

```
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/0.3/G/10

/home/nicole/Jupyter/JG3/Data/0.3/G/10
```

```
In [4]: ;ls

Correlation.G5.G.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
```

```
In [5]: ;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

```
In [6]: ;awk '{print $1}' GenNF.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
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 G
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=false)
nothing
df      = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);           # without 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 J
nothing
```

```
In [31]: vG      = 0.692
vRes     = 1.615
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,nIter, outFreq=5000);
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
2726.314449 seconds (23.04 G allocations: 723.593 GB, 7.15% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 9.49455
 4.24758
```

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

```
Out[33]: 4.24758163953954
```

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

```
Out[34]: 6.8710645966526585
```

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

```
Out[35]: 200-element Array{Float64,1}:
```

```
-0.068263  
-0.038699  
-0.0710559  
0.000922297  
0.0970738  
0.0281959  
0.168358  
0.166733  
-0.0813685  
0.117954  
0.0912766  
-0.0331006  
-0.0325105  
⋮  
0.0644235  
0.167837  
-0.0319943  
-0.00792183  
0.00399425  
0.132967  
-0.0384884  
-0.00879601  
-0.00209629  
-0.0106346  
0.00532854  
-0.0228593
```

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

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

```
In [38]: 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 [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 epsilon
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.873
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.981
```

```
Out[39]: 0.8726034425735077
```

```
In [40]: TBV = a[posAi]
mean(TBV)
```

```
Out[40]: 10.863178833333334
```

```
In [41]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[41]: 1.3748472642904896
```

```
In [42]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.970
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.060
```

```
Out[42]: 0.969980848167892
```

```
In [43]: TBV = a[posAi]
         mean(TBV)
```

```
Out[43]: 11.821125222222223
```

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

```
Out[44]: 2.362676580789582
```

```
In [45]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg3)
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.824
```

```
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV =  0.974
```

```
Out[45]: 0.8237829231813196
```

```
In [46]: TBV = a[posAi]
         mean(TBV)
```

```
Out[46]: 10.642114282051281
```

```
In [47]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[47]: 1.146886652790699
```

```
In [48]: 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 epsilon
        @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
        JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.695
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.129
```

```
Out[48]: 0.6947293346195149
```

```
In [49]: TBV = a[posAi]
        G0TBV=mean(TBV)
```

```
Out[49]: 9.696585499999998
```

```
In [50]: GEBV = aHat1[posAi]
        G0GEBV=mean(GEBV)
```

```
Out[50]: 0.11153536901525242
```

```
In [51]: 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 epsilon
        @printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
        JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.685
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.019
```

```
Out[51]: 0.6851436325704882
```

```
In [52]: TBV = a[posAi]
        G1TBV=mean(TBV)
```

```
Out[52]: 10.27287525
```



```
In [53]: GEBV = aHat1[posAi]
         G1GEBV=mean(GEBV)
```

```
Out[53]: 0.7751186689593285
```

```
In [54]: 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 epsilon
         @printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
         JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.703
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.021
```

```
Out[54]: 0.7025591816356748
```

```
In [55]: TBV = a[posAi]
         G2TBV=mean(TBV)
```

```
Out[55]: 10.721563625
```

```
In [56]: GEBV = aHat1[posAi]
         G2GEBV=mean(GEBV)
```

```
Out[56]: 1.2616208153703201
```

```
In [57]: 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 epsilon
         @printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
         JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.692
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.013
```

```
Out[57]: 0.6921224134305931
```

```
In [58]: TBV = a[posAi]
        G3TBV=mean(TBV)
```

```
Out[58]: 11.139553874999997
```

```
In [59]: GEBV = aHat1[posAi]
        G3GEBV=mean(GEBV)
```

```
Out[59]: 1.6735978394734756
```

```
In [60]: 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 epsilon
        @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
        JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.723
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.012
```

```
Out[60]: 0.7230942347957039
```

```
In [61]: TBV = a[posAi]
        G4TBV=mean(TBV)
```

```
Out[61]: 11.491697875
```

```
In [62]: GEBV = aHat1[posAi]
        G4GEBV=mean(GEBV)
```

```
Out[62]: 2.0318235760848933
```

```
In [63]: 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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.968
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.060
```

```
Out[63]: 0.9677065487292444
```

```
In [64]: TBV = a[posAi]
G5TBV=mean(TBV)
```

```
Out[64]: 11.856796875000002
```

```
In [65]: GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

```
Out[65]: 2.3953873168396678
```

```
In [66]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 = 0.968
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.027
```

```
Out[66]: 0.9675080229937508
```

```
In [67]: TBV = a[posAi]
mean(TBV)
```

```
Out[67]: 10.841814999999997
```

```
In [68]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[68]: 1.4546604765621074
```

```
In [69]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.974
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.042
```

```
Out[69]: 0.9739252597939747
```

```
In [70]: TBV = a[posAi]
         mean(TBV)
```

```
Out[70]: 11.16823
```

