

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

```
In [2]: function getPos(ped,IDs)  
        posAi = Array{Int64,1}(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/0.5/M/4  
  
/home/nicole/Jupyter/JG3/Data/0.5/M/4
```

In [4]: ;ls

```
Correlation.G5.M.C.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.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 G4.Genotype.ID;wc G5.Genotype.ID
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",calculateInbreeding
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      = 0.759
vG       = 0.759
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
2374.055292 seconds (23.03 G allocations: 723.571 GB, 7.69% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
8.76633
```

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

```
Out[33]: 150-element Array{Float64,1}:  
  0.0423141  
 -0.195197  
  0.037057  
 -0.0998706  
  0.0416117  
  0.221133  
  0.120625  
  0.0671526  
  0.120642  
  0.102385  
 -0.189438  
  0.00485046  
 -0.0545351  
  ⋮  
 -0.148733  
 -0.0464746  
  0.03505  
  0.113112  
  0.0658994  
 -0.0223412  
  0.139168  
  0.0306669  
  0.0174051  
  0.0822491  
  0.0398437  
 -0.0699232
```

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

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

```
Out[35]: 45918-element Array{Float64,1}:
 -0.490856
  0.27245
 -0.234821
 -0.697251
 -0.239329
  0.0832808
 -0.885095
 -0.02272
 -0.0943112
  0.119414
  0.347689
  0.238579
 -0.236976
  ⋮
 -0.199523
  0.232568
  0.169976
  0.67837
 -0.573396
 -0.380013
  0.30169
  0.2005
 -1.05566
  0.0309865
 -0.282179
 -0.162832
```

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

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

```
In [38]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ', header=:ID,
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=:ID,
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 correlation
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.910
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.000
```

```
Out[39]: 0.9102979090857439
```

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

```
Out[40]: 1.6798266608075507
```

```
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 ) # 1
         @printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.861
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.994
```

```
Out[41]: 0.8614808000415495
```

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

```
Out[42]: 2.936478262937788
```

```
In [43]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=
         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 = %6.3f\n", reg3)
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.880
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.969
```

```
Out[43]: 0.8799122325824088
```

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

```
Out[44]: 1.3898301372390343
```

```
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", reg4)
         JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.718
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.879
```

```
Out[45]: 0.7178389333533057
```

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

```
Out[46]: 0.13761450103238448
```

```
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", r
         JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.769
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.992
```

```
Out[47]: 0.7688681228800157
```

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

```
Out[48]: 0.8869775780851656
```

```
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", r
         JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.765
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.021
```

```
Out[49]: 0.7652959124686993
```

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

```
Out[50]: 1.4790368581471598
```

```
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", r
         JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.761
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.009
```

```
Out[51]: 0.7606968706844037
```



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

```
Out[52]: 2.0304083375387427
```

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

```
SSBRJC from Gibbs - G4.ID : correlation = 0.748
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.005
```

```
Out[53]: 0.7482929079580287
```

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

```
Out[54]: 2.5626931935844333
```

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

```
SSBRJC from Gibbs - G5.ID : correlation = 0.843
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.956
```

```
Out[55]: 0.8431508224031612
```

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

```
Out[56]: 2.982229496457419
```

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

```
Out[57]: 2.095251918372253
```

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

```
Out[58]: 5-element Array{Float64,1}:
          0.886978
          1.47904
          2.03041
          2.56269
          2.98223
```

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

```
Out[59]: 2-element Array{Float64,1}:
  9.03752
  0.955511
```

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

```
Out[60]: 0.4455580431371651
```

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

```
Out[61]: 0.5722232628989719
```

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

```
Out[62]: 0.4257357953004269
```

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

```
Out[63]: 0.9555114128404681
```

```
In [64]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
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 = %6.3f\n", reg9 )
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.845
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.946
```

```
Out[64]: 0.845114035876607
```

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

```
Out[65]: 1.7159614257717117
```

```
In [66]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 = %6.3f\n", reg9)
JCA11 = cor9
```

SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.860

SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.914

Out[66]: 0.8596647850966257

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

Out[67]: 2.145369908452431

```
In [68]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 = %6.3f\n", reg10)
JCA11 = cor10
```

SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.837

SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.851

Out[68]: 0.8374312463327277

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

Out[69]: 2.602105413701321

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 = %6.3f\n", reg11)
JCA11 = cor11
```

SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.825

SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.817

Out[70]: 0.8254010887821609

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

```
Out[71]: 3.0463167251142753
```

```
In [72]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         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 = %6.3f\n", reg12)
         JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.804
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.828
```

```
Out[72]: 0.8036804445384365
```

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

```
Out[73]: 3.34258850086397
```

```
In [74]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
         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 = %6.3f\n", reg13)
         JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.843
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.956
```

```
Out[74]: 0.8431508224031612
```

```
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]: 11.887073375
```

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

```
Out[78]: 2.982229496457419
```

```
In [79]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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 = %6.3f\n", reg14)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.700
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.898
```

```
Out[79]: 0.6998029455443067
```

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

```
Out[80]: 0.09714406706470943
```

```
In [81]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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 = %6.3f\n", reg14)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.754
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.005
```

```
Out[81]: 0.7543999239235571
```

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

```
Out[82]: 0.8547111080757486
```

```
In [83]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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 = %6.3f\n", reg15)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.749
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.023
```

```
Out[83]: 0.7492564444470121
```

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

```
Out[84]: 1.4502402285175655
```

```
In [85]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
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 = %6.3f\n", reg16)
JCall = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.744
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.002
```

```
Out[85]: 0.7443198589165966
```

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

```
Out[86]: 2.004359404523986
```

```
In [87]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
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 = %6.3f\n", reg17)
JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.735
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[87]: 0.7349764799591081
```

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

```
Out[88]: 2.5426958780131637
```

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

```
Out[89]: SSBR.NumSSBayes(54918,45918,9000,40000,39000,1000,150)
```