

```
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/10  
  
/home/nicole/Jupyter/JG3/Data/0.1/G/10
```

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

```
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.PBLUP.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPGAll
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      = 0.567
         vRes    = 5.110
         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
         2706.859957 seconds (23.05 G allocations: 723.882 GB, 7.21% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          8.75232
          3.33048
```

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

```
Out[33]: 3.3304779613303497
```

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

```
Out[34]: 6.041398781924631
```

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

```
Out[35]: 200-element Array{Float64,1}:
 -0.0404275
 -0.00871455
 -0.0431552
  0.0111246
  0.0698565
  0.163685
  0.0667667
  0.0658752
 -0.0311363
  0.0502384
  0.0391377
 -0.0145831
  0.11209
  ⋮
  0.0193635
  0.0506424
 -0.0198795
  0.0201025
  0.0756011
 -0.054966
  0.0169874
  0.00847195
 -0.00731564
  0.0465176
  0.0847266
 -0.0116786
```

```
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 = 0.777
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.988
```

```
Out[39]: 0.777357511469966
```

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

```
Out[40]: 9.7854824375
```

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

```
Out[41]: 1.0265316624634122
```

```
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 = 0.940
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.106
```

```
Out[42]: 0.9398383445845095
```

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

```
Out[43]: 10.445068
```

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

```
Out[44]: 1.7198741918642722
```

```
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 = 0.702
```

```
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.972
```

```
Out[45]: 0.7016955315373118
```

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

```
Out[46]: 9.633270384615386
```

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

```
Out[47]: 0.8665295402939829
```

```
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 = 0.526
```

```
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.283
```

```
Out[48]: 0.5259754141157061
```



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

```
Out[49]: 8.97592725
```

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

```
Out[50]: 0.08996649097393596
```

```
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 =  0.563
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.052
```

```
Out[51]: 0.5629706399184501
```

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

```
Out[52]: 9.44069875
```

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

```
Out[53]: 0.6522945353858611
```

```
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 = 0.594
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.060
```

```
Out[54]: 0.593625473674049
```

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

```
Out[55]: 9.689194499999997
```

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

```
Out[56]: 0.9709798484211821
```

```
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 = 0.628
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.100
```

```
Out[57]: 0.6284467236148451
```

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

```
Out[58]: 9.93373975
```

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

```
Out[59]: 1.2247635301596305
```

```
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 = 0.696
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.122
```

```
Out[60]: 0.6964992479729157
```

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

```
Out[61]: 10.203327875000003
```

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

```
Out[62]: 1.4793755489339369
```

```
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 = 0.938
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.107
```

```
Out[63]: 0.9381011326873064
```

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

```
Out[64]: 10.4700065
```

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

```
Out[65]: 1.7418100209059266
```

```
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)
        JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation =  0.916
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.042
```

```
Out[66]: 0.9157922863717165
```

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

```
Out[67]: 9.903660000000002
```

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

```
Out[68]: 1.2320746011664854
```

```
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 = 0.927
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.041
```

```
Out[69]: 0.9269648906683154
```

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

```
Out[70]: 9.956415
```

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

```
Out[71]: 1.3076162135256888
```

```
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 = 0.952
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.131
```

```
Out[72]: 0.9521321465796937
```

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

```
Out[73]: 10.173700000000002
```

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

```
Out[74]: 1.4877174743617718
```

```
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 = 0.957
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.135
```

```
Out[75]: 0.9573213687649692
```

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

```
Out[76]: 10.452524999999998
```

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

```
Out[77]: 1.71828840206221
```

```
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 = 0.931
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.081
```

```
Out[78]: 0.9307117110016623
```

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

```
Out[79]: 10.7415
```

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

```
Out[80]: 1.9762411065390242
```

```
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 = 0.938
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.107
```

```
Out[81]: 0.9381011326873064
```

```
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]: 10.4700065
```

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

```
Out[85]: 1.7418100209059266
```

```
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 = 0.511
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 1.609
```

```
Out[86]: 0.5114251579576606
```

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

```
Out[87]: 8.952139230769228
```

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

```
Out[88]: 0.06068166763566545
```

```
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 = 0.545
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.074
```

```
Out[89]: 0.5447317534900897
```

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

```
Out[90]: 9.427475256410256
```



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

```
Out[91]: 0.6354914154335577
```

```
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)
         JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.576
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.060
```

```
Out[92]: 0.5758521129039882
```

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

```
Out[93]: 9.67677128205128
```

