In [1]:
```julia
include("/home/nicole/Jupyter/SSBRnoJ/src/SSBR.jl")
using SSBR
```

In [2]:
```julia
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]:
```julia
; cd Data/0.5/G/6
```

/home/nicole/Jupyter/JG3/Data/0.5/G/6

```
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 (

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

```
In [31]: vRes    = 0.912
         vG      = 0.912
         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 =  0.887
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.977
```

Out[34]: 0.8874110503252064

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

Out[35]: 10.199740145833333

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

Out[36]: 1.5251149353656235

```
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 =  0.560
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.935
```

Out[37]: 0.559948484173743

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

Out[38]: 11.505419444444444

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

Out[39]: 2.8925493565749867

```
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 =  0.874
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.990
```

Out[40]: 0.8738312866017834

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

Out[41]: 9.898429538461539

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

Out[42]: 1.2095531458557702

```
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 =  0.732
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.962
```

Out[43]: 0.7323531978729594

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

Out[44]: 8.683999375

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

Out[45]: 0.005556015522373465

```
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 =  0.766
         SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.989
```

Out[46]: 0.7658380411017554

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

Out[47]: 9.382714874999998

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

Out[48]: 0.6890557447239849

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", re
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.766
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.989
```

Out[49]: 0.7658992534211417

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

Out[50]: 9.982135999999997

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

Out[51]: 1.289869786297254

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", re
JCAll = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.753
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.973
```

Out[52]: 0.753231796413395

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

Out[53]: 10.526489125

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

Out[54]: 1.837667278547946

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

```
         SSBRJC from Gibbs - G4.ID : correlation =  0.716
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.920
```

Out[55]: 0.7158789136901965

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

Out[56]: 11.062736000000001

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

Out[57]: 2.3780148931718204

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

```
         SSBRJC from Gibbs - G5.ID : correlation =  0.409
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.911
```

Out[58]: 0.40944131973243164

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

Out[59]: 11.560365500000001

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

Out[60]: 2.950525893930361

```
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 =  0.906
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.049
```

Out[61]: 0.9063060736702027

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

Out[62]: 10.039674999999999

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

Out[63]: 1.377070751422532

```
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 =  0.872
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.011
```

Out[64]: 0.8720636545138885

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

Out[65]: 10.57286

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

Out[66]: 1.8947013573209528

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 =  0.904
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.037
```

Out[67]: 0.9035665031322626

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

Out[68]: 11.076469999999999

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

Out[69]: 2.3971575515613135

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 =  0.842
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.902
```

Out[70]: 0.8417749949604869

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

Out[71]: 11.597399999999999

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

Out[72]: 2.9425813857440613

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 =   0.417
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.809
```

Out[73]: 0.41723115322474985

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

Out[74]: 12.042850000000001

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

Out[75]: 3.532174242611098

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 =   0.409
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   0.911
```

Out[76]: 0.40944131973243164

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]: 11.560365500000001

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

Out[80]: 2.950525893930361

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 = !
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.712
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.957
```

Out[81]: 0.7115960805745596

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

Out[82]: 8.649238461538461

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

Out[83]: −0.029611028987887016

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 = !
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.750
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.988
```

Out[84]: 0.7504180273999741

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

Out[85]: 9.352198333333334

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

Out[86]: 0.6581417546573959

```
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 =   0.752
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   0.988
```

Out[87]: 0.751785666891681

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

Out[88]: 9.954076153846152

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

Out[89]: 1.2614777923161242

```
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 =   0.739
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =   0.975
```

Out[90]: 0.7394274270641495

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

Out[91]: 10.499029871794875

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

Out[92]: 1.8093361475941991

```
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 =   0.705
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   0.928
```

Out[93]: 0.7050976011130451

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

Out[94]: 11.037604871794871

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

Out[95]: 2.348421063699019

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

Out[96]: SSBR.NumSSBayes(54914,45914,9000,40000,39000,1000,0)