```
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/8
```

/home/nicole/Jupyter/JG3/Data/0.1/G/8

```
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    = 0.584
         vRes  = 5.259
         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 =  0.677
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.053
```

Out[34]: 0.6771679720410126

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

Out[35]: 10.476803083333333

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

Out[36]: 0.6852249421552665

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 =  0.408
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.954
```

Out[37]: 0.40819601375604353

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

Out[38]: 11.115723222222222

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

Out[39]: 1.3129256434440375

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 =  0.657
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.076
```

Out[40]: 0.6571226518198615

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

Out[41]: 10.329359974358974

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

Out[42]: 0.5403709341655502

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 =   0.559
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =   1.709
```

Out[43]: 0.5586605959255406

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

Out[44]: 9.66376525

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

Out[45]: 0.0016956368102155701

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 =   0.528
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.995
```

Out[46]: 0.5277314256324311

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

Out[47]: 10.160527499999999

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

Out[48]: 0.27433934118303643

```
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 =   0.526
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   0.971

Out[49]: 0.5256986624619121

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

Out[50]: 10.374001375

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

Out[51]: 0.5640044788415086

```
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 =   0.558
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.034

Out[52]: 0.5579641066003176

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

Out[53]: 10.638668000000001

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

Out[54]: 0.8378391827020936

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 =  0.537
SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV =  1.082
```

Out[55]: 0.5369348072475338

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

Out[56]: 10.886312875

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

Out[57]: 1.0918658371552326

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 =   0.332
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.995
```

Out[58]: 0.331620316013532

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

Out[59]: 11.137543500000001

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

Out[60]: 1.341605176239512

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 =   0.775
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =   0.899
```

Out[61]: 0.774586277720948

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

Out[62]: 10.648155

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

Out[63]: 0.5335741452885593

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 = 0.802
SSBRJC from Gibbs – G1.Genotype.ID : regression of TBV on GEBV = 0.973

Out[64]: 0.8017689479569426

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

Out[65]: 10.596925

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

Out[66]: 0.8576570977278961

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 = 0.795
SSBRJC from Gibbs – G2.Genotype.ID : regression of TBV on GEBV = 1.048

Out[67]: 0.7951150138021333

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

Out[68]: 10.925364999999998

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

Out[69]: 1.097885530654935

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 =  0.764
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.086
```

Out[70]: 0.7644300475559737

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

Out[71]: 11.14334

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

Out[72]: 1.343038423708684

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 =  0.475
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.047
```

Out[73]: 0.47540733349618464

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

Out[74]: 11.392020000000002

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

Out[75]: 1.5852917080211242

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 =  0.332
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.995
```

Out[76]: 0.331620316013532

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]: 11.137543500000001

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

Out[80]: 1.341605176239512

```
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 =  0.535
         SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.834
```

Out[81]: 0.535408617874801

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

Out[82]: 9.638524487179488

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

Out[83]: -0.011942273663588118

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 =  0.515
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.011
```

Out[84]: 0.5152139920436628

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

Out[85]: 10.14933782051282

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

Out[86]: 0.2593824756306041

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 =  0.507
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.964
```

Out[87]: 0.5072713971629191

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

Out[88]: 10.35986384615385

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

Out[89]: 0.5503152211027029

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 =  1.033
```

Out[90]: 0.5444716402819496

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

Out[91]: 10.625727692307693

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

Out[92]: 0.824885356009617

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 =  0.531
SSBRJC from Gibbs – G4.noGenotype.ID : regression of TBV on GEBV =  1.086
```

Out[93]: 0.531195526390873

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

Out[94]: 10.873346025641025

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

Out[95]: 1.0792138917484149

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

Out[96]: SSBR.NumSSBayes(54898,45898,9000,40000,39000,1000,0)