

```
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/0.1/G/3  
  
/home/nicole/Jupyter/JG3/Data/0.1/G/3
```

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

```
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.JC.txt
Regression.G5.G.PBLUP.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPGA11
meanOfSNPGG0
meanOfSNPGG1
meanOfSNPGG2
meanOfSNPGG3
meanOfSNPGG4
meanOfSNPGG5
noGenotype.ID
sim.bv
sim.phenotype
```

```
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      = 0.865
vRes     = 7.792
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
3977.992656 seconds (23.06 G allocations: 724.048 GB, 7.63% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 8.95311
 2.03708
```

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

```
Out[33]: 2.0370778746011258
```

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

```
Out[34]: 5.495095625458314
```

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

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

```
 0.00504531  
-0.104857  
 0.100888  
 0.0399788  
 0.126248  
 0.129299  
 0.114909  
 0.133771  
-0.0250808  
 0.0296212  
 0.0466886  
-0.0322658  
 0.034427  
  ⋮  
 0.026918  
-0.0131774  
-0.0211765  
 0.0126716  
 0.0590998  
 0.0410567  
-0.0502458  
-0.0337809  
-0.0329549  
-0.0127472  
-0.0529514  
-0.0282255
```

```
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 = 0.773
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.967
```

```
Out[39]: 0.7730965726333431
```

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

```
Out[40]: 10.273093
```

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

```
Out[41]: 1.3172848502124974
```

```
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 = 0.928
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.118
```

```
Out[42]: 0.9281347134548033
```

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

```
Out[43]: 11.030237777777776
```

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

```
Out[44]: 2.1288331369850026
```

```
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)
         JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.706
```

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

```
Out[45]: 0.7064484507005065
```

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

```
Out[46]: 10.098367282051282
```

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

```
Out[47]: 1.1300044763419193
```



```
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 = 0.548
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.303
```

```
Out[48]: 0.5480621944039294
```

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

```
Out[49]: 9.244850249999999
```

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

```
Out[50]: 0.11419646997381182
```

```
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 = 0.546
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.062
```

```
Out[51]: 0.5464160516098159
```

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

```
Out[52]: 9.896761625
```

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

```
Out[53]: 0.9023530155333163
```

```
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 =  0.609
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.076
```

```
Out[54]: 0.6091362646336732
```

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

```
Out[55]: 10.160266124999998
```

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

```
Out[56]: 1.2508171904758811
```

```
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 =  0.597
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.060
```

```
Out[57]: 0.5973405305252762
```

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

```
Out[58]: 10.491404249999999
```

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

```
Out[59]: 1.5937549369109505
```

```
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 =  0.658
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.085
```

```
Out[60]: 0.6580557985972478
```

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

```
Out[61]: 10.792163
```

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

```
Out[62]: 1.893548720405763
```

```
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 = 0.926
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.119
```

```
Out[63]: 0.9259446994658769
```

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

```
Out[64]: 11.053112749999999
```

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

```
Out[65]: 2.1490387679752616
```

```
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 = 0.917
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.029
```

```
Out[66]: 0.9172323159856771
```

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

```
Out[67]: 10.552165
```

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

```
Out[68]: 1.7166292199151016
```

```
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 = 0.951
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.145
```

```
Out[69]: 0.9513419292892559
```

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

```
Out[70]: 10.432319999999999
```

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

```
Out[71]: 1.605812621908096
```

```
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 = 0.929
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.083
```

```
Out[72]: 0.9286407070998751
```

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

```
Out[73]: 10.804575000000002
```

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

```
Out[74]: 1.9466088699767676
```

```
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 =  0.925
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.090
```

```
Out[75]: 0.9251075486224902
```

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

```
Out[76]: 11.123205
```

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

```
Out[77]: 2.196476261121293
```

```
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 = 0.918
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.111
```

```
Out[78]: 0.9177678719967547
```

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

```
Out[79]: 11.323925
```

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

```
Out[80]: 2.3704134723933503
```

```
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 = 0.926
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.119
```

```
Out[81]: 0.9259446994658769
```

```
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]: 11.053112749999999
```

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

```
Out[85]: 2.1490387679752616
```

```
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 =  0.542
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.745
```

```
Out[86]: 0.5419632939862745
```

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

```
Out[87]: 9.21132935897436
```

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

```
Out[88]: 0.073108450744548
```



```
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 =  0.525
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.077
```

```
Out[89]: 0.5252210789346861
```

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

```
Out[90]: 9.883029358974357
```

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

```
Out[91]: 0.8843155897288347
```

```
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 =  0.595
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.083
```

```
Out[92]: 0.5947208316330476
```

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

```
Out[93]: 10.143745384615382
```

