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/0.3/G/9
```

/home/nicole/Jupyter/JG3/Data/0.3/G/9

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

```
Correlation.G5.G.C.txt
Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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.PBLUP.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 G4.Genotype.ID;wc G5.Genotype
```

```
    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.ID;wc G4.noGenotype.ID;wc G
```

```
   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",calculateInbreeding=false)
         nothing
         df      = read_genotypes("GenNF.txt",numSSBayes)
         M_Mats = make_MMats(df,A_Mats,ped);                          # without centering
         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 J
         nothing
```

```
In [31]: vG     = 0.746
         vRes   = 1.742
         nIter  = 50000
         @time aHat1,alphaHat,betaHat,epsiHat =
         ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter, outFreq=5000);
         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
2493.541830 seconds (23.05 G allocations: 723.786 GB, 7.71% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
          10.0876
```

```
In [33]: using DataFrames
```

In [34]:
```
df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',header=false)
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 [35]:
```
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 epsilon
@printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n", reg1)
JCAll = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation =  0.855
SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.983
```

Out[35]: 0.8546961358566392

In [36]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[36]: 1.3440881475036064

In [37]:
```
IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV = %6.3f\n", reg2)
JCAll = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.950
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.099
```

Out[37]: 0.9499220615024351

In [38]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[38]: 2.2752078153024073

```
In [39]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV = %6.3f\n", reg3)
         JCAll = cor3
```

```
         SSBRJC from Gibbs - noGenotype.ID : correlation =  0.804
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.974
```

Out[39]: 0.8039268366136948

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

Out[40]: 1.1292143780115753

```
In [41]: 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 epsilon
         @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G0.ID : correlation =  0.699
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  1.166
```

Out[41]: 0.6993562542543743

```
In [42]: GEBV = aHat1[posAi]
         G0GEBV=mean(GEBV)
```

Out[42]: 0.11982985836453566

In [43]:
```
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 epsilon
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.685
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.064
```

Out[43]: 0.6850574410371226

In [44]:
```
GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

Out[44]: 0.7929510735323629

In [45]:
```
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 epsilon
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
JCAll = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.667
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.017
```

Out[45]: 0.6669547228785127

In [46]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[46]: 1.2686605035473477

```
In [47]: 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 epsilon
         @printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
         JCAll = cor6
```

```
         SSBRJC from Gibbs - G3.ID : correlation =   0.662
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.008
```

Out[47]: 0.6615437893962616

```
In [48]: GEBV = aHat1[posAi]
         G3GEBV=mean(GEBV)
```

Out[48]: 1.6101242143586865

```
In [49]: 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 epsilon
         @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
         JCAll = cor7
```

```
         SSBRJC from Gibbs - G4.ID : correlation =   0.710
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.031
```

Out[49]: 0.7099761681788441

```
In [50]: GEBV = aHat1[posAi]
         G4GEBV=mean(GEBV)
```

Out[50]: 1.9678804740347837

In [51]:
```
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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.947
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.099
```

Out[51]: 0.9473516333427221

In [52]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[52]: 2.305082761183923

In [53]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCAll = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.942
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.104
```

Out[53]: 0.9423415209057493

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

Out[54]: 1.488881680568126

In [55]:
```julia
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg9)
JCAll = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation =  0.954
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.102
```

Out[55]: 0.9539910433609303

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

Out[56]: 1.781721588545559

In [57]:
```julia
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg10)
JCAll = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =  0.943
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.070
```

Out[57]: 0.9430016125126869

In [58]:
```julia
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[58]: 1.991098064576716

In [59]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg11)
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =  0.943
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.055
```

Out[59]: 0.94344164438341

In [60]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[60]: 2.327190278186964

In [61]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg12)
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =  0.933
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.054
```

Out[61]: 0.9331423482303156

In [62]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[62]: 2.5921496293740516

In [63]:
```
IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg13)
JCAll = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation =  0.947
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.099
```

Out[63]: 0.9473516333427221

In [64]:
```
writedlm("Correlation.G5.G.N.txt",cor13)
```

In [65]:
```
writedlm("Regression.G5.G.N.txt",reg13)
```

In [66]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[66]: 12.347483624999992

In [67]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[67]: 2.305082761183923

In [68]:
```
IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.688
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.254
```

Out[68]: 0.68840717598286

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

Out[69]: 0.08472596548752057

In [70]:
```
IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs – G1.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg14)
JCAll = cor14
```

```
SSBRJC from Gibbs – G1.noGenotype.ID : correlation =  0.667
SSBRJC from Gibbs – G1.noGenotype.ID : regression of TBV on GEBV =  1.076
```

Out[70]: 0.666659973600869

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

Out[71]: 0.7675979834038196

In [72]:
```
IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs – G2.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg15)
JCAll = cor15
```

```
SSBRJC from Gibbs – G2.noGenotype.ID : correlation =  0.654
SSBRJC from Gibbs – G2.noGenotype.ID : regression of TBV on GEBV =  1.020
```

Out[72]: 0.6540673808426356

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

Out[73]: 1.2501364635209533

In [74]:
```
IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg16)
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.645
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.006
```

Out[74]: 0.6450078384968105

In [75]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[75]: 1.591737905029756

In [76]:
```
IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg17)
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.696
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.029
```

Out[76]: 0.696439028440206

In [77]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[77]: 1.9518735726158285

In [78]:
```
numSSBayes
```

Out[78]: SSBR.NumSSBayes(54907,45907,9000,40000,39000,1000,200)