

```
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/9  
  
/home/nicole/Jupyter/JG3/Data/0.5/M/9
```

In [4]: ;ls

```
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.J.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.ID
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",calculateInbreedingCoefficients,
nothing
df = read_genotypes("MarNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped); # with M_Mats
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 X_Mats
nothing
```

```
In [31]: vRes = 0.547
vG = 0.547
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
4528.615715 seconds (23.05 G allocations: 724.233 GB, 7.18% gc time)
```

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

```
Out[32]: 1-element Array{Float64,1}:
10.0546
```

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

```
Out[33]: 150-element Array{Float64,1}:
 -0.0810941
  0.138958
 -0.0236479
  0.0184244
 -0.00107173
  0.00284777
  0.0634995
  0.0252944
 -0.0745516
 -0.0200068
 -0.0854636
 -0.222438
  0.00620302
  ⋮
  0.0727527
  0.217404
 -0.111329
 -0.0671389
 -0.0826853
  0.00409777
 -0.0375747
  0.00942249
  0.0267316
  0.100388
  0.0748276
  0.0651361
```

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

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

```
Out[35]: 45966-element Array{Float64,1}:
 -0.0962287
  0.37877
  0.227108
 -0.379818
 -0.225992
  0.520559
 -0.734337
 -1.39754
  0.0654208
 -0.546834
 -0.453048
  0.377907
 -0.422266
  ⋮
 -0.333731
 -0.332939
 -0.330858
  0.382106
 -0.0181531
 -0.469871
 -0.44133
 -0.626526
  0.0676477
 -0.780288
  0.365988
  0.272491
```

```
In [36]: writedlm("epsiEstimatesN",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 = 0.891
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.995
```

```
Out[39]: 0.890768413015037
```

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

```
Out[40]: 1.3462452805895573
```

```
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 = 0.783
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.988
```

```
Out[41]: 0.783322947177808
```

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

```
Out[42]: 2.304506018736111
```

```
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 = 0.864
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.956
```

```
Out[43]: 0.863615286692672
```

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

```
Out[44]: 1.1251081871711217
```

```
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 = 0.670
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.776
```

```
Out[45]: 0.670428434391193
```

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

```
Out[46]: 0.10800011626364758
```

```
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 = 0.762
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.969
```

```
Out[47]: 0.7622928417489911
```

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

```
Out[48]: 0.7269425586896809
```

```
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 = 0.752
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.006
```

```
Out[49]: 0.7523911817725919
```

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

```
Out[50]: 1.2133898983846028
```

```
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 = 0.745
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.002
```

```
Out[51]: 0.7446047839670967
```



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

```
Out[52]: 1.6546130789086815
```

```
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 = 0.727
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.011
```

```
Out[53]: 0.7271371085323837
```

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

```
Out[54]: 2.0404733602050498
```

```
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 = 0.759
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.941
```

```
Out[55]: 0.7591703075389445
```

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

```
Out[56]: 2.334052671085681
```

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

```
Out[57]: 1.607110112396
```

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

```
Out[58]: 5-element Array{Float64,1}:
          0.726943
          1.21339
          1.65461
          2.04047
          2.33405
```

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

```
Out[59]: 2-element Array{Float64,1}:
          10.3382
           0.941445
```

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

```
Out[60]: 0.25969834341036896
```

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

```
Out[61]: 0.39937518948266976
```

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

```
Out[62]: 0.2444918260424943
```

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

```
Out[63]: 0.9414454587265284
```

```
In [64]: IDs = readtable("G0.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 - 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 = 0.822
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.961
```

```
Out[64]: 0.8217694879970253
```

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

```
Out[65]: 1.469197188482108
```

```
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 = 0.764

SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.837

Out[66]: 0.7639503871509314

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

Out[67]: 1.7839070311739422

```
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 = 0.760

SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.829

Out[68]: 0.7595838175947408

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

Out[69]: 2.1048535770678813

```
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 = 0.712

SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.752

Out[70]: 0.7115288926955221

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

```
Out[71]: 2.37538546349749
```

```
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 = 0.672
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.770
```

```
Out[72]: 0.6719174081327711
```

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

```
Out[73]: 2.607320739476311
```

```
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 = 0.759
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.941
```

```
Out[74]: 0.7591703075389445
```

```
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]: 12.535571875
```

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

```
Out[78]: 2.334052671085681
```

```
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 = 0.652
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.788
```

```
Out[79]: 0.6522813257085451
```

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

```
Out[80]: 0.07309762723240501
```

```
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 = 0.748
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.976
```

```
Out[81]: 0.7475709169204591
```

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

```
Out[82]: 0.6998409055490588
```

```
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 = 0.737
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[83]: 0.7366016393480617
```

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

```
Out[84]: 1.1905318553414415
```

```
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 = 0.732
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[85]: 0.7318345588949637
```

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

```
Out[86]: 1.636131735714097
```

```
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 = 0.717
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.000
```

```
Out[87]: 0.7169634902538733
```

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

```
Out[88]: 2.025938812018607
```

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

```
Out[89]: SSBR.NumSSBayes(54966,45966,9000,40000,39000,1000,150)
```