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/M/8
```

/home/nicole/Jupyter/JG3/Data/0.5/M/8

In [4]: `;ls`

```
Correlation.G5.M.C.txt
Correlation.G5.M.J.txt
Correlation.G5.M.JC.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
MarNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C.txt
Regression.G5.M.J.txt
Regression.G5.M.JC.txt
all.ID
alphaEstimatesC
alphaEstimatesJ
alphaEstimatesJC
epsiEstimatesC
epsiEstimatesJ
epsiEstimatesJC
genotype.ID
meanOfSNPMAll
meanOfSNPMG0
meanOfSNPMG1
meanOfSNPMG2
meanOfSNPMG3
meanOfSNPMG4
meanOfSNPMG5
noGenotype.ID
sim.bv
sim.phenotype
```

In [5]: `;awk '{print $1}' PedAll.txt | sort -b > all.ID`

In [6]: `;awk '{print $1}' MarNF.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",calculateInbreedin
         nothing
         df      = read_genotypes("MarNF.txt",numSSBayes)
         M_Mats = make_MMats(df,A_Mats,ped);                              # with
         y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes);
         Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
         X_Mats, W_Mats = make_XWMats(Z_Mats,M_Mats,numSSBayes)          # no
         nothing
```

```
In [31]: vRes   = 0.627
         vG     = 0.627
         nIter  = 50000
         @time aHat1,alphaHat,betaHat,epsiHat =
         ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter,
         nothing
```

```
        This is iteration 5000
        This is iteration 10000
        This is iteration 15000
        This is iteration 20000
        This is iteration 25000
        This is iteration 30000
        This is iteration 35000
        This is iteration 40000
        This is iteration 45000
        This is iteration 50000
        2346.534382 seconds (23.06 G allocations: 724.302 GB, 7.72% gc time)
```

```
In [32]: betaHat
```

```
Out[32]: 1-element Array{Float64,1}:
          9.74843
```

```
In [33]: alphaHat
```

```
Out[33]: 150-element Array{Float64,1}:
          0.0393003
         -0.0602824
         -0.0408026
          0.110512
         -0.0362045
          0.238743
         -0.220963
         -0.0493724
          0.0971384
         -0.022809
         -0.0317123
          0.0242011
          0.0449498
          ⋮
          0.0174452
          0.116284
          0.0553401
         -0.129857
         -0.0440287
          0.112198
          0.00406022
          0.0892276
         -0.0677271
         -0.0168545
         -0.0645819
          0.019636
```

```
In [34]: writedlm("alphaEstimatesN",alphaHat)
```

In [35]: `epsiHat`

Out[35]: 45971-element Array{Float64,1}:
```
   0.0148412
   0.524518
  -0.259009
   0.0194983
  -0.432002
  -0.567165
   0.169841
  -0.617147
  -0.00476548
  -0.750035
   0.285758
   0.435914
  -0.128092
   ⋮
   0.11051
   0.211233
  -0.536037
   0.121553
  -0.230616
   0.350356
  -0.206178
   0.332375
   0.0815422
  -0.396854
  -0.111287
  -0.394874
```

In [36]: `writedlm("epsiEstimatesN",epsiHat)`

In [37]: **using** `DataFrames`

In [38]:
```julia
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 [39]:
```julia
IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor1 = cor(a[posAi],aHat1[posAi])[1,1]
reg1 = linreg(aHat1[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 =  0.899
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.987
```

Out[39]: 0.8994185288229136

```
In [40]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[40]: 1.3882284938957

```
In [41]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=
         posAi = getPos(ped,IDs)
         cor2 = cor(a[posAi],aHat1[posAi])[1,1]
         reg2 = linreg(aHat1[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 =  0.844
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.966
```

Out[41]: 0.8443343118986067

```
In [42]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[42]: 2.438541892723576

```
In [43]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
         posAi = getPos(ped,IDs)
         cor3 = cor(a[posAi],aHat1[posAi])[1,1]
         reg3 = linreg(aHat1[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 =  0.867
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.960
```

Out[43]: 0.8672243181044066

```
In [44]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[44]: 1.1458484787815748

```
In [45]: IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false
         posAi = getPos(ped,IDs)
         cor4 = cor(a[posAi],aHat1[posAi])[1,1]
         reg4 = linreg(aHat1[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 =  0.694
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.835
```

Out[45]: 0.6937853301243453

```
In [46]:  GEBV = aHat1[posAi]
          G1GEBV=mean(GEBV)
```

Out[46]: 0.1123463117044741

```
In [47]:  IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=false
          posAi = getPos(ped,IDs)
          cor4 = cor(a[posAi],aHat1[posAi])[1,1]
          reg4 = linreg(aHat1[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 =   0.760
          SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   0.975
```

Out[47]: 0.7597102402678484

```
In [48]:  GEBV = aHat1[posAi]
          G1GEBV=mean(GEBV)
```

Out[48]: 0.7256313480906004

```
In [49]:  IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=false
          posAi = getPos(ped,IDs)
          cor5 = cor(a[posAi],aHat1[posAi])[1,1]
          reg5 = linreg(aHat1[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 =   0.760
          SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.014
```

Out[49]: 0.7604362562313545

```
In [50]:  GEBV = aHat1[posAi]
          G2GEBV=mean(GEBV)
```

Out[50]: 1.2331010829572917

```
In [51]:  IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=false
          posAi = getPos(ped,IDs)
          cor6 = cor(a[posAi],aHat1[posAi])[1,1]
          reg6 = linreg(aHat1[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 =   0.758
          SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   0.993
```