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

```
Out[94]: 1.2329763781809864
```

```
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 = 0.582
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.059
```

```
Out[95]: 0.5816713247268842
```

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

```
Out[96]: 10.47520423076923
```

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

```
Out[97]: 1.5783005439824802
```

```
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 = 0.647
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.083
```

```
Out[98]: 0.6473061231915976
```

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

```
Out[99]: 10.778528076923077
```

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

```
Out[100]: 1.8813214190727479
```

```
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)
          JCA11 = 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]: 10.778528076923077
```

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

```
Out[103]: 1.8813214190727479
```

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

```
Out[104]: SSBR.NumSSBayes(54925,45925,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45925x1 Array{Float64,2}:
```

```
-0.00351127  
-0.88779  
-0.515213  
-0.503732  
-0.00234055  
-0.752192  
-0.751902  
-0.751756  
-0.00117028  
-0.752311  
-0.962595  
-0.501463  
-0.943826  
:  
-0.943827  
-0.962573  
-0.00117096  
-0.757162  
-0.757761  
-0.770001  
-0.500439  
-0.971862  
-0.504093  
-0.88779  
-0.878488  
-0.00117096
```

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

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

```
-0.982252  
-0.981408  
-0.981388  
-0.981248  
-0.981212  
-0.981152  
-0.981146  
-0.980864  
-0.980837  
-0.980797  
-0.98078  
-0.980755  
-0.980747  
:  
5.55842e-17  
5.55843e-17  
5.55846e-17  
5.56168e-17  
5.56346e-17  
5.56576e-17  
5.58194e-17  
5.61715e-17  
5.62624e-17  
5.81617e-17  
6.11258e-17  
7.5085e-17
```

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

```
Out[107]: 45925x1 Array{Float64,2}:  
  -0.986533  
  -0.985645  
  -0.985623  
  -0.985619  
  -0.985597  
  -0.985302  
  -0.985283  
  -0.984749  
  -0.984482  
  -0.984458  
  -0.984087  
  -0.983828  
  -0.983065  
  ⋮  
  6.11258e-17  
  6.20241e-17  
  6.42309e-17  
  6.56163e-17  
  6.76734e-17  
  7.46666e-17  
  7.5085e-17  
  7.55122e-17  
  7.94764e-17  
  8.8797e-17  
  1.00747e-16  
  1.11193e-16
```

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

```
Out[108]: 43891x1 Array{Float64,2}:
```

```
-0.986533  
-0.985645  
-0.985623  
-0.985619  
-0.985597  
-0.985302  
-0.985283  
-0.984749  
-0.984482  
-0.984458  
-0.984087  
-0.983828  
-0.983065  
:  
-7.2166e-36  
-7.2166e-36  
-7.21477e-36  
-7.21477e-36  
-7.2124e-36  
-7.21238e-36  
-7.20807e-36  
-2.79335e-49  
-2.79335e-49  
-1.79591e-67  
-1.79591e-67  
-1.77799e-67
```

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

```
Out[109]: 1334x1 Array{Float64,2}:
```

```
8.00737e-52
8.01203e-52
8.02378e-52
8.02378e-52
8.04974e-52
8.08804e-52
8.08804e-52
1.60051e-51
1.60147e-51
1.602e-51
1.60241e-51
1.60241e-51
1.60241e-51
:
6.11258e-17
6.20241e-17
6.42309e-17
6.56163e-17
6.76734e-17
7.46666e-17
7.5085e-17
7.55122e-17
7.94764e-17
8.8797e-17
1.00747e-16
1.11193e-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}:
```

```
0.209333 1.20333 0.986111 1.85578 ... 1.00722 0.591778 1.80378 0.875
```

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

```
Out[112]: 1x200 Array{Float64,2}:
```

```
0.215 1.38 0.805 1.865 1.72 ... 0.4 0.895 0.9 0.735 1.78 0.93
```



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

```
Out[113]: 1x200 Array{Float64,2}:  
 0.205  1.44  0.77  1.855  1.71  0.44  ...  0.96  0.965  0.63  1.845  0.91
```

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

```
Out[114]: 1x200 Array{Float64,2}:  
 0.24  1.24  0.955  1.825  1.685  0.585  ...  0.955  0.955  0.62  1.84  0.915
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
 0.27  1.195  0.985  1.865  1.745  0.71  ...  1.015  1.015  0.57  1.845  0.85
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
 0.19  1.12  1.08  1.86  1.71  0.74  1.34  ...  1.045  1.05  0.575  1.775  0.83
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
 0.2075  1.19437  0.9945  1.856  1.71962  ...  1.011  0.5875  1.80212  0.8735
```

```
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)
```