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

```
Out[94]: 0.9577301657047566
```

```
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 = 0.612
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.099
```

```
Out[95]: 0.6120707753160116
```

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

```
Out[96]: 9.920437564102563
```

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

```
Out[97]: 1.2121090462646922
```

```
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 =  0.687
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.124
```

```
Out[98]: 0.6868852055388422
```

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

```
Out[99]: 10.18952858974359
```

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

```
Out[100]: 1.4666354064312426
```

```
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]: 10.18952858974359
```

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

```
Out[103]: 1.4666354064312426
```

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

```
Out[104]: SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45913x1 Array{Float64,2}:  
  -0.00117096  
  -0.00117096  
  -0.00234399  
  -0.887703  
  -0.503813  
  -0.501314  
  -0.834648  
  -0.751902  
  -0.752047  
  -0.8138  
  -0.96281  
  -0.524885  
  -0.943798  
  ⋮  
  -0.971996  
  -0.499552  
  -0.75644  
  -0.752048  
  -0.752751  
  -0.00117371  
  -0.977545  
  -0.504988  
  -0.887713  
  -0.878293  
  -0.00117302  
  -0.0836296
```

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

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

```
-0.984285  
-0.981255  
-0.981142  
-0.980986  
-0.980801  
-0.98079  
-0.97999  
-0.979804  
-0.979575  
-0.979406  
-0.979179  
-0.978947  
-0.978924  
:  
5.6385e-17  
5.64449e-17  
5.66645e-17  
5.6834e-17  
5.71109e-17  
6.06723e-17  
6.10414e-17  
6.31568e-17  
6.6215e-17  
6.65635e-17  
7.1097e-17  
1.21953e-16
```

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

```
Out[107]: 45913x1 Array{Float64,2}:
```

```
-0.986201  
-0.986147  
-0.985915  
-0.985641  
-0.985619  
-0.985566  
-0.984411  
-0.984392  
-0.984336  
-0.984285  
-0.984131  
-0.983883  
-0.982702  
:  
6.05964e-17  
6.06723e-17  
6.10251e-17  
6.10414e-17  
6.31568e-17  
6.34522e-17  
6.6215e-17  
6.63189e-17  
6.65635e-17  
7.1097e-17  
1.11783e-16  
1.21953e-16
```

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

```
Out[108]: 43863x1 Array{Float64,2}:
```

```
-0.986201  
-0.986147  
-0.985915  
-0.985641  
-0.985619  
-0.985566  
-0.984411  
-0.984392  
-0.984336  
-0.984285  
-0.984131  
-0.983883  
-0.982702  
:  
-1.01499e-35  
-7.25083e-36  
-7.2166e-36  
-7.2163e-36  
-7.2124e-36  
-7.21238e-36  
-7.21231e-36  
-7.20816e-36  
-7.17441e-36  
-5.07496e-36  
-2.79335e-49  
-2.57125e-65
```

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

```
Out[109]: 1334x1 Array{Float64,2}:
 2.42284e-67
 8.00267e-52
 8.01203e-52
 1.12687e-51
 1.59304e-51
 1.60053e-51
 1.60147e-51
 1.60148e-51
 1.60241e-51
 2.1823e-51
 2.40203e-51
 2.80034e-51
 2.81314e-51
 ⋮
 6.05964e-17
 6.06723e-17
 6.10251e-17
 6.10414e-17
 6.31568e-17
 6.34522e-17
 6.6215e-17
 6.63189e-17
 6.65635e-17
 7.1097e-17
 1.11783e-16
 1.21953e-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}:
 0.137667  1.50933  0.633333  1.87133  ...  0.831  0.806778  1.87111  1.02278
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.15  1.57  0.615  1.85  1.685  0.45  ...  0.885  0.875  0.755  1.85  0.975
```



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

```
Out[113]: 1x200 Array{Float64,2}:  
 0.135  1.57  0.62  1.87  1.685  0.46  ...  0.84  0.83  0.755  1.855  1.045
```

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

```
Out[114]: 1x200 Array{Float64,2}:  
 0.125  1.55  0.615  1.865  1.705  0.575  ...  0.855  0.845  0.755  1.885  1.03
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
 0.145  1.515  0.62  1.9  1.775  0.68  ...  0.595  0.9  0.89  0.77  1.88  0.995
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
 0.145  1.44  0.685  1.855  1.74  0.75  ...  0.845  0.835  0.82  1.89  1.005
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
 0.137375  1.50687  0.633625  1.87175  ...  0.828  0.81125  1.871  1.02438
```

```
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)
```

