

```
In [1]: include("/home/nicole/Jupyter/SSBRJ/src/SSBR.jl")
        using SSBR
```

```
In [2]: function getPos(ped,IDs)
        posAi = Array{Int64,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/0.5/G/9

        /home/nicole/Jupyter/JG3/Data/0.5/G/9
```

```
In [4]: ;ls
        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
        all.ID
        genotype.ID
        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.ID
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
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
nothing
df      = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);           # with
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
nothing
```

```
In [31]: vRes      = 0.547
vG       = 0.547
nIter    = 50000
@time aHat1,alphaHat,betaHat,epsHat =
ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,
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
4334.528330 seconds (23.08 G allocations: 724.613 GB, 7.00% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 10.0862
  5.33179
```

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

```
Out[33]: 5.331786110896389
```

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

```
Out[34]: 7.709016993038771
```

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

```
Out[35]: 200-element Array{Float64,1}:
 0.167635
 0.0825889
-0.0290098
 0.0499552
-0.00785691
-0.0131825
 0.00247348
 0.00196123
 0.0221479
-0.0095612
-0.0107736
 0.167361
 0.179632
  ⋮
-0.0225407
-0.0339254
 0.00136923
 0.136875
 0.130145
 0.00870659
 0.1458
-0.000974521
 0.00409424
 0.0342967
 0.048291
-0.0332861
```

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

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

```
In [38]: df = readtable("sim.bv", eltypes=[UTF8String, Float64], separator = ' ', header=:a
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 correlation
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.913
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.966
```

```
Out[39]: 0.9134976644441363
```

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

```
Out[40]: 11.428397729166667
```

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

```
Out[41]: 1.3423635758589203
```

```
In [42]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=
         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 ) # 1
         @printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3:
         JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.978
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.068
```

```
Out[42]: 0.9779061844309465
```

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

```
Out[43]: 12.488875555555556
```

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

```
Out[44]: 2.4257300783069122
```

```
In [45]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',head
         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 ) ;
         @printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6
         JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.874
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.949
```

```
Out[45]: 0.873690201631623
```

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

```
Out[46]: 11.183672076923077
```

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

```
Out[47]: 1.092355921447845
```

```
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 e
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", r
JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.676
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.796
```

```
Out[48]: 0.6757711324406883
```

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

```
Out[49]: 10.275937750000002
```

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

```
Out[50]: 0.10083402574293765
```

```
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 e
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", r
JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.780
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.971
```

```
Out[51]: 0.7796520418539746
```

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

```
Out[52]: 10.713453375
```

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

```
Out[53]: 0.6435061827414812
```

```
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 e
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.772
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.997
```

```
Out[54]: 0.7718142354495753
```

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

```
Out[55]: 11.205781749999998
```

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

```
Out[56]: 1.1469051184873091
```

```
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 e
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.767
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.994
```

```
Out[57]: 0.7672438474075506
```

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

```
Out[58]: 11.694766500000002
```

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

```
Out[59]: 1.6240134756688263
```

```
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 e
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.773
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.006
```

```
Out[60]: 0.772791985833217
```

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

```
Out[61]: 12.144875125
```

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

```
Out[62]: 2.0701581885942835
```

```
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 e
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", r
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.975
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.066
```

```
Out[63]: 0.9747271482320861
```

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

```
Out[64]: 12.535571875
```

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

```
Out[65]: 2.468764463918683
```



```
In [66]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 )
@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 = 0.984
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.056
```

```
Out[66]: 0.9838742164042266
```

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

```
Out[67]: 11.166174999999999
```

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

```
Out[68]: 1.2206553284689472
```

```
In [69]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 )
@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 = 0.977
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.033
```

```
Out[69]: 0.9769301251382634
```

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

```
Out[70]: 11.69979
```

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

```
Out[71]: 1.693465179573559
```

```
In [72]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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)
@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 = 0.966
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.054
```

```
Out[72]: 0.966265277637063
```

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

```
Out[73]: 12.181799999999999
```

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

```
Out[74]: 2.1314509660926664
```

```
In [75]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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)
@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 = 0.955
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.036
```

```
Out[75]: 0.95485772264658
```

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

```
Out[76]: 12.595339999999998
```

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

```
Out[77]: 2.519166861215527
```

```
In [78]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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)
@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 = 0.958
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.064
```

```
Out[78]: 0.9579435356860841
```

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

```
Out[79]: 12.933420000000002
```

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

```
Out[80]: 2.8425366317129974
```

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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)
@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 = 0.975
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.066
```

```
Out[81]: 0.9747271482320861
```

```
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]: 12.535571875
```

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

```
Out[85]: 2.468764463918683
```

```
In [86]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.653
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.790
```

```
Out[86]: 0.6532056989844824
```

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

```
Out[87]: 10.253111153846152
```

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

```
Out[88]: 0.07212065900637331
```

```
In [89]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.763
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.973
```

```
Out[89]: 0.7626033847356012
```

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

```
Out[90]: 10.688162692307694
```

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

```
Out[91]: 0.6165841571816842
```

```
In [92]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
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)
@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 = 0.753
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.996
```

