```
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/4
```

/home/nicole/Jupyter/JG3/Data/0.1/G/4

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

```
Correlation.G5.G.C.txt
Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.N.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
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 G
```
```
 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
```

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

In [31]:
```
vRes    = 0.871
vG      = 7.839
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 = ' ',head
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
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
JCAll = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.485
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.210
```

Out[34]: 0.48514850111829694

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

Out[35]: 10.450745875

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

Out[36]: 1.4560282550790429

```
In [37]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header
         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 ) # 
         @printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3
         JCAll = cor2
```

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.234
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.149
```

Out[37]: 0.23436021776870444

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

Out[38]: 11.171621444444444

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

Out[39]: 4.190585175150528

```
In [40]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
         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 ) 
         @printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV = %6
         JCAll = cor3
```

```
         SSBRJC from Gibbs - noGenotype.ID : correlation =  0.411
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.192
```

Out[40]: 0.4107158611628223

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

Out[41]: 10.284389974358973

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

Out[42]: 0.8249766581394693

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 e
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =   0.696
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.555
```

Out[43]: 0.6960357620643675

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

Out[44]: 9.452027

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

Out[45]: 0.0007354386117282612

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 e
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =   0.312
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.122
```

Out[46]: 0.31219708008397856

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

Out[47]: 10.110348125

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

Out[48]: 0.553176427899261

```
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 e
         @printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", r
         JCAll = cor5
```

```
         SSBRJC from Gibbs - G2.ID : correlation =   0.322
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   0.125
```

Out[49]: 0.3218239192939809

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

Out[50]: 10.389132875000001

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

Out[51]: 0.9873078090984532

```
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 e
         @printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", r
         JCAll = cor6
```

```
         SSBRJC from Gibbs - G3.ID : correlation =   0.317
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.120
```

Out[52]: 0.3167103336735439

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

Out[53]: 10.644380375

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

Out[54]: 1.2625339090226324

```
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 e
         @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =   0.322
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   0.117
```

Out[55]: 0.32156672570372796

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

Out[56]: 10.913760875

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

Out[57]: 1.674883397895851

```
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 e
         @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.185
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.126
```

Out[58]: 0.1849437739564974

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

Out[59]: 11.194825999999999

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

Out[60]: 4.257532547946331

```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         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 )
         @printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.582
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.609
```

Out[61]: 0.5823936210533236

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

Out[62]: 10.763530000000001

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

Out[63]: 1.5814336945026495

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         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 )
         @printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6
         JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.619
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.558
```

Out[64]: 0.6188972493680428

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

Out[65]: 10.638454999999997

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

Out[66]: 2.94020121842501

In [67]:
```
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.602
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.543
```

Out[67]: 0.6021194765439356

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

Out[68]: 10.915555

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

Out[69]: 3.2660477736032902

In [70]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.642
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.602
```

Out[70]: 0.6424758986604978

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

Out[71]: 11.159884999999997

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

Out[72]: 3.6589282430010615

In [73]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =   0.235
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.229
```

Out[73]: 0.23543281106467534

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

Out[74]: 11.4525

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

Out[75]: 6.828420034388545

In [76]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =   0.185
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   0.126
```

Out[76]: 0.1849437739564974

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]: 11.194825999999999

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

Out[80]: 4.257532547946331

In [81]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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", cor1
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.682
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.541
```

Out[81]: 0.6819416643057913

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

Out[82]: 9.418398717948719

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

Out[83]: −0.03979528589829537

In [84]:
```
IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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", cor1
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.300
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.117
```

Out[84]: 0.2997237192251827

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

Out[85]: 10.096806923076924

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

Out[86]: 0.4919706403962647

In [87]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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", cor1!
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = '
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.310
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.120
```

Out[87]: 0.31028892021973914

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

Out[88]: 10.375634871794873

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

Out[89]: 0.9288785792393547

In [90]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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", cor1(
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = '
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.304
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.116
```

Out[90]: 0.3044357284007

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

Out[91]: 10.631162307692307

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

Out[92]: 1.201087900459083

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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", cor1
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 
         JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.311
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.118
```

Out[93]: 0.3107504237121776

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

Out[94]: 10.899947051282052

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

Out[95]: 1.5427414328575773

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

Out[96]: SSBR.NumSSBayes(54893,45893,9000,40000,39000,1000,0)