

```
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/0.5g2k/G/1

/home/nicole/Jupyter/JG3/Data/0.5g2k/G/1
```

```
In [4]: ;ls
```

```
Correlation.G5.G.JC.txt
Correlation.G5.G.N.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]: vRes    = 0.865
vG       = 0.865
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
7078.500594 seconds (23.87 G allocations: 737.122 GB, 2.70% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 31.3246
  3.76293
```

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

```
Out[33]: 3.7629342706160984
```

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

```
Out[34]: 17.54378432325699
```

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

```
Out[35]: 2000-element Array{Float64,1}:
```

```
 0.034729  
-0.00338819  
-0.00568932  
 0.0100436  
 0.0236593  
 0.00580749  
 0.0296522  
 0.0291092  
-0.0243338  
 0.0237916  
 0.0246274  
-0.0169823  
-0.014356  
  ⋮  
-0.00029304  
 0.00477821  
 0.00483385  
 0.00864985  
 0.00403217  
 0.00131294  
 0.00746932  
 0.00523126  
-0.0132825  
-0.00709559  
 0.0221378  
 0.0414128
```

```
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 = 0.921
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.987
```

```
Out[39]: 0.9206520644987592
```

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

```
Out[40]: 33.1377618125
```

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

```
Out[41]: 1.8236012011706966
```

```
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 = 0.923
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.044
```

```
Out[42]: 0.9234639773355418
```

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

```
Out[43]: 34.61326044444444
```

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

```
Out[44]: 3.2923846229155362
```

```
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 = 0.886
```

```
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.973
```

```
Out[45]: 0.8863238227662239
```

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

```
Out[46]: 32.79726212820513
```

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

```
Out[47]: 1.484651180768041
```

```
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 = 0.735
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.929
```

```
Out[48]: 0.7351726971315338
```

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

```
Out[49]: 31.545710125
```

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

```
Out[50]: 0.14520147412212306
```

```
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 = 0.777
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.003
```

```
Out[51]: 0.7767400097926019
```

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

```
Out[52]: 32.22381812500001
```



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

```
Out[53]: 0.9279137075230538
```

```
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 = 0.768
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.996
```

```
Out[54]: 0.7680064152870382
```

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

```
Out[55]: 32.85196787500001
```

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

```
Out[56]: 1.5784180470644842
```

```
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 = 0.768
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.007
```

```
Out[57]: 0.7681070992176466
```

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

```
Out[58]: 33.450599625
```

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

```
Out[59]: 2.1681482300229935
```

```
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 =  0.770
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.026
```

```
Out[60]: 0.7696102777913572
```

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

```
Out[61]: 34.074856874999995
```

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

```
Out[62]: 2.770414071575121
```

```
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 = 0.910
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.033
```

```
Out[63]: 0.9097283297074624
```

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

```
Out[64]: 34.67961825
```

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

```
Out[65]: 3.351511676716402
```

```
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 = 0.930
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.010
```

```
Out[66]: 0.9300834204780857
```

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

```
Out[67]: 32.896510000000006
```

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

```
Out[68]: 1.7732149925036855
```

```
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 = 0.933
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.995
```

```
Out[69]: 0.9326006447599688
```

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

```
Out[70]: 33.481749999999999
```

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

```
Out[71]: 2.2743219091600073
```

```
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 = 0.935
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.011
```

```
Out[72]: 0.9346403051091838
```

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

```
Out[73]: 34.062104999999995
```

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

```
Out[74]: 2.790314147045048
```

```
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 =  0.921
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.027
```

```
Out[75]: 0.9207417269077107
```

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

```
Out[76]: 34.689359999999999
```

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

```
Out[77]: 3.3649592030750637
```

```
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)
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.883
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.950
```

```
Out[78]: 0.8832496218691842
```

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

```
Out[79]: 35.282265
```

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

```
Out[80]: 3.894030710759265
```

```
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)
JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.910
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.033
```

```
Out[81]: 0.9097283297074624
```

```
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]: 34.67961825
```

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

```
Out[85]: 3.351511676716402
```

```
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 =  0.714
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.941
```

```
Out[86]: 0.7144431832701278
```

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

```
Out[87]: 31.511074230769232
```

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

```
Out[88]: 0.10345753775336504
```

```
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 = 0.760
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.011
```

```
Out[89]: 0.7597655472051461
```

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

```
Out[90]: 32.191563461538465
```

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

```
Out[91]: 0.8933904203015934
```

```
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 = 0.750
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.996
```

```
Out[92]: 0.7499723278213039
```

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

```
Out[93]: 32.82093871794873
```



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

```
Out[94]: 1.5473437880906236
```

```
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)
         JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.750
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.004
```

```
Out[95]: 0.7501507279480297
```

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

```
Out[96]: 33.41883653846154
```