```
Out[92]: 0.7534377029953834
```

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

```
Out[93]: 11.180755641025641
```

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

```
Out[94]: 1.1216603531640947
```

```
In [95]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
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)
@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 = 0.752
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[95]: 0.7515031905842594
```

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

```
Out[96]: 11.671674871794874
```

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

```
Out[97]: 1.6010608247573728
```

```
In [98]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.759
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.004
```

```
Out[98]: 0.7588403516787727
```

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

```
Out[99]: 12.124656025641027
```

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

```
Out[100]: 2.0503536131297015
```

```
In [101]: IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg18)
JCall = cor18
```

```
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]: 12.124656025641027
```

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

```
Out[103]: 2.0503536131297015
```

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

```
Out[104]: SSBR.NumSSBayes(54966,45966,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45966x1 Array{Float64,2}:  
  -0.013436  
  -0.5  
  -0.00349581  
  -0.913858  
  -0.503951  
  -0.503889  
  -0.00116959  
  -0.817037  
  -0.752156  
  -0.752192  
  -0.00233987  
  -0.751899  
  -0.962571  
  ⋮  
  -0.94522  
  -0.962573  
  -0.756471  
  -0.752339  
  -0.751903  
  1.86707e-17  
  -0.966064  
  -0.504107  
  -0.887683  
  -0.878393  
  -0.168172  
  6.49633e-20
```

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

```
Out[106]: 8001x1 Array{Float64,2}:  
  -0.990145  
  -0.984727  
  -0.983551  
  -0.981443  
  -0.981314  
  -0.981147  
  -0.981132  
  -0.98088  
  -0.980876  
  -0.980848  
  -0.980847  
  -0.980837  
  -0.980808  
  ⋮  
  5.56389e-17  
  5.56598e-17  
  5.56907e-17  
  5.57473e-17  
  5.57627e-17  
  5.58374e-17  
  5.63186e-17  
  5.65768e-17  
  6.61924e-17  
  7.14323e-17  
  8.88178e-17  
  1.2259e-16
```



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

```
Out[107]: 45966x1 Array{Float64,2}:  
  -0.990145  
  -0.986216  
  -0.985984  
  -0.985915  
  -0.985665  
  -0.985546  
  -0.985536  
  -0.985405  
  -0.985217  
  -0.984727  
  -0.984479  
  -0.984386  
  -0.983639  
  ⋮  
  6.76027e-17  
  7.10931e-17  
  7.14323e-17  
  7.52907e-17  
  7.54313e-17  
  7.75322e-17  
  7.92816e-17  
  8.88178e-17  
  9.02541e-17  
  9.40576e-17  
  9.99201e-17  
  1.2259e-16
```

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

```
Out[108]: 43930x1 Array{Float64,2}:  
  -0.990145  
  -0.986216  
  -0.985984  
  -0.985915  
  -0.985665  
  -0.985546  
  -0.985536  
  -0.985405  
  -0.985217  
  -0.984727  
  -0.984479  
  -0.984386  
  -0.983639  
  ⋮  
  -7.22508e-36  
  -7.2166e-36  
  -7.2166e-36  
  -4.91411e-36  
  -7.60646e-65  
  -3.80323e-65  
  -2.34411e-65  
  -1.17206e-65  
  -9.00332e-67  
  -4.50166e-67  
  -3.55912e-67  
  -3.55912e-67
```

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

```
Out[109]: 1367x1 Array{Float64,2}:
 2.60249e-81
 8.44487e-81
 1.60289e-51
 1.60289e-51
 1.61185e-51
 3.07671e-51
 3.20102e-51
 3.20294e-51
 3.20577e-51
 3.95084e-51
 4.05474e-51
 4.05474e-51
 4.6261e-51
 ⋮
 6.76027e-17
 7.10931e-17
 7.14323e-17
 7.52907e-17
 7.54313e-17
 7.75322e-17
 7.92816e-17
 8.88178e-17
 9.02541e-17
 9.40576e-17
 9.99201e-17
 1.2259e-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}:
 0.238444  1.88844  0.443  1.97044  ...  0.486222  1.13878  1.76722  1.1695
 6
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.165  1.82  0.46  1.955  1.66  0.24  ...  0.595  0.595  0.915  1.835  1.1
 55
```

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

```
Out[113]: 1x200 Array{Float64,2}:
 0.175  1.86  0.41  1.945  1.665  0.2  ...  0.505  0.505  1.04  1.77  1.145
```

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

```
Out[114]: 1x200 Array{Float64,2}:
 0.225  1.905  0.41  1.97  1.66  0.205  ...  0.53  0.53  1.095  1.79  1.12
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
  0.225  1.895  0.4  1.97  1.675  0.21  ...  0.455  0.455  1.155  1.725  1.2  
  15
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
  0.265  1.91  0.475  1.985  1.595  0.21  ...  0.485  0.485  1.185  1.775  
  1.15
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
  0.241875  1.88975  0.4445  1.97113  ...  0.48275  1.14637  1.76575  1.1711  
  2
```

```
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)
```