

```
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/0.5/G/1

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

```
In [4]: ;ls

Correlation.G5.G.C.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.N.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
```

```
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      = 0.668
vG       = 0.668
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
3307.237927 seconds (23.05 G allocations: 723.785 GB, 7.33% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 9.9075
 4.9784
```

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

```
Out[33]: 4.978395980569135
```

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

```
Out[34]: 7.442949221836349
```

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

```
Out[35]: 200-element Array{Float64,1}:
 -0.0512977
  0.0157711
 -0.0169307
 -0.036971
 -0.049871
  0.0253603
  0.00317008
  0.00361254
  0.00258071
 -0.00244807
  0.0101341
 -0.00653252
  0.137584
  ⋮
  0.0804077
  0.161798
 -0.0361745
 -0.0222072
  0.148515
  0.113387
 -0.0545158
 -0.00472721
 -0.0186448
  0.00931601
 -0.0245961
  0.121572
```

```
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 correlation
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.915
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.967
```

```
Out[39]: 0.914920257259231
```

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

```
Out[40]: 11.392354354166669
```

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

```
Out[41]: 1.4856759412269482
```

```
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 = %6.3f\n", reg2)
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.981
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV =  1.082
```

```
Out[42]: 0.9806631919449872
```

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

```
Out[43]: 12.525361111111112
```

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

```
Out[44]: 2.6487246534219158
```

```
In [45]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=
         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 = %6.3f\n", reg3)
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.877
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV =  0.952
```

```
Out[45]: 0.8767659424096729
```

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

```
Out[46]: 11.130891256410255
```

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

```
Out[47]: 1.2172800845665712
```

```
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 = 0.710
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.854
```

```
Out[48]: 0.7096047232136792
```

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

```
Out[49]: 10.1364735
```

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

```
Out[50]: 0.12355065740230088
```

```
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 = 0.779
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.989
```

```
Out[51]: 0.7794581748453483
```

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

```
Out[52]: 10.634187875
```

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

```
Out[53]: 0.7438215774952153
```

```
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 = 0.770
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.988
```

```
Out[54]: 0.7695278734384888
```

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

```
Out[55]: 11.175617749999997
```

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

```
Out[56]: 1.296366042216726
```

```
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 = 0.770
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.995
```

```
Out[57]: 0.7699715501539183
```

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

```
Out[58]: 11.683383124999999
```

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

```
Out[59]: 1.800110645221962
```

```
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 = 0.789
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.007
```

```
Out[60]: 0.7893496800725618
```

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

```
Out[61]: 12.150585625
```

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

```
Out[62]: 2.257274868415466
```

```
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 = 0.978
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.080
```

```
Out[63]: 0.9782068585200807
```

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

```
Out[64]: 12.573878249999998
```

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

```
Out[65]: 2.69293185661002
```



```
In [66]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.975
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.097
```

```
Out[66]: 0.9748835604207324
```

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

```
Out[67]: 11.136659999999997
```

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

```
Out[68]: 1.4003390541826253
```

```
In [69]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.980
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.043
```

```
Out[69]: 0.9799808449372412
```

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

```
Out[70]: 11.721100000000002
```

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

```
Out[71]: 1.9010462097432912
```

```
In [72]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.974
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.061
```

```
Out[72]: 0.9735809105265136
```

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

```
Out[73]: 12.206114999999997
```

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

```
Out[74]: 2.3559627762318716
```

```
In [75]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.976
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.066
```

```
Out[75]: 0.9764521083653007
```

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

```
Out[76]: 12.621465
```

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

```
Out[77]: 2.730481515745591
```

```
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)
JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.963
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.071
```

```
Out[78]: 0.9625654266686775
```

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

```
Out[79]: 13.000779999999999
```

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

```
Out[80]: 3.0875055836820255
```

```
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)
JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.978
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.080
```

```
Out[81]: 0.9782068585200807
```

```
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]: 12.573878249999998
```

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

```
Out[85]: 2.69293185661002
```

```
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 = 0.690
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.855
```

```
Out[86]: 0.6900796678621672
```

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

```
Out[87]: 10.110827692307693
```

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

```
Out[88]: 0.09081249338229257
```

```
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 = 0.762
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[89]: 0.7623191105767572
```

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

```
Out[90]: 10.606318333333332
```

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

```
Out[91]: 0.7141491510273159
```

```
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 = 0.752
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.988
```

```
Out[92]: 0.7516176240352204
```

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

```
Out[93]: 11.14919474358974
```

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

```
Out[94]: 1.2691968951906967
```

```
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 = 0.754
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[95]: 0.7535649385170222
```

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

```
Out[96]: 11.659329743589744
```

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