Out[51]: 0.7580697551956522

In [52]:
```
GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

Out[52]: 1.6810386038236624

In [53]:
```
IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat1[posAi])[1,1]
reg7 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.ID : correlation = %6.3f\n", cor7 ) # with ei
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =   0.760
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.998
```

Out[53]: 0.7599881301296156

In [54]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[54]: 2.1007640311759186

In [55]:
```
IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat1[posAi])[1,1]
reg8 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.ID : correlation = %6.3f\n", cor8 ) # with ei
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.821
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.924
```

Out[55]: 0.8211763438935322

In [56]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[56]: 2.4764895856222524

In [57]:
```
GEBVG5G1=G5GEBV-G1GEBV
```

Out[57]: 1.7508582375316522

In [58]:
```
GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]
```

Out[58]:
```
5-element Array{Float64,1}:
 0.725631
 1.2331
 1.68104
 2.10076
 2.47649
```

In [59]:
```
reg8 = linreg(aHat1[posAi], a[posAi])
```

Out[59]:
```
2-element Array{Float64,1}:
  10.0218
   0.923817
```

In [60]:
```
VarGEBV=var(aHat1[posAi])
```

Out[60]: `0.2984589246058511`

In [61]:
```
VarTBV=var(a[posAi])
```

Out[61]: `0.3777318285763221`

In [62]:
```
Cov=cov(aHat1[posAi], a[posAi])
```

Out[62]: `0.27572141926369326`

In [63]:
```
b=Cov/VarGEBV
```

Out[63]: `0.9238169695471988`

In [64]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
#TBV = a[posAi]
#GEBV = aHat1[posAi]
#reg = linreg(X,Y)
#reg = linreg(GEBV, TBV)[2,1]
reg9 = linreg(aHat1[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 =  0.848
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.957
```

Out[64]: `0.8480781183621401`

In [65]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[65]: `1.4112837992695069`

```
In [66]:  IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
          posAi = getPos(ped,IDs)
          cor9 = cor(a[posAi],aHat1[posAi])[1,1]
          #TBV = a[posAi]
          #GEBV = aHat1[posAi]
          #reg = linreg(X,Y)
          #reg = linreg(GEBV, TBV)[2,1]
          reg9 = linreg(aHat1[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 =  0.838
          SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.939
```

Out[66]: 0.8380930468652116

```
In [67]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[67]: 1.8169171310547665

```
In [68]:  IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
          posAi = getPos(ped,IDs)
          cor10 = cor(a[posAi],aHat1[posAi])[1,1]
          reg10 = linreg(aHat1[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 =  0.853
          SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.953
```

Out[68]: 0.8533141670149981

```
In [69]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[69]: 2.156889930826136

```
In [70]:  IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
          posAi = getPos(ped,IDs)
          cor11 = cor(a[posAi],aHat1[posAi])[1,1]
          reg11 = linreg(aHat1[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 =  0.839
          SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.898
```

Out[70]: 0.8393667061739709

In [71]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[71]: 2.496353902653324

In [72]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor12 = cor(a[posAi],aHat1[posAi])[1,1]
reg12 = linreg(aHat1[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 =  0.768
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.814
```

Out[72]: 0.7682304082603862

In [73]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[73]: 2.7933569838670707

In [74]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor13 = cor(a[posAi],aHat1[posAi])[1,1]
reg13 = linreg(aHat1[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 =  0.821
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.924
```

Out[74]: 0.8211763438935322

In [75]:
```
writedlm("Correlation.G5.M.N.txt",cor13)
```

In [76]:
```
writedlm("Regression.G5.M.N.txt",reg13)
```

In [77]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[77]: 12.309573500000003

In [78]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[78]: 2.4764895856222524

```
In [79]:  IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          posAi = getPos(ped,IDs)
          cor14 = cor(a[posAi],aHat1[posAi])[1,1]
          reg14 = linreg(aHat1[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 =  0.676
          SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.842
```

Out[79]: 0.6760358931269145

```
In [80]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[80]: 0.07904022227972965

```
In [81]:  IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          posAi = getPos(ped,IDs)
          cor14 = cor(a[posAi],aHat1[posAi])[1,1]
          reg14 = linreg(aHat1[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 =  0.744
          SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.981
```

Out[81]: 0.744266815792929

```
In [82]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[82]: 0.6976496613479295

```
In [83]:  IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          posAi = getPos(ped,IDs)
          cor15 = cor(a[posAi],aHat1[posAi])[1,1]
          reg15 = linreg(aHat1[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 =  0.744
          SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.010
```

Out[83]: 0.7439871491407806

```
In [84]:  GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[84]: 1.209414189422193

```
In [85]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         posAi = getPos(ped,IDs)
         cor16 = cor(a[posAi],aHat1[posAi])[1,1]
         reg16 = linreg(aHat1[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 =  0.744
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.987
```

Out[85]: 0.7439615579551342

```
In [86]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[86]: 1.6601330833408505

```
In [87]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         posAi = getPos(ped,IDs)
         cor17 = cor(a[posAi],aHat1[posAi])[1,1]
         reg17 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : correlation = %6.3f\n", cor17
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = %
         JCAll = cor17
```

```
         SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.749
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.989
```

Out[87]: 0.7486806970310309

```
In [88]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[88]: 2.083005237517171

```
In [89]: numSSBayes
```

Out[89]: SSBR.NumSSBayes(54971,45971,9000,40000,39000,1000,150)