

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

```
In [2]: function getPos(ped,IDs)  
        posAi = Array{Int64,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  
  
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    = 0.759
         vG      = 0.759
         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
2429.894092 seconds (23.03 G allocations: 723.584 GB, 7.52% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          8.00816
         -3.65805
```

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

```
Out[33]: -3.6580453186805526
```

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

```
Out[34]: 2.175058520737801
```

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

```
Out[35]: 150-element Array{Float64,1}:  
  0.0346815  
 -0.20837  
  0.00825384  
 -0.107679  
  0.0457779  
  0.196204  
 -0.00887381  
  0.00066845  
  0.0764819  
  0.0998801  
 -0.189303  
 -0.00125355  
 -0.0514862  
  ⋮  
 -0.198004  
 -0.053184  
  0.00475439  
  0.103322  
  0.0535587  
 -0.0469517  
  0.074577  
 -0.00357876  
 -0.0125654  
  0.0524954  
  0.00199501  
 -0.108019
```

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

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

```
Out[37]: 45918-element Array{Float64,1}:
 -0.483429
  0.270558
 -0.219506
 -0.701117
 -0.270023
  0.0933451
 -0.882446
 -0.00614576
 -0.0997451
  0.138335
  0.353502
  0.258112
 -0.250832
  ⋮
 -0.203612
  0.25083
  0.133299
  0.666472
 -0.549961
 -0.366502
  0.317344
  0.23377
 -1.04594
  0.0179089
 -0.280796
 -0.158987
```

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

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

```
In [40]: 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 [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 = 0.910
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.999
```

```
Out[41]: 0.9102823107559451
```

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

```
Out[42]: 2.4381125566004607
```

```
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 = 0.862
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.991
```

```
Out[43]: 0.8615130725862511
```

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

```
Out[44]: 3.695584634666834
```

```
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 = 0.880
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.968
```

```
Out[45]: 0.8798979791181917
```

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

```
Out[46]: 2.1479266924312976
```

```
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 = 0.718
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.880
```

```
Out[47]: 0.7179168405906159
```

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

```
Out[48]: 0.8946017754302693
```

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

```
Out[49]: 0.7687812744916867
```

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

```
Out[50]: 1.6422115305284641
```

```
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 = 0.766
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.023
```

```
Out[51]: 0.7657531793714358
```

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

```
Out[52]: 2.238209964630987
```

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

```
Out[53]: 0.7605420465960144
```

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

```
Out[54]: 2.7901918828915253
```

```
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 = 0.748
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.001
```

```
Out[55]: 0.7475465312597654
```

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

```
Out[56]: 3.322156921881364
```

```
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 = 0.843
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.952
```

```
Out[57]: 0.8432187025186697
```

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

```
Out[58]: 2-element Array{Float64,1}:
         8.32456
         0.952212
```

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

```
Out[59]: 0.4487231241597648
```

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

```
Out[60]: 0.5722232628989719
```

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

```
Out[61]: 0.42727965142581015
```



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

```
Out[62]: 0.9522122405122143
```

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

```
Out[63]: 3.741303264240155
```

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

```
Out[64]: 2.099091733711691
```

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

```
Out[65]: 5-element Array{Float64,1}:
 1.64221
 2.23821
 2.79019
 3.32216
 3.7413
```

```
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 = 0.847
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.949
```

```
Out[66]: 0.8468835520475435
```

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

```
Out[67]: 2.466304539454275
```

```
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 = 0.861
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.925
```

```
Out[68]: 0.86135870741867
```

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

```
Out[69]: 2.910646282361583
```

```
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 = 0.836
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.855
```

```
Out[70]: 0.8358176491598097
```

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

```
Out[71]: 3.3638051372928675
```

```
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 = 0.827
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.809
```

```
Out[72]: 0.826859727093117
```

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

```
Out[73]: 3.805878756546632
```

```
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 = 0.803
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.820
```

```
Out[74]: 0.8027730046305371
```

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

```
Out[75]: 4.102543274746022
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10,
         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 = 0.952
```

```
Out[76]: 0.8432187025186697
```

```
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]: 11.887073375
```

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

```
Out[80]: 3.741303264240155
```

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', head=10,
         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 = 0.700
```

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

```
Out[81]: 0.6997933149737658
```

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

```
Out[82]: 0.8543017045578588
```

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

```
Out[83]: 0.7543265894209119
```

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

```
Out[84]: 1.609687562532743
```

```
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 = 0.750
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.025
```

```
Out[85]: 0.7497644618676685
```

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

```
Out[86]: 2.209348549947349
```

```
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 = 1.003
```

```
Out[87]: 0.7441671846676274
```

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

```
Out[88]: 2.7641486297208813
```

```
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 = 0.734
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.989
```

```
Out[89]: 0.734245210731174
```

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

```
Out[90]: 3.3021470153976544
```

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

```
Out[91]: SSBR.NumSSBayes(54918,45918,9000,40000,39000,1000,150)
```

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

```
Out[92]: 45918x1 Array{Float64,2}:
-1.00018
-0.989621
-0.988966
-0.988656
-0.986208
-0.985971
-0.985931
-0.985615
-0.985572
-0.985545
-0.985116
-0.985082
-0.984151
⋮
8.08e-17
8.40541e-17
8.56774e-17
8.88017e-17
9.25384e-17
1.00706e-16
1.11122e-16
1.11366e-16
1.11879e-16
1.44033e-16
1.49661e-16
1.682e-16
```

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

```
Out[93]: 43970x1 Array{Float64,2}:  
  -1.00018  
  -0.989621  
  -0.988966  
  -0.988656  
  -0.986208  
  -0.985971  
  -0.985931  
  -0.985615  
  -0.985572  
  -0.985545  
  -0.985116  
  -0.985082  
  -0.984151  
  ⋮  
  -1.08419e-35  
  -7.22966e-36  
  -7.22085e-36  
  -7.22085e-36  
  -7.20816e-36  
  -7.20815e-36  
  -7.0501e-36  
  -8.72921e-51  
  -3.55174e-67  
  -1.78225e-67  
  -1.77587e-67  
  -8.91125e-68
```

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

```
Out[94]: 1281x1 Array{Float64,2}:  
 1.97869e-83  
 8.02654e-52  
 1.59956e-51  
 1.60053e-51  
 1.60531e-51  
 2.1823e-51  
 2.56016e-51  
 2.74883e-51  
 3.19912e-51  
 4.8006e-51  
 4.80207e-51  
 5.46964e-51  
 2.23532e-50  
 ⋮  
 8.08e-17  
 8.40541e-17  
 8.56774e-17  
 8.88017e-17  
 9.25384e-17  
 1.00706e-16  
 1.11122e-16  
 1.11366e-16  
 1.11879e-16  
 1.44033e-16  
 1.49661e-16  
 1.682e-16
```