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

```
Out[71]: 1.775688761206374
```

```
In [72]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.969
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.030
```

```
Out[72]: 0.9694045336157409
```

```
In [73]: TBV = a[posAi]
         mean(TBV)
```

```
Out[73]: 11.556379999999997
```

```
In [74]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[74]: 2.1164942579364525
```

```
In [75]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.968
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.046
```

```
Out[75]: 0.9677877421550491
```

```
In [76]: TBV = a[posAi]
         mean(TBV)
```

```
Out[76]: 11.872939999999998
```

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

```
Out[77]: 2.409023154687712
```

```
In [78]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 = 0.949

SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.032

Out[78]: 0.9493967345158146

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

Out[79]: 12.239395

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

Out[80]: 2.749086811551856

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 = 0.968

SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.060

Out[81]: 0.9677065487292444

```
In [82]: writedlm("Correlation.G5.G.J.txt",cor13)
```

```
In [83]: writedlm("Regression.G5.G.J.txt",reg13)
```

```
In [84]: TBVG5Gall = a[posAi]
         TBVG5G=mean(TBVG5Gall)
```

```
Out[84]: 11.856796875000002
```

```
In [85]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[85]: 2.3953873168396678
```

```
In [86]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.675
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.194
```

```
Out[86]: 0.6754333312008877
```

```
In [87]: TBV = a[posAi]
         mean(TBV)
```

```
Out[87]: 9.66722064102564
```

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

```
Out[88]: 0.07709626369353816
```

```
In [89]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.665
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.031
```

```
Out[89]: 0.6645637811905697
```

```
In [90]: TBV = a[posAi]
mean(TBV)
```

```
Out[90]: 10.249917435897435
```

```
In [91]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[91]: 0.7494630255683786
```

```
In [92]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.686
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.023
```

```
Out[92]: 0.6856182844748149
```

```
In [93]: TBV = a[posAi]
mean(TBV)
```

```
Out[93]: 10.700158076923076
```



```
In [94]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[94]: 1.2397009835096502
```

```
In [95]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.677
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.013
```

```
Out[95]: 0.6771219017395685
```

```
In [96]: TBV = a[posAi]
         mean(TBV)
```

```
Out[96]: 11.120749102564101
```

```
In [97]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[97]: 1.6547407801090082
```

```
In [98]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.710
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.010
```

```
Out[98]: 0.710203978342464
```

```
In [99]: TBV = a[posAi]
         mean(TBV)
```

```
Out[99]: 11.472526153846156
```

```
In [100]: GEBV = aHat1[posAi]
          mean(GEBV)
```

```
Out[100]: 2.01343221107292
```

```
In [101]: IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor18 = cor(a[posAi],aHat1[posAi])[1,1]
         reg18 = linreg(aHat1[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - G5.noGenotype.ID : correlation = %6.3f\n", cor18 ) # with epsilon
         @printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg18)
         JCall = cor17
```

```
LoadError: BoundsError: attempt to access 0-element Array{UInt8,1}
         at index [1]
while loading In[101], in expression starting on line 1
```

```
[inlined code] from /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:167
in readnrows! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:222
in readtable! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:774
in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:862
in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:956
```

```
In [102]: TBVG5NGall = a[posAi]
         TBVG5NG=mean(TBVG5NGall)
```

```
Out[102]: 11.472526153846156
```

```
In [103]: GEBVG5NGall = aHat1[posAi]
         GEBVG5NG=mean(GEBVG5NGall)
```

```
Out[103]: 2.01343221107292
```

```
In [104]: numSSBayes
```

```
Out[104]: SSBR.NumSSBayes(54892,45892,9000,40000,39000,1000,200)
```

```
In [105]: J_Vecs.J1
```

```
Out[105]: 45892x1 Array{Float64,2}:
```

```
 2.60005e-19  
 1.62313e-18  
-0.0122664  
-0.896974  
-0.503803  
-0.501463  
-0.000877842  
-0.752447  
-0.00117165  
-0.773699  
-0.970029  
-0.501737  
-0.943859  
 ⋮  
-0.963018  
-0.166913  
-0.756583  
-0.848193  
-0.772861  
 9.75163e-20  
-0.962529  
-0.602934  
-0.887812  
-0.878291  
-0.00234123  
-0.0835489
```

```
In [106]: sortrows(J_Vecs.J1[end-8000:end,:])
```

```
Out[106]: 8001x1 Array{Float64,2}:
```

```
-0.985943  
-0.985716  
-0.985637  
-0.983624  
-0.982885  
-0.981819  
-0.981743  
-0.981624  
-0.981311  
-0.981248  
-0.981203  
-0.981173  
-0.980891  
:  
5.5659e-17  
5.56821e-17  
5.5712e-17  
5.57874e-17  
5.57971e-17  
5.59795e-17  
5.65144e-17  
5.69226e-17  
5.83331e-17  
5.88104e-17  
6.05998e-17  
6.63939e-17
```

