```
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/0.3/G/2
```

```
/home/nicole/Jupyter/JG3/Data/0.3/G/2
```

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

```
Correlation.G5.G.C.txt
Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.N.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.C.txt
Regression.G5.G.J.txt
Regression.G5.G.JC.txt
Regression.G5.G.N.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
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
nothing
```

In [31]:
```
vG      = 0.731
vRes    = 1.706
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 =  0.814
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.981
```

Out[34]: 0.8136292457972425

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

Out[35]: 12.347678479166667

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

Out[36]: 1.0865877740217493

```
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 =  0.460
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.843
```

Out[37]: 0.4601885500047226

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

Out[38]: 13.24399111111111

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

Out[39]: 2.0359804385288975

```
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 =  0.796
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.004
```

Out[40]: 0.7955493006018552

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

Out[41]: 12.140837102564102

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

Out[42]: 0.8674971591354844

```
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 = 0.693
          SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.222

Out[43]: 0.6932526656300552

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

Out[44]: 11.238509625

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

Out[45]: -0.0015907410096458

```
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 =  0.672
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.984
```

Out[46]: 0.6718957632411496

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

Out[47]: 11.813502

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

Out[48]: 0.5090691580135336

```
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 =  0.663
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.961
```

Out[49]: 0.6628459942525847

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

Out[50]: 12.230377375000002

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

Out[51]: 0.9490930565415064

```
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 =   0.632
          SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.934

Out[52]: 0.6319106812031616

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

Out[53]: 12.594595625

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

Out[54]: 1.3238367643948081

```
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 =   0.596
          SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   0.867

Out[55]: 0.5959505386016802

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

Out[56]: 12.932307125

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

Out[57]: 1.6630609028118506

```
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 =  0.339
         SSBRJC from Gibbs – G5.ID : regression of TBV on GEBV =  0.807
```

Out[58]: 0.33921580783632344

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

Out[59]: 13.276779125000001

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

Out[60]: 2.0760575033784434

```
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 =  0.837
         SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.942
```

Out[61]: 0.8372777692106419

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

Out[62]: 12.406154999999998

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

Out[63]: 0.9993524706953939

```
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 =  0.873
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.018
```

Out[64]: 0.8727435381629977

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

Out[65]: 12.63826

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

Out[66]: 1.3864372712744397

```
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 =  0.834
         SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.034
```

Out[67]: 0.8344204780773031

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

Out[68]: 12.992820000000002

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

Out[69]: 1.7088471008814494

```
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 =  0.798
         SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.873
```

Out[70]: 0.798060119598914

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

Out[71]: 13.258989999999999

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

Out[72]: 1.997198711066258

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 =  0.379
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.724
```

Out[73]: 0.37891893347567085

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

Out[74]: 13.612210000000005

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

Out[75]: 2.484984044745119

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 =   0.339
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   0.807
```

Out[76]: 0.33921580783632344

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]: 13.276779125000001

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

Out[80]: 2.0760575033784434

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 =   0.672
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   1.240
```

Out[81]: 0.6723126292222221

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

Out[82]: 11.20857

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

Out[83]: -0.027255951566185276

```
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 =  0.655
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.987
```

Out[84]: 0.6553828484874605

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

Out[85]: 11.79235435897436

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

Out[86]: 0.4865725397247925

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 =   0.648
SSBRJC from Gibbs – G2.noGenotype.ID : regression of TBV on GEBV =   0.957
```

Out[87]: 0.6475981006911736

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

Out[88]: 12.210827564102566

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

Out[89]: 0.9296121836097131

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 =   0.618
SSBRJC from Gibbs – G3.noGenotype.ID : regression of TBV on GEBV =   0.933
```

Out[90]: 0.6178516238130365

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

Out[91]: 12.577559871794872

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

Out[92]: 1.3065710734545144

```
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 =  0.585
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.872
```

Out[93]: 0.5852049843080149

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

Out[94]: 12.91487371794872

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

Out[95]: 1.6419859504545875

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

Out[96]: SSBR.NumSSBayes(54934,45934,9000,40000,39000,1000,0)