

```
In [1]: include("/home/nicole/Jupyter/SSBRJ/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/8

/home/nicole/Jupyter/JG3/Data/0.5/M/8
```

```
In [4]: ;ls

MarNF.txt
PedAll.txt
Phe.txt
PheAll.txt
```

```
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
      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);
      y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
      J_Vecs = make_JVecs(numSSBayes,A_Mats)
      Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
      X_Mats, W_Mats = make_XWMats(J_Vecs,Z_Mats,M_Mats,numSSBayes)
      nothing
```

```
In [31]: vRes    = 0.627
         vG      = 0.627
         nIter   = 50000
         @time aHat1,alphaHat,betaHat,epsHat =
         ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,1
         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
2352.018158 seconds (23.06 G allocations: 724.316 GB, 7.90% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          10.3039
          -1.13055
```

```
In [33]: mu  = betaHat[1]
         mug = betaHat[2]
```

```
Out[33]: -1.1305457472571776
```

```
In [34]: (mu+mug)/2
```

```
Out[34]: 4.586679303497354
```

```
In [35]: alphaHat
```

```
Out[35]: 150-element Array{Float64,1}:
 0.0343527
-0.0707594
-0.0538777
 0.103682
-0.0336962
 0.227726
-0.235083
-0.0466235
 0.0881982
-0.0269293
-0.0422537
 0.0127945
 0.0392995
  ⋮
 0.00902642
 0.114879
 0.0529728
-0.13617
-0.0561895
 0.111548
-0.00264962
 0.0749876
-0.0748121
-0.0219469
-0.0735245
 0.0122876
```

```
In [36]: writedlm("alphaEstimatesJC",alphaHat)
```

```
In [37]: epsiHat
```

```
Out[37]: 45971-element Array{Float64,1}:
 0.0200375
 0.541196
-0.263365
 0.0259778
-0.439365
-0.560613
 0.170588
-0.620238
-0.0192957
-0.74968
 0.286701
 0.438347
-0.130199
 ⋮
 0.100619
 0.215019
-0.529363
 0.119492
-0.236492
 0.350377
-0.200365
 0.334002
 0.0769383
-0.39636
-0.109128
-0.38822
```

```
In [38]: writedlm("epsiEstimatesJC",epsiHat)
```

```
In [39]: using DataFrames
```

```
In [40]: 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 [41]: 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 e
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", 1
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.900
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.987
```

```
Out[41]: 0.8995907564079892
```

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

```
Out[42]: 0.8326786610705273
```

```
In [43]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=1)
         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 ) # w.
         @printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.847
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.970
```

```
Out[43]: 0.8465317998616496
```

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

```
Out[44]: 1.8828258282946482
```

```
In [45]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=1)
         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 = 0.867
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.960
```

```
Out[45]: 0.8672659722573374
```

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

```
Out[46]: 0.5903370070957302
```

```
In [47]: 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 ep
         @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
         JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.694
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.835
```

```
Out[47]: 0.6937658036918248
```

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

```
Out[48]: -0.44372278679315136
```

```
In [49]: 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 ep
         @printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg
         JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.760
```

```
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.975
```

```
Out[49]: 0.7597060984228923
```

```
In [50]: GEBV = aHat1[posAi]
         G1GEBV=mean(GEBV)
```

```
Out[50]: 0.16997846530514757
```

```
In [51]: 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 ep
         @printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg
         JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.761
```

```
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.015
```

```
Out[51]: 0.7606089853863225
```

```
In [52]: GEBV = aHat1[posAi]
         G2GEBV=mean(GEBV)
```

```
Out[52]: 0.6780599291434785
```

```
In [53]: 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 ep
         @printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg
         JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.758
```

```
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.994
```

```
Out[53]: 0.7582991350584262
```

```
In [54]: GEBV = aHat1[posAi]
        G3GEBV=mean(GEBV)
```

```
Out[54]: 1.1258252747210895
```

```
In [55]: 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", reg
        JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.760
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.999
```

```
Out[55]: 0.7604416334765007
```

```
In [56]: GEBV = aHat1[posAi]
        G4GEBV=mean(GEBV)
```

```
Out[56]: 1.5452031942438507
```

```
In [57]: 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", reg
        JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.824
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.928
```

```
Out[57]: 0.8237839242335403
```

```
In [58]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[58]: 2-element Array{Float64,1}:
         10.5269
          0.928099
```

```
In [59]: VarGEBV=var(aHat1[posAi])
```

```
Out[59]: 0.2975924103074429
```

```
In [60]: VarTBV=var(a[posAi])
```

```
Out[60]: 0.3777318285763221
```

```
In [61]: Cov=cov(aHat1[posAi], a[posAi])
```

```
Out[61]: 0.2761951376316828
```



```
In [62]: b=Cov/VarGEBV
```

```
Out[62]: 0.9280987285473626
```

```
In [63]: GEBV = aHat1[posAi]
         G5GEBV=mean(GEBV)
```

```
Out[63]: 1.9207278898027493
```

```
In [64]: GEBVG5G1=G5GEBV-G1GEBV
```

```
Out[64]: 1.7507494244976018
```

```
In [65]: GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]
```

```
Out[65]: 5-element Array{Float64,1}:
          0.169978
          0.67806
          1.12583
          1.5452
          1.92073
```

```
In [66]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 ) ;
          JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.847
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.958
```

```
Out[66]: 0.8474825800894672
```