```
Out[97]: 1.7762549818752018
```

```
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 = 0.778
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.005
```

```
Out[98]: 0.7775954658481696
```

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

```
Out[99]: 12.128785769230769
```

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

```
Out[100]: 2.2359869013573492
```

```
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]: 12.128785769230769
```

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

```
Out[103]: 2.2359869013573492
```

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

```
Out[104]: SSBR.NumSSBayes(54906,45906,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45906x1 Array{Float64,2}:
  9.22014e-19
 -0.00117028
 -0.887669
 -0.506888
 -0.501171
 -0.0122736
 -0.752051
 -0.771989
 -0.752044
 -0.971901
 -0.501765
 -0.959207
 -0.513216
  ⋮
 -0.961393
 -0.963504
 -2.89386e-35
 -0.838608
 -0.752192
 -0.751756
  1.2987e-19
 -0.962573
 -0.638225
 -0.91827
 -0.878362
 -0.00156891
```

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

```
Out[106]: 8001x1 Array{Float64,2}:  
  -0.999676  
  -0.983545  
  -0.981624  
  -0.981231  
  -0.981231  
  -0.980891  
  -0.980888  
  -0.980879  
  -0.980864  
  -0.980808  
  -0.980732  
  -0.979785  
  -0.979419  
  ⋮  
  5.56413e-17  
  5.56418e-17  
  5.57142e-17  
  5.574e-17  
  5.59134e-17  
  5.62542e-17  
  5.7199e-17  
  5.76026e-17  
  5.90253e-17  
  6.67238e-17  
  1.10761e-16  
  1.10949e-16
```



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

```
Out[107]: 45906x1 Array{Float64,2}:  
  -0.999676  
  -0.997643  
  -0.988757  
  -0.987284  
  -0.985823  
  -0.985587  
  -0.985551  
  -0.985066  
  -0.984633  
  -0.984498  
  -0.984346  
  -0.984273  
  -0.984156  
  ⋮  
   6.08279e-17  
   6.14904e-17  
   6.60531e-17  
   6.67238e-17  
   6.67549e-17  
   7.5108e-17  
   8.07893e-17  
   8.88438e-17  
   9.974e-17  
   1.0006e-16  
   1.10761e-16  
   1.10949e-16
```

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

```
Out[108]: 43936x1 Array{Float64,2}:  
  -0.999676  
  -0.997643  
  -0.988757  
  -0.987284  
  -0.985823  
  -0.985587  
  -0.985551  
  -0.985066  
  -0.984633  
  -0.984498  
  -0.984346  
  -0.984273  
  -0.984156  
  ⋮  
  -7.21871e-36  
  -7.20816e-36  
  -7.20816e-36  
  -7.20812e-36  
  -7.20812e-36  
  -7.20395e-36  
  -7.05053e-36  
  -4.91411e-36  
  -2.5921e-65  
  -5.33294e-67  
  -2.66647e-67  
  -1.78216e-67
```

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

```
Out[109]: 1264x1 Array{Float64,2}:
 8.00262e-52
 8.02614e-52
 1.60052e-51
 1.60476e-51
 1.60523e-51
 1.60523e-51
 2.40174e-51
 3.19885e-51
 3.20388e-51
 3.20953e-51
 4.53675e-51
 4.80349e-51
 6.42512e-51
 ⋮
 6.08279e-17
 6.14904e-17
 6.60531e-17
 6.67238e-17
 6.67549e-17
 7.5108e-17
 8.07893e-17
 8.88438e-17
 9.974e-17
 1.0006e-16
 1.10761e-16
 1.10949e-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}:
 0.124111  1.60911  0.649  1.86378  1.61022  ...  0.537444  1.81689  0.9158
89
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.09  1.665  0.58  1.88  1.63  0.305  ...  0.3  0.885  0.885  0.63  1.8
0.96
```

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

```
Out[113]: 1x200 Array{Float64,2}:
 0.125  1.665  0.575  1.885  1.65  ...  0.17  0.96  0.96  0.53  1.79  0.915
```

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

```
Out[114]: 1x200 Array{Float64,2}:
 0.14  1.535  0.71  1.84  1.59  0.37  ...  0.985  0.985  0.525  1.805  0.88
5
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
  0.125  1.575  0.72  1.87  1.585  0.375  ...  0.93  0.93  0.575  1.805  0.9  
  15
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
  0.125  1.63  0.61  1.86  1.62  0.44  0.84  ...  0.97  0.975  0.505  1.83  
  0.93
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
  0.1245  1.6085  0.65025  1.86338  ...  0.954  0.5355  1.81825  0.91525
```

```
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)
```