

```
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/0.3/G/7  
  
        /home/nicole/Jupyter/JG3/Data/0.3/G/7
```

```
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      = 0.647
         vRes    = 1.510
         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
         5695.655064 seconds (23.07 G allocations: 724.282 GB, 5.98% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          10.928
           4.82435
```

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

```
Out[33]: 4.824353026660432
```

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

```
Out[34]: 7.876161410794295
```

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

```
Out[35]: 200-element Array{Float64,1}:
 -0.00853233
  0.0488296
  0.0221144
 -0.0116155
 -0.0646552
 -0.0575412
  0.0103845
  0.0117738
 -0.00483299
 -0.00324496
 -0.0204249
  0.114542
 -0.010131
  ⋮
  0.0600011
  0.0010459
  0.0221588
  0.104237
  0.00305041
  0.12481
  0.025278
 -0.0661095
 -0.0657976
  0.15231
  0.0591654
  0.0727759
```

```
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 = 0.870
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.982
```

```
Out[39]: 0.8697268973114844
```

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

```
Out[40]: 12.235168791666666
```

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

```
Out[41]: 1.3082214946263002
```

```
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 = 0.969
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.077
```

```
Out[42]: 0.9689451334055432
```

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

```
Out[43]: 13.178626777777776
```

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

```
Out[44]: 2.2819643188917893
```

```
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 = 0.817
```

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

```
Out[45]: 0.8165587163338986
```

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

```
Out[46]: 12.017447717948718
```

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

```
Out[47]: 1.0835116121034947
```

```
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 = 0.678
```

```
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.103
```

```
Out[48]: 0.6779540521262883
```



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

```
Out[49]: 11.133240249999998
```

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

```
Out[50]: 0.10301083810600191
```

```
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 =  0.692
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.030
```

```
Out[51]: 0.6922899448875884
```

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

```
Out[52]: 11.645055249999997
```

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

```
Out[53]: 0.7172393771003304
```

```
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 = 0.681
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.021
```

```
Out[54]: 0.6814816015958269
```

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

```
Out[55]: 12.077482625
```

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

```
Out[56]: 1.171612186752157
```

```
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 = 0.676
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.005
```

```
Out[57]: 0.6758855784858367
```

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

```
Out[58]: 12.473388625
```

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

```
Out[59]: 1.5791550613599514
```

```
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 =  0.719
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.039
```

```
Out[60]: 0.7191278488507639
```

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

```
Out[61]: 12.865080375
```

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

```
Out[62]: 1.960396698498473
```

```
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 =  0.967
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.079
```

```
Out[63]: 0.9668939506204771
```

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

```
Out[64]: 13.216765625
```

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

```
Out[65]: 2.317914805940887
```

```
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 = 0.963
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.058
```

```
Out[66]: 0.9632648680789913
```

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

```
Out[67]: 12.152225000000001
```

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

```
Out[68]: 1.3546523623579427
```

```
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)
JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.961
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.032
```

```
Out[69]: 0.9612122919564642
```

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

```
Out[70]: 12.496020000000001
```

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

```
Out[71]: 1.6396816016066784
```

```
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)
JCall = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.969
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.052
```

```
Out[72]: 0.9689446249744698
```

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

```
Out[73]: 12.88939
```

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

```
Out[74]: 1.9868764596340354
```

```
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 = 0.962
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.072
```

```
Out[75]: 0.9615562652829238
```

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

```
Out[76]: 13.247625000000001
```

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

```
Out[77]: 2.341833748126609
```

```
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 = 0.954
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.060
```

```
Out[78]: 0.9538041020019468
```

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

```
Out[79]: 13.58232
```

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

```
Out[80]: 2.6487579407697783
```

```
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 =  0.967
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.079
```

```
Out[81]: 0.9668939506204771
```

```
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]: 13.216765625
```

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

```
Out[85]: 2.317914805940887
```

```
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 =  0.659
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.165
```

```
Out[86]: 0.6590699909754837
```

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

```
Out[87]: 11.107112435897434
```

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

```
Out[88]: 0.07091746568928549
```

```
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 =  0.675
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.039
```

```
Out[89]: 0.6751028251572084
```

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

```
Out[90]: 11.62323564102564
```



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

```
Out[91]: 0.6935870123693983
```

```
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 =  0.663
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.022
```

```
Out[92]: 0.6627549511887236
```

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

```
Out[93]: 12.056664487179487
```

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

```
Out[94]: 1.1507079746269804
```

```
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 =  0.658
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.002
```

```
Out[95]: 0.657625876993169
```