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

```
Out[97]: 2.137460769175505
```

```
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)
         JCA11 = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.753
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.023
```

```
Out[98]: 0.7527484762862764
```

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

```
Out[99]: 34.043897692307695
```

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

```
Out[100]: 2.741603388519118
```

```
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]: 34.043897692307695
```

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

```
Out[103]: 2.741603388519118
```

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

```
Out[104]: SSBR.NumSSBayes(54920,45920,9000,40000,39000,1000,2000)
```

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

```
Out[105]: 45920x1 Array{Float64,2}:
```

```
-0.000878092  
-0.00204767  
-0.00233782  
-0.897853  
-0.503513  
-0.513777  
-0.00350946  
-0.801365  
-0.752509  
-0.752336  
-0.460361  
-0.752051  
-0.962619  
⋮  
-0.943834  
-0.962551  
-0.75644  
-0.789066  
-0.751756  
-0.0134389  
-0.9663  
-0.503513  
-0.918243  
-0.898679  
-0.00116309  
-0.00170564
```

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

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

```
-0.988498  
-0.986059  
-0.984904  
-0.982868  
-0.981992  
-0.981646  
-0.981543  
-0.981299  
-0.981279  
-0.981267  
-0.981161  
-0.980909  
-0.980825  
:  
5.55843e-17  
5.56573e-17  
5.56654e-17  
5.5698e-17  
5.57141e-17  
5.66287e-17  
5.67965e-17  
5.78149e-17  
5.82959e-17  
6.62156e-17  
8.08732e-17  
9.73636e-17
```

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

```
Out[107]: 45920x1 Array{Float64,2}:
```

```
-0.988706  
-0.988498  
-0.986511  
-0.986059  
-0.985867  
-0.985788  
-0.985507  
-0.985314  
-0.985279  
-0.985184  
-0.984904  
-0.984202  
-0.984131  
:  
7.409e-17  
7.43324e-17  
7.52995e-17  
7.8916e-17  
8.08732e-17  
8.81587e-17  
8.87214e-17  
9.73636e-17  
1.02118e-16  
1.11275e-16  
1.11862e-16  
1.1197e-16
```

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

```
Out[108]: 43884x1 Array{Float64,2}:
```

```
-0.988706  
-0.988498  
-0.986511  
-0.986059  
-0.985867  
-0.985788  
-0.985507  
-0.985314  
-0.985279  
-0.985184  
-0.984904  
-0.984202  
-0.984131  
:  
-7.2166e-36  
-7.21238e-36  
-7.21238e-36  
-6.61366e-36  
-3.49169e-50  
-7.60646e-65  
-8.95569e-66  
-6.89096e-66  
-1.05058e-66  
-5.29884e-67  
-5.25288e-67  
-2.64942e-67
```

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

```
Out[109]: 1357x1 Array{Float64,2}:  
 5.37979e-83  
 5.88289e-83  
 1.60147e-51  
 1.60147e-51  
 1.60335e-51  
 1.60476e-51  
 1.61001e-51  
 2.38638e-51  
 2.74418e-51  
 3.07361e-51  
 3.19826e-51  
 3.20435e-51  
 3.20959e-51  
 ⋮  
 7.409e-17  
 7.43324e-17  
 7.52995e-17  
 7.8916e-17  
 8.08732e-17  
 8.81587e-17  
 8.87214e-17  
 9.73636e-17  
 1.02118e-16  
 1.11275e-16  
 1.11862e-16  
 1.1197e-16
```

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

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

```
Out[111]: 1x2000 Array{Float64,2}:  
 0.291556  1.38511  0.763  1.90178  ...  0.657  0.511444  1.04611  0.672444
```

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

```
Out[112]: 1x2000 Array{Float64,2}:  
 0.195  1.595  0.625  1.93  1.71  0.37  ...  1.47  0.685  0.56  0.955  0.595
```

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

```
Out[113]: 1x2000 Array{Float64,2}:  
 0.22  1.505  0.695  1.88  1.715  0.4  ...  1.455  0.645  0.56  1.005  0.615
```

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

```
Out[114]: 1x2000 Array{Float64,2}:  
 0.23  1.405  0.82  1.89  1.72  0.395  ...  1.465  0.615  0.55  1.06  0.635
```

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

```
Out[115]: 1x2000 Array{Float64,2}:  
 0.305  1.41  0.725  1.9  1.785  0.385  ...  1.435  0.65  0.57  0.965  0.655
```

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

```
Out[116]: 1x2000 Array{Float64,2}:  
 0.33  1.305  0.8  1.915  1.815  0.375  ...  1.545  0.695  0.46  1.085  0.72
```

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

```
Out[117]: 1x2000 Array{Float64,2}:  
 0.296  1.37775  0.76675  1.90163  ...  0.656875  0.507875  1.05012  0.676
```

```
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)
```


