

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

In [4]: ;ls

```
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.JC.txt
all.ID
alphaEstimatesJ
alphaEstimatesJC
epsiEstimatesJ
epsiEstimatesJC
genotype.ID
meanOfSNPMA11
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",calculateInbreeding
nothing
df      = read_genotypes("MarNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped,center=true);           # 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      = 0.714
vG       = 0.714
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
2388.704963 seconds (23.04 G allocations: 723.736 GB, 7.46% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
10.5168
```

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

```
Out[33]: 150-element Array{Float64,1}:  
  -0.0511688  
  -0.115607  
   0.196472  
   0.0247497  
  -0.0285359  
   0.0988894  
  -0.0885265  
   0.0506333  
  -0.0691985  
   0.034203  
  -0.0599119  
  -0.0296326  
   0.0382986  
   ⋮  
  -0.12435  
   0.129464  
  -0.1103  
  -0.0529531  
   0.165205  
   0.0296973  
  -0.148262  
   0.034057  
   0.0424689  
   0.0699243  
  -0.0499534  
   0.0605296
```

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

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

```
Out[35]: 45930-element Array{Float64,1}:
 0.483664
 0.193591
 0.299089
 0.251221
-0.164474
 0.296757
-0.214947
 0.196153
-0.205759
-0.0445675
 0.409274
-0.166966
-0.366344
  ⋮
-0.450971
-0.000529153
-0.788038
 0.100398
-0.766421
-0.600181
-0.152897
 0.491772
 0.517489
-0.12128
-0.736403
 0.654348
```

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

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

```
In [38]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ', header=:a
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 correlation
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.898
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.997
```

```
Out[39]: 0.8980693194548445
```

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

```
Out[40]: 0.1398402531135769
```

```
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 = 0.802
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.967
```

```
Out[41]: 0.8024121033191799
```

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

```
Out[42]: 1.2477165880879517
```

```
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 = 0.870
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.966
```

```
Out[43]: 0.8704994485251227
```

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

```
Out[44]: -0.11582351649589426
```

```
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 = 0.709
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.860
```

```
Out[45]: 0.7093541737528876
```

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

```
Out[46]: -1.267547271562283
```

```
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 =  0.761
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.983
```

```
Out[47]: 0.76051915558157
```

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

```
Out[48]: -0.5603515446151832
```

```
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 =  0.749
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.996
```

```
Out[49]: 0.7491694765939771
```

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

```
Out[50]: -0.006607315209380545
```

```
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 =  0.733
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.973
```

```
Out[51]: 0.733196324600902
```



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

```
Out[52]: 0.46322660700915935
```

```
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 = 0.741
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.998
```

```
Out[53]: 0.7409451738310643
```

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

```
Out[54]: 0.9267791928911561
```

```
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 = 0.778
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.923
```

```
Out[55]: 0.7782186546304508
```

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

```
Out[56]: 1.283541850167993
```

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

```
Out[57]: 1.8438933947831762
```

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

```
Out[58]: 5-element Array{Float64,1}:
          -0.560352
          -0.00660732
           0.463227
           0.926779
           1.28354
```

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

```
Out[59]: 2-element Array{Float64,1}:
 10.7525
  0.923
```

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

```
Out[60]: 0.33889528347017783
```

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

```
Out[61]: 0.4767229049180523
```

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

```
Out[62]: 0.31280047851535403
```

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

```
Out[63]: 0.9230003891242703
```

```
In [64]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
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 =  0.805
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.999
```

```
Out[64]: 0.8048951116214481
```

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

```
Out[65]: 0.22312107123050529
```

```
In [66]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
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 =  0.765
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.858
```

```
Out[66]: 0.7646228117343004
```

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

```
Out[67]: 0.6370612189809444
```

```
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)
         JCall = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.766
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.864
```

```
Out[68]: 0.7655191056483671
```

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

```
Out[69]: 0.9732835931759004
```

```
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)
         JCall = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.765
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.795
```

```
Out[70]: 0.764854333045188
```

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

```
Out[71]: 1.3843006559470064
```

```
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 = 0.752
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.782
```

```
Out[72]: 0.7524040460517722
```

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

```
Out[73]: 1.5878059179037436
```

```
In [74]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 = 0.778
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.923
```

```
Out[74]: 0.7782186546304508
```

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

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

```
In [77]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[77]: 1.283541850167993
```

```
In [78]: 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)
         JCall = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.693
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.874
```

```
Out[78]: 0.6925079155743108
```

```
In [79]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[79]: -1.3057695367620983
```

```
In [80]: 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 = 0.745
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[80]: 0.7454271331903105
```

```
In [81]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[81]: -0.5910544359894429
```

```
In [82]: 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 = 0.734
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[82]: 0.7339164268571134
```

```
In [83]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[83]: -0.031732723116695415
```

```
In [84]: 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)
JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.716
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.965
```

```
Out[84]: 0.7161503650737407
```

```
In [85]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[85]: 0.4396093237030608
```

```
In [86]: 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 = 0.730
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.987
```

```
Out[86]: 0.7300593632653223
```

```
In [87]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[87]: 0.9098297896857049
```

```
In [88]: numSSBayes
```

```
Out[88]: SSBR.NumSSBayes(54930,45930,9000,40000,39000,1000,150)
```