68]: 12.469374999999998

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

Out[69]: 1.2351562459697467

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 =  0.782
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.998
```

Out[70]: 0.7818983417148903

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

Out[71]: 12.78123

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

Out[72]: 1.5511796251061392

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 =  0.474
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.946
```

Out[73]: 0.47375907061513034

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

Out[74]: 12.961149999999998

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

Out[75]: 1.8741977460403447

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 =  0.350
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.959
```

Out[76]: 0.3496945738390492

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]: 12.725047124999998

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

Out[80]: 1.560103559534095

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 =  0.558
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  2.022
```

Out[81]: 0.5583723017314023

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

Out[82]: 11.025473461538466

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

Out[83]: -0.016813605918549877

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 =  0.473
SSBRJC from Gibbs – G1.noGenotype.ID : regression of TBV on GEBV =  0.956
```

Out[84]: 0.47265743454804765

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

Out[85]: 11.680810897435897

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

Out[86]: 0.3325191650688396

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 =  0.489
SSBRJC from Gibbs – G2.noGenotype.ID : regression of TBV on GEBV =  0.932
```

Out[87]: 0.48863140991493315

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

Out[88]: 11.930857307692309

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

Out[89]: 0.64755695651816

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 =   0.544
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =   1.009
```

Out[90]: 0.5444042118296459

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

Out[91]: 12.20332358974359

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

Out[92]: 0.9321659791455248

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 =   0.521
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   0.959
```

Out[93]: 0.520611616883218

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

Out[94]: 12.477597051282052

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

Out[95]: 1.2320458104432268

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

Out[96]: SSBR.NumSSBayes(54874,45874,9000,40000,39000,1000,0)