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

```
Out[67]: 0.8557272228800717
```

```
In [68]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 ) ;
          JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.840
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.945
```

```
Out[68]: 0.8398143567647407
```

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

```
Out[69]: 1.2632914576628562
```

```
In [70]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 = 0.856
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.959
```

```
Out[70]: 0.8557014864834738
```

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

```
Out[71]: 1.601946100268133
```

```
In [72]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 = 0.841
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.902
```

```
Out[72]: 0.8412723984887436
```

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

```
Out[73]: 1.94033717561862
```

```
In [74]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 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 = 0.772
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.820
```

```
Out[74]: 0.7715518241064774
```

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

```
Out[75]: 2.2367447247195043
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',heads = ["ID", "G5"],
         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 = 0.824
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.928
```

```
Out[76]: 0.8237839242335403
```

```
In [77]: writedlm("Correlation.G5.M.JC.txt",cor13)
```

```
In [78]: writedlm("Regression.G5.M.JC.txt",reg13)
```

```
In [79]: TBVG5Gall = a[posAi]
         TBVG5G=mean(TBVG5Gall)
```

```
Out[79]: 12.309573500000003
```

```
In [80]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[80]: 1.9207278898027493
```

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',heads = ["ID", "G0"],
         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 = 0.676
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.842
```

```
Out[81]: 0.6760291057183113
```

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

```
Out[82]: -0.4770420178104135
```

```
In [83]: 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)
JCall = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.744
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[83]: 0.7442374839202777
```

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

```
Out[84]: 0.1419447988344371
```

```
In [85]: 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)
JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.744
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.010
```

```
Out[85]: 0.7441216174451126
```

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

```
Out[86]: 0.6543705401402822
```

```
In [87]: 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 = 0.988
```

```
Out[87]: 0.7441728515230324
```

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

```
Out[88]: 1.1049403541852554
```

```
In [89]: 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", JCall)
JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.749
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[89]: 0.749110857577159
```

```
In [90]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[90]: 1.5274713601290903
```

```
In [91]: numSSBayes
```

```
Out[91]: SSBR.NumSSBayes(54971,45971,9000,40000,39000,1000,150)
```

```
In [92]: J1 = sortrows(J_Vecs.J1)
```

```
Out[92]: 45971x1 Array{Float64,2}:
-0.987719
-0.98594
-0.98576
-0.985627
-0.985599
-0.98553
-0.985326
-0.985309
-0.985242
-0.984632
-0.984502
-0.984372
-0.983764
⋮
7.44482e-17
7.56223e-17
7.72039e-17
7.92431e-17
8.89064e-17
8.9058e-17
9.10725e-17
9.40848e-17
1.02917e-16
1.03764e-16
1.07511e-16
1.117e-16
```

```
In [93]: J1[J1 .< 0.0,:]
```

```
Out[93]: 43929x1 Array{Float64,2}:  
  -0.987719  
  -0.98594  
  -0.98576  
  -0.985627  
  -0.985599  
  -0.98553  
  -0.985326  
  -0.985309  
  -0.985242  
  -0.984632  
  -0.984502  
  -0.984372  
  -0.983764  
  ⋮  
  -7.23354e-36  
  -7.22719e-36  
  -7.22591e-36  
  -7.22591e-36  
  -7.2166e-36  
  -7.16402e-36  
  -5.41807e-36  
  -4.91411e-36  
  -8.72921e-51  
  -7.61204e-65  
  -3.80602e-65  
  -1.77903e-67
```

```
In [94]: J1[J1 .> 0.0,:]
```

```
Out[94]: 1313x1 Array{Float64,2}:  
 8.45106e-81  
 8.01203e-52  
 8.02238e-52  
 1.20305e-51  
 1.53665e-51  
 1.59073e-51  
 1.60241e-51  
 1.60448e-51  
 1.60476e-51  
 1.60617e-51  
 1.61185e-51  
 3.07329e-51  
 3.21189e-51  
 ⋮  
 7.44482e-17  
 7.56223e-17  
 7.72039e-17  
 7.92431e-17  
 8.89064e-17  
 8.9058e-17  
 9.10725e-17  
 9.40848e-17  
 1.02917e-16  
 1.03764e-16  
 1.07511e-16  
 1.117e-16
```