

```
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/5

        /home/nicole/Jupyter/JG3/Data/0.5/M/5
```

```
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.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.ID;wc G4.noGenotype.ID;wc G5.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,center=true); # with centering
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) # with W_Mats
nothing
```

```
In [31]: vRes    = 0.699
         vG      = 0.699
         nIter   = 50000
         @time aHat1,alphaHat,betaHat,epsiHat =
         ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,
         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
2446.035573 seconds (23.03 G allocations: 723.516 GB, 7.43% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          10.7162
          -1.0195
```

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

```
Out[33]: -1.0194968490394707
```

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

```
Out[34]: 4.848342985477104
```

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

```
Out[35]: 150-element Array{Float64,1}:
 -0.110785
  0.122651
  0.0468765
  0.0416842
 -0.0729382
  0.00339768
  0.0534751
 -0.0407642
 -0.148908
 -0.241639
 -0.0280031
  0.0790511
 -0.0844509
  ⋮
 -0.18507
 -0.0705208
  0.0172563
 -0.000720576
  0.116333
  0.121689
  0.0128185
  0.0512721
 -0.185962
 -0.168228
 -0.118687
 -0.0273101
```

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

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

```
Out[37]: 45913-element Array{Float64,1}:
 0.252875
-0.0431041
-0.471639
 0.202473
-0.690494
-0.112445
 0.131993
-0.0782717
 0.806249
-0.11617
-0.25705
 0.266111
 0.300137
  ⋮
-0.122781
-0.0186311
-1.00691
 0.793447
-0.754392
 0.664985
 0.122724
 0.64676
-0.467261
-0.289332
-0.57115
-0.127743
```

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

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

```
In [40]: 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 [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 correlation
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.902
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.992
```

```
Out[41]: 0.901961455292321
```

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

```
Out[42]: 0.7773342125961784
```

```
In [43]: 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 = 0.850
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.018
```

```
Out[43]: 0.849647933982504
```

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

```
Out[44]: 1.9420310082445782
```

```
In [45]: 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[45]: 0.87026675351284
```

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

```
Out[46]: 0.5085580289850093
```

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

```
SSBRJC from Gibbs - G0.ID : correlation = 0.700
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.854
```

```
Out[47]: 0.7004559036062312
```

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

```
Out[48]: -0.6384883470416499
```

```
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 e
         @printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.764
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.982
```

```
Out[49]: 0.7644024160658126
```

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

```
Out[50]: 0.05883153342751628
```

```
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 e
         @printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.762
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.010
```

```
Out[51]: 0.761671608021321
```

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

```
Out[52]: 0.6068807937155822
```

```
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 e
         @printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", r
         JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.748
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.026
```

```
Out[53]: 0.7481714270505306
```

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

```
Out[54]: 1.089761960879753
```

```
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 e
         @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", r
         JCA11 = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.753
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.033
```

```
Out[55]: 0.7527800759804291
```

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

```
Out[56]: 1.5633580817021313
```

```
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 e
         @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", r
         JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.832
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.990
```

```
Out[57]: 0.8320200841775656
```

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

```
Out[58]: 2-element Array{Float64,1}:
         10.8286
         0.989707
```

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

```
Out[59]: 0.3904078547922037
```

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

```
Out[60]: 0.5524134329322257
```

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

```
Out[61]: 0.3863893954990718
```



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

```
Out[62]: 0.9897070224284531
```

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

```
Out[63]: 1.9836612528937376
```

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

```
Out[64]: 1.9248297194662214
```

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

```
Out[65]: 5-element Array{Float64,1}:
          0.0588315
          0.606881
          1.08976
          1.56336
          1.98366
```

```
In [66]: 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 )
         JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.836
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.938
```

```
Out[66]: 0.8360539835230361
```

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

```
Out[67]: 0.8349844203668664
```

```
In [68]: 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 )
         JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.802
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.845
```

```
Out[68]: 0.8017255944487065
```

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

```
Out[69]: 1.2485813826855152
```

```
In [70]: 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 = 0.810
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.890
```

```
Out[70]: 0.8100455798785532
```

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

```
Out[71]: 1.6001187954085208
```

```
In [72]: 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 = 0.805
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.942
```

```
Out[72]: 0.8054111407885491
```

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

```
Out[73]: 2.0024997867613785
```

```
In [74]: 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 = 0.770
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.870
```

```
Out[74]: 0.7702227159055562
```

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

```
Out[75]: 2.358760870034227
```

```
In [76]: 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 = 0.832
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[76]: 0.8320200841775656
```

```
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]: 12.791862625000002
```

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

```
Out[80]: 1.9836612528937376
```

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', head=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 = 0.682
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.867
```

```
Out[81]: 0.6821634230522955
```

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

```
Out[82]: -0.6762697000521246
```

```
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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation = 0.750
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[83]: 0.7495781437611287
```

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

```
Out[84]: 0.02832512703628554
```

```
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)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.748
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.012
```

```
Out[85]: 0.7481184083645399
```

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

```
Out[86]: 0.5814131526465325
```

```
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)
JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.733
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.021
```

```
Out[87]: 0.7332900931273706
```

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

```
Out[88]: 1.0663584268827886
```

```
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", reg17)
JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.739
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.024
```

```
Out[89]: 0.7394274628718286
```

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

```
Out[90]: 1.5429631384115647
```

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

```
Out[91]: SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,150)
```

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

```
Out[92]: 45913x1 Array{Float64,2}:
-1.00043
-0.985971
-0.985679
-0.985673
-0.985559
-0.985515
-0.985433
-0.985336
-0.984686
-0.984432
-0.984228
-0.984108
-0.984089
⋮
6.48111e-17
6.52054e-17
6.63179e-17
6.93627e-17
7.27749e-17
7.41413e-17
7.42107e-17
1.03621e-16
1.10998e-16
1.11071e-16
1.11477e-16
1.16402e-16
```

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

```
Out[93]: 43945x1 Array{Float64,2}:  
  -1.00043  
  -0.985971  
  -0.985679  
  -0.985673  
  -0.985559  
  -0.985515  
  -0.985433  
  -0.985336  
  -0.984686  
  -0.984432  
  -0.984228  
  -0.984108  
  -0.984089  
  ⋮  
  -7.2166e-36  
  -7.2166e-36  
  -7.21448e-36  
  -7.21447e-36  
  -7.20922e-36  
  -7.20922e-36  
  -7.20808e-36  
  -2.1823e-51  
  -7.62092e-65  
  -3.81046e-65  
  -2.55514e-65  
  -3.56081e-67
```

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

```
Out[94]: 1285x1 Array{Float64,2}:  
 8.46092e-81  
 8.00384e-52  
 1.60051e-51  
 1.60077e-51  
 1.60077e-51  
 1.60193e-51  
 1.60194e-51  
 1.60241e-51  
 1.60365e-51  
 1.60365e-51  
 1.60382e-51  
 1.60429e-51  
 2.1823e-51  
 ⋮  
 6.48111e-17  
 6.52054e-17  
 6.63179e-17  
 6.93627e-17  
 7.27749e-17  
 7.41413e-17  
 7.42107e-17  
 1.03621e-16  
 1.10998e-16  
 1.11071e-16  
 1.11477e-16  
 1.16402e-16
```