```
In [107]: J1 = sortrows(J_Vecs.J1)
```

```
Out[107]: 45892x1 Array{Float64,2}:
```

```
-0.986186  
-0.985943  
-0.985716  
-0.985637  
-0.985583  
-0.985556  
-0.985522  
-0.985468  
-0.985386  
-0.984727  
-0.983624  
-0.9829  
-0.982885  
:  
5.93898e-17  
5.98122e-17  
6.05998e-17  
6.61593e-17  
6.63939e-17  
7.29002e-17  
7.40974e-17  
7.66015e-17  
7.95265e-17  
8.00701e-17  
8.94951e-17  
1.07769e-16
```

```
In [108]: J1[J1 .< 0.0,:]
```

```
Out[108]: 43886x1 Array{Float64,2}:
```

```
-0.986186  
-0.985943  
-0.985716  
-0.985637  
-0.985583  
-0.985556  
-0.985522  
-0.985468  
-0.985386  
-0.984727  
-0.983624  
-0.9829  
-0.982885  
:  
-7.21236e-36  
-7.15953e-36  
-7.08388e-36  
-7.34861e-66  
-7.3438e-66  
-7.16964e-66  
-3.67431e-66  
-3.6719e-66  
-3.51402e-67  
-1.78007e-67  
-1.76496e-67  
-1.75701e-67
```

```
In [109]: J1[J1 .> 0.0,:]
```

```
Out[109]: 1305x1 Array{Float64,2}:  
 3.90135e-83  
 8.15325e-82  
 8.1586e-82  
 7.94868e-52  
 8.01673e-52  
 1.58257e-51  
 1.58974e-51  
 1.60146e-51  
 1.60241e-51  
 1.60241e-51  
 1.60241e-51  
 1.60335e-51  
 3.06642e-51  
 ⋮  
 5.93898e-17  
 5.98122e-17  
 6.05998e-17  
 6.61593e-17  
 6.63939e-17  
 7.29002e-17  
 7.40974e-17  
 7.66015e-17  
 7.95265e-17  
 8.00701e-17  
 8.94951e-17  
 1.07769e-16
```

```
In [110]: G = convert(Array,readtable("GenNF.txt", separator = ' ',header=false));
```

```
In [111]: GAll=mean(G[:,2:end],1)
```

```
Out[111]: 1x200 Array{Float64,2}:  
 0.357556  1.49378  0.599778  1.87278  ...  0.510444  1.86633  0.619444
```

```
In [112]: GG0=mean(G[1:200,2:end],1)
```

```
Out[112]: 1x200 Array{Float64,2}:  
 0.25  1.56  0.555  1.88  1.755  0.385  ...  1.015  1.015  0.595  1.8  0.785
```

```
In [113]: GG1=mean(G[201:400,2:end],1)
```

```
Out[113]: 1x200 Array{Float64,2}:  
 0.295  1.505  0.63  1.865  1.705  0.54  ...  1.065  1.065  0.53  1.81  0.715
```

```
In [114]: GG2=mean(G[401:600,2:end],1)
```

```
Out[114]: 1x200 Array{Float64,2}:  
 0.315  1.515  0.655  1.875  1.715  0.595  ...  1.125  1.125  0.49  1.86  0.64
```

```
In [115]: GG3=mean(G[601:800,2:end],1)
```

```
Out[115]: 1x200 Array{Float64,2}:  
 0.36  1.475  0.605  1.865  1.78  0.66  ...  1.16  1.16  0.465  1.835  0.625
```

```
In [116]: GG4=mean(G[801:1000,2:end],1)
```

```
Out[116]: 1x200 Array{Float64,2}:  
 0.425  1.465  0.585  1.865  1.825  0.635  ...  1.195  1.2  0.49  1.91  0.515
```

```
In [117]: GG5=mean(G[1001:9000,2:end],1)
```

```
Out[117]: 1x200 Array{Float64,2}:  
 0.361125  1.4925  0.599  1.87312  ...  1.13038  0.51  1.86925  0.614875
```

```
In [118]: writedlm("meanOfSNPGAll",GAll)
```

```
In [119]: writedlm("meanOfSNPGG0",GG0)
```

```
In [120]: writedlm("meanOfSNPGG1",GG1)
```

```
In [121]: writedlm("meanOfSNPGG2",GG2)
```

```
In [122]: writedlm("meanOfSNPGG3",GG3)
```

```
In [123]: writedlm("meanOfSNPGG4",GG4)
```

```
In [124]: writedlm("meanOfSNPGG5",GG5)
```


