

```
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/2  
  
/home/nicole/Jupyter/JG3/Data/0.1/G/2
```

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

```
Correlation.G5.G.C.txt
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.C.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      = 0.705
vRes     = 6.350
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
3703.453910 seconds (23.05 G allocations: 723.896 GB, 7.55% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 10.3977
  3.74563
```

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

```
Out[33]: 3.7456307800577817
```

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

```
Out[34]: 7.0716832905697595
```

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

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

```
 0.0650794  
-0.026114  
 0.112051  
 0.0505976  
-0.0250953  
-0.016014  
 0.0163764  
 0.0416008  
-0.033231  
 0.0278257  
 0.0388535  
 0.0764332  
-0.0205215  
  ⋮  
-0.0217762  
-0.0503402  
 0.147426  
 0.0394074  
 0.0522408  
-0.00714481  
 0.0166507  
 0.047933  
 0.0532274  
-0.00288438  
 0.018561  
 0.0116349
```

```
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 = 0.757
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.959
```

```
Out[39]: 0.75683083226994
```

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

```
Out[40]: 11.532842479166668
```

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

```
Out[41]: 1.1546025076764308
```

```
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 = 0.931
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.136
```

```
Out[42]: 0.9314136958526791
```

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

```
Out[43]: 12.12047388888889
```

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

```
Out[44]: 1.8101462080072783
```

```
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 = 0.692
```

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

```
Out[45]: 0.6920508368786971
```

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

```
Out[46]: 11.397235230769232
```

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

```
Out[47]: 1.003323192215466
```



```
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 = 0.543
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.268
```

```
Out[48]: 0.5425800745317604
```

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

```
Out[49]: 10.65073
```

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

```
Out[50]: 0.10767159028389903
```

```
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 = 0.555
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.060
```

```
Out[51]: 0.5548363490694148
```

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

```
Out[52]: 11.261764999999999
```

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

```
Out[53]: 0.8334995956255845
```

```
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 = 0.587
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.059
```

```
Out[54]: 0.5868320664752184
```

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

```
Out[55]: 11.491451625000002
```

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

```
Out[56]: 1.1493525886638933
```

```
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 = 0.592
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.060
```

```
Out[57]: 0.5916185933187351
```

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

```
Out[58]: 11.69377025
```

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

```
Out[59]: 1.3871654412038015
```

```
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 =  0.659
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.069
```

```
Out[60]: 0.6594134479645521
```

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

```
Out[61]: 11.964299125
```

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

```
Out[62]: 1.6265347993319557
```

```
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 = 0.931
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.139
```

```
Out[63]: 0.93104659903869
```

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

```
Out[64]: 12.135038874999998
```

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

```
Out[65]: 1.8233910309494494
```

```
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 = 0.911
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.082
```

```
Out[66]: 0.9114174227602373
```

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

```
Out[67]: 11.856909999999997
```

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

```
Out[68]: 1.5602746807044001
```

```
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 = 0.945
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.096
```

```
Out[69]: 0.9451322674006786
```

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

```
Out[70]: 11.74462
```

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

```
Out[71]: 1.4936023262392748
```

```
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 = 0.937
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.103
```

```
Out[72]: 0.9369049433208749
```

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

```
Out[73]: 11.890899999999998
```

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

```
Out[74]: 1.6409681783553896
```

```
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 =  1.081
```

```
Out[75]: 0.9214448567860343
```

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

```
Out[76]: 12.230025000000003
```

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

```
Out[77]: 1.8571788598419083
```

```
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 = 0.922
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.170
```

```
Out[78]: 0.9215291662424618
```

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

```
Out[79]: 12.297315
```

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

```
Out[80]: 1.9689140772085634
```

```
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 = 0.931
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.139
```

```
Out[81]: 0.93104659903869
```

```
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]: 12.135038874999998
```

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

```
Out[85]: 1.8233910309494494
```

```
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 =  0.525
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.648
```

```
Out[86]: 0.5245086944596931
```

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

```
Out[87]: 10.619802307692307
```

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

```
Out[88]: 0.07042535719619386
```



```
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 =  0.539
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.081
```

```
Out[89]: 0.5385108971079328
```

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

```
Out[90]: 11.249384102564102
```

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

```
Out[91]: 0.8165738845842079
```

```
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 =  0.574
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.065
```

```
Out[92]: 0.574465636983547
```

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

```
Out[93]: 11.48120935897436
```

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

```
Out[94]: 1.1367470607230858
```

```
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 = 0.576
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.057
```

```
Out[95]: 0.5758388542477102
```

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

```
Out[96]: 11.680020128205127
```

