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/0.5a0/M/2
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/2

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

```
Correlation.G5.M.C*.txt
Correlation.G5.M.C.txt
Correlation.G5.M.J.txt
Correlation.G5.M.JC*.txt
Correlation.G5.M.JC.txt
Correlation.G5.M.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
MarNF.txt
MarNFCenter.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C*.txt
Regression.G5.M.C.txt
Regression.G5.M.J.txt
Regression.G5.M.JC*.txt
Regression.G5.M.JC.txt
Regression.G5.M.N.txt
all.ID
alphaEstimatesC
alphaEstimatesJ
alphaEstimatesJC
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
alphaEstimatesN
epsiEstimatesC
epsiEstimatesJ
epsiEstimatesJC
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
epsiEstimatesN
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 (
```

```
 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);                              # wit
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   = 0.323
vG     = 0.323
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
3453.884224 seconds (23.05 G allocations: 724.068 GB, 7.30% gc time)
```

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

Out[32]:
```
1-element Array{Float64,1}:
 2.5592
```

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

```
Out[33]: 150-element Array{Float64,1}:
          0.0556282
          0.0752604
          0.0368649
          0.0620793
          0.235575
         -0.00187676
         -0.0107445
         -0.0619366
         -0.108716
          0.0605105
         -0.0261941
         -0.0343297
          0.00807523
          ⋮
         -0.183942
         -0.040783
          0.0476992
          0.0919452
          0.0775822
          0.0576932
         -0.00136548
         -0.0301384
          0.0411589
          0.0191305
          0.0166336
          0.00294003
```

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

```
In [35]: epsiHat
```

```
Out[35]: 45954-element Array{Float64,1}:
            0.0903891
           -0.242293
           -0.266195
           -0.282066
           -0.101087
           -0.192796
            0.110253
           -0.234639
           -0.0633728
           -0.0395489
            1.27747
            0.283518
           -0.0815261
            ⋮
            0.588886
           -0.223928
            0.0552311
           -0.282992
            0.476608
           -0.102237
           -0.0898605
           -0.0549042
            0.170971
            0.266727
           -0.267003
           -0.263962
```

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

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

```
In [38]: 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]: 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 =  0.893
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.962
```

```
Out[39]: 0.892598895851336
```

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

Out[40]: 1.0724202502840476

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 =  0.893
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.096
```

Out[41]: 0.8934993908136715

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

Out[42]: 1.8960849203800334

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 =  0.851
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.914
```

Out[43]: 0.851211478530807

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

Out[44]: 0.8823437879542049

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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.574
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.579
```

Out[45]: 0.5736266266248048

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

Out[46]: 0.08900324389132597

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 =  0.766
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.952
```

Out[47]: 0.7660352302620459

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

Out[48]: 0.5513938230570452

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 =  0.774
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.022
```

Out[49]: 0.7736944998997977

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

Out[50]: 0.9561960626063133

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 =  0.765
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.050
```

Out[51]: 0.7645109302486234

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

Out[52]: 1.2833042687651

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

```
SSBRJC from Gibbs - G4.ID : correlation =   0.772
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.067
```

Out[53]: 0.77201553449966

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

Out[54]: 1.6279616913140869

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

```
SSBRJC from Gibbs - G5.ID : correlation =   0.879
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.070
```

Out[55]: 0.8785120431620345

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

Out[56]: 1.9266624120704148

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

Out[57]: 1.3752685890133696

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

Out[58]:
```
5-element Array{Float64,1}:
 0.551394
 0.956196
 1.2833
 1.62796
 1.92666
```

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

Out[59]:
```
2-element Array{Float64,1}:
  2.49443
  1.0702
```

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

Out[60]: `0.18128335956001798`

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

Out[61]: `0.2690228966395174`

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

Out[62]: `0.19400874762572445`

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

Out[63]: `1.0701961178157307`

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 =  0.886
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.054
```

Out[64]: `0.8862708277795737`

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

Out[65]: `1.0703944410750312`

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 =  0.873
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.993
```

Out[66]: 0.873362892098551

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

Out[67]: 1.4197162430600037

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 =  0.893
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.997
```

Out[68]: 0.8928883885381677

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

Out[69]: 1.6266245750001007

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 =  0.871
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.980
```

Out[70]: 0.8709343496061115

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

Out[71]: 1.9482001082456701

```
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 =  0.832
         SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.928
```

Out[72]: 0.8315516906040411

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

Out[73]: 2.192389566904103

```
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 =  0.879
         SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.070
```

Out[74]: 0.8785120431620345

```
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]: 4.55633275

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

Out[78]: 1.9266624120704148

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 = ⁹
JCAll = cor14
```

```
SSBRJC from Gibbs – G0.noGenotype.ID : correlation =   0.549
SSBRJC from Gibbs – G0.noGenotype.ID : regression of TBV on GEBV =   0.567
```

Out[79]: 0.5488610131073259

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

Out[80]: 0.06383936704046173

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 = ⁹
JCAll = cor14
```

```
SSBRJC from Gibbs – G1.noGenotype.ID : correlation =   0.747
SSBRJC from Gibbs – G1.noGenotype.ID : regression of TBV on GEBV =   0.952
```

Out[81]: 0.7472310914708594

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

Out[82]: 0.5291291456210719

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 = ⁹
JCAll = cor15
```

```
SSBRJC from Gibbs – G2.noGenotype.ID : correlation =   0.759
SSBRJC from Gibbs – G2.noGenotype.ID : regression of TBV on GEBV =   1.021
```

Out[83]: 0.7592817077036517

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

Out[84]: 0.9390055879295496

```
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", cor1(
         @printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = '
         JCAll = cor16
```

```
         SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.748
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.045
```

Out[85]: 0.7482566252141115

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

Out[86]: 1.2662556574963673

```
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", cor1'
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = '
         JCAll = cor17
```

```
         SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.759
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.059
```

Out[87]: 0.7594610213252104

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

Out[88]: 1.6134891816835737

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

Out[89]: SSBR.NumSSBayes(54954,45954,9000,40000,39000,1000,150)