```
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/1
```

```
         /home/nicole/Jupyter/JG3/Data/0.3/G/1
```

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

```
         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.JC.txt
         Regression.G5.G.N.txt
         all.ID
         genotype.ID
         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",calculateInbreedir
         nothing
         y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
         Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
         nothing
```

```
In [31]: vRes    = 1.405
         vG      = 0.602
         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 c
         @printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
         JCAll = cor1

        SSBRJC from Gibbs - all.ID : correlation =  0.823
        SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.997
```

Out[34]: 0.8231274450122179

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

Out[35]: 11.204598604166668

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

Out[36]: 1.0342479651757412

```
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 ) # u
         @printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3:
         JCAll = cor2
```

```
         SSBRJC from Gibbs - genotype.ID : correlation =   0.513
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   0.960
```

Out[37]: 0.5128056350268517

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

Out[38]: 12.134408888888888

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

Out[39]: 2.0005151781377744

```
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 =   0.803
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   1.016
```

Out[40]: 0.803240726373825

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

Out[41]: 10.990027000000001

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

Out[42]: 0.8112632237229644

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 =  0.671
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.161
```

Out[43]: 0.6714913218773987

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

Out[44]: 10.16234475

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

Out[45]: 0.0030431780746628958

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 =  0.680
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.041
```

Out[46]: 0.6802185058360255

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

Out[47]: 10.63602175

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

Out[48]: 0.437733963290391

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

```
SSBRJC from Gibbs - G2.ID : correlation =   0.673
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.015
```

Out[49]: 0.6726107999698935

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

Out[50]: 11.01344775

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

Out[51]: 0.8309475840959759

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

```
SSBRJC from Gibbs - G3.ID : correlation =   0.670
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.999
```

Out[52]: 0.6704093282769289

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

Out[53]: 11.427672249999999

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

Out[54]: 1.244776202140067

```
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 =   0.635
          SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.956
```

Out[55]: 0.6348363371624534

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

Out[56]: 11.812994499999999

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

Out[57]: 1.643943946863036

```
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 =   0.393
          SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.975
```

Out[58]: 0.3931979224973303

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

Out[59]: 12.175110624999999

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

Out[60]: 2.045042916590315

```
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 =  0.845
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.025
```

Out[61]: 0.8450460908285522

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

Out[62]: 11.108905

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

Out[63]: 0.8657007452008889

```
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 =  0.843
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.996
```

Out[64]: 0.8426979922511936

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

Out[65]: 11.386879999999996

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

Out[66]: 1.2218228912604499

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 =  0.850
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.965
```

Out[67]: 0.8498293536180686

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

Out[68]: 11.794975

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

Out[69]: 1.6508130251064312

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 =  0.846
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.974
```

Out[70]: 0.8457567725893791

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

Out[71]: 12.206025

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

Out[72]: 2.0367580884333303

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 =  0.514
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.968
```

Out[73]: 0.5138975862444392

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

Out[74]: 12.547189999999999

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

Out[75]: 2.4463716025861633

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 =  0.393
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.975
```

Out[76]: 0.3931979224973303

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]: 12.175110624999999

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

Out[80]: 2.045042916590315

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", cor14
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.651
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.174
```

Out[81]: 0.6514537647102134

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

Out[82]: 10.138073974358976

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

Out[83]: −0.019076246723445472

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", cor14
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.666
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.049
```

Out[84]: 0.6662500112108529

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

Out[85]: 10.616768974358976

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

Out[86]: 0.41762911898346644

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", cor15
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =   0.657
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   1.021
```

Out[87]: 0.6569223039689391

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

Out[88]: 10.993408589743588

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

Out[89]: 0.809925393300836

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", cor16
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =   0.653
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =   1.001
```

Out[90]: 0.6529527840692406

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

Out[91]: 11.407714487179486

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

Out[92]: 1.2244689742863935

```
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 =  0.624
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.960
```

Out[93]: 0.6235511580981267

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

Out[94]: 11.794168974358971

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

Out[95]: 1.6233688787675713

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

Out[96]: SSBR.NumSSBayes(54925,45925,9000,40000,39000,1000,0)