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

```
Out[97]: 1.3751138150848756
```

```
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 = 0.650
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.067
```

```
Out[98]: 0.6503745845153317
```

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

```
Out[99]: 11.955760256410256
```

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

```
Out[100]: 1.6177558434889654
```

```
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]: 11.955760256410256
```

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

```
Out[103]: 1.6177558434889654
```

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

```
Out[104]: SSBR.NumSSBayes(54914,45914,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45914x1 Array{Float64,2}:
```

```
-0.00234034  
-0.00117165  
0.0  
-0.890411  
-0.66947  
-0.501767  
-0.499782  
-0.751904  
-0.751757  
-0.758043  
2.60082e-19  
-0.752046  
-0.962551  
⋮  
-0.962702  
-0.00117096  
-0.757153  
-0.804366  
-0.77316  
-0.00204584  
-0.962559  
-0.50439  
-0.943782  
-0.918927  
-0.170121  
1.29927e-19
```

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

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

```
-0.984587  
-0.984391  
-0.984313  
-0.984145  
-0.982731  
-0.981255  
-0.981142  
-0.981005  
-0.980943  
-0.980926  
-0.98092  
-0.980862  
-0.980797  
:  
5.55843e-17  
5.55843e-17  
5.56087e-17  
5.5934e-17  
5.62014e-17  
5.62787e-17  
6.07117e-17  
6.11314e-17  
6.58332e-17  
6.63457e-17  
7.57849e-17  
1.11393e-16
```

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

```
Out[107]: 45914x1 Array{Float64,2}:  
  -0.999837  
  -0.986258  
  -0.984587  
  -0.984391  
  -0.984313  
  -0.984294  
  -0.984145  
  -0.983586  
  -0.982731  
  -0.982593  
  -0.982044  
  -0.982033  
  -0.982001  
  ⋮  
  7.41326e-17  
  7.41573e-17  
  7.42549e-17  
  7.43014e-17  
  7.57849e-17  
  7.7172e-17  
  8.91647e-17  
  9.00641e-17  
  9.45996e-17  
  9.56915e-17  
  1.11393e-16  
  1.13846e-16
```

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

```
Out[108]: 43894x1 Array{Float64,2}:
```

```
-0.999837  
-0.986258  
-0.984587  
-0.984391  
-0.984313  
-0.984294  
-0.984145  
-0.983586  
-0.982731  
-0.982593  
-0.982044  
-0.982033  
-0.982001  
:  
-7.2293e-36  
-7.2293e-36  
-7.21672e-36  
-7.21344e-36  
-7.21344e-36  
-7.21343e-36  
-7.21238e-36  
-7.20923e-36  
-7.20916e-36  
-7.20688e-36  
-7.18932e-36  
-2.56687e-65
```

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

```
Out[109]: 1314x1 Array{Float64,2}:  
  1.59635e-51  
  1.6017e-51  
  1.6017e-51  
  1.60243e-51  
  1.60523e-51  
  1.60908e-51  
  2.23649e-51  
  2.40468e-51  
  4.80937e-51  
  5.03913e-51  
  9.53202e-51  
  1.73648e-50  
  6.30157e-50  
  ⋮  
  7.41326e-17  
  7.41573e-17  
  7.42549e-17  
  7.43014e-17  
  7.57849e-17  
  7.7172e-17  
  8.91647e-17  
  9.00641e-17  
  9.45996e-17  
  9.56915e-17  
  1.11393e-16  
  1.13846e-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}:  
  0.166556  1.47833  0.804222  1.82989  ...  0.546111  1.82489  0.865778
```

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

```
Out[112]: 1x200 Array{Float64,2}:  
  0.125  1.5  0.785  1.82  1.505  0.305  ...  0.885  0.885  0.67  1.78  0.995
```



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

```
Out[113]: 1x200 Array{Float64,2}:  
 0.14  1.57  0.68  1.885  1.6  0.295  ...  0.93  0.93  0.58  1.815  0.935
```

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

```
Out[114]: 1x200 Array{Float64,2}:  
 0.19  1.55  0.7  1.87  1.58  0.365  ...  0.4  0.96  0.96  0.56  1.82  0.915
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
 0.175  1.475  0.8  1.83  1.535  0.34  ...  0.385  1.0  1.0  0.56  1.82  0.835
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
 0.175  1.46  0.855  1.82  1.495  0.365  ...  1.07  1.07  0.495  1.845  0.825
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
 0.16725  1.47425  0.80925  1.828  1.529  ...  1.011  0.54275  1.826  0.861375
```

```
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)
```