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

```
Out[96]: 12.45353641025641
```

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

```
Out[97]: 1.5595991975967036
```

```
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 =  0.705
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.038
```

```
Out[98]: 0.7049699662227561
```

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

```
Out[99]: 12.846689615384614
```

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

```
Out[100]: 1.9427464102351062
```

```
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]: 12.846689615384614
```

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

```
Out[103]: 1.9427464102351062
```

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

```
Out[104]: SSBR.NumSSBayes(54942,45942,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45942x1 Array{Float64,2}:  
  -0.00114213  
  -0.00117096  
    2.60005e-19  
  -0.918157  
  -0.504722  
  -0.501466  
  -0.00224277  
  -0.82738  
  -0.834464  
  -0.772731  
  -0.752191  
  -0.962529  
  -0.943827  
    ⋮  
  -0.94386  
  -0.973758  
  -0.00233986  
  -0.75644  
  -0.751765  
  -0.751902  
  -0.962529  
  -0.878235  
  -0.504376  
  -0.918167  
  -0.00235304  
  -0.00117131
```

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

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

```
-0.98221  
-0.98178  
-0.981282  
-0.98128  
-0.981251  
-0.981245  
-0.981231  
-0.981152  
-0.981142  
-0.980947  
-0.980913  
-0.980895  
-0.98085  
:  
5.55112e-17  
5.55713e-17  
5.55842e-17  
5.56595e-17  
5.56744e-17  
5.57885e-17  
5.65978e-17  
5.83886e-17  
6.33741e-17  
6.64764e-17  
8.85368e-17  
8.88593e-17
```

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

```
Out[107]: 45942x1 Array{Float64,2}:  
  -0.985636  
  -0.985575  
  -0.985548  
  -0.985536  
  -0.985285  
  -0.985264  
  -0.984177  
  -0.983911  
  -0.983722  
  -0.983544  
  -0.982976  
  -0.982691  
  -0.982491  
  :  
  7.40532e-17  
  7.47313e-17  
  7.74044e-17  
  8.85368e-17  
  8.87612e-17  
  8.87612e-17  
  8.87964e-17  
  8.88593e-17  
  8.89114e-17  
  8.89115e-17  
  8.91533e-17  
  1.07076e-16
```

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

```
Out[108]: 43877x1 Array{Float64,2}:
```

```
-0.985636  
-0.985575  
-0.985548  
-0.985536  
-0.985285  
-0.985264  
-0.984177  
-0.983911  
-0.983722  
-0.983544  
-0.982976  
-0.982691  
-0.982491  
:  
-1.0814e-35  
-7.24659e-36  
-7.22508e-36  
-7.20816e-36  
-7.20393e-36  
-7.0434e-36  
-5.67514e-36  
-5.40698e-36  
-7.59646e-65  
-4.8926e-65  
-3.56013e-67  
-3.55653e-67
```

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

```
Out[109]: 1371x1 Array{Float64,2}:  
 8.00267e-52  
 1.20059e-51  
 1.56395e-51  
 1.59959e-51  
 1.60053e-51  
 1.60172e-51  
 1.60334e-51  
 3.20344e-51  
 3.20668e-51  
 3.20668e-51  
 3.20668e-51  
 4.70357e-51  
 4.70357e-51  
 ⋮  
 7.40532e-17  
 7.47313e-17  
 7.74044e-17  
 8.85368e-17  
 8.87612e-17  
 8.87612e-17  
 8.87964e-17  
 8.88593e-17  
 8.89114e-17  
 8.89115e-17  
 8.91533e-17  
 1.07076e-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}:  
 0.0716667  1.88444  0.622778  ...  0.322111  1.15467  1.80622  1.43589
```

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

```
Out[112]: 1x200 Array{Float64,2}:  
 0.1  1.775  0.58  1.935  1.585  0.145  ...  0.585  0.585  0.82  1.835  1.255
```



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

```
Out[113]: 1x200 Array{Float64,2}:  
 0.105  1.82  0.565  1.935  1.56  0.135  ...  0.425  0.425  0.965  1.78  1.405
```

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

```
Out[114]: 1x200 Array{Float64,2}:  
 0.08  1.855  0.61  1.95  1.49  0.145  ...  0.325  0.325  1.155  1.77  1.48
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
 0.075  1.92  0.63  1.97  1.42  0.095  ...  0.24  0.24  1.18  1.775  1.515
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
 0.055  1.925  0.635  1.965  1.415  ...  0.295  0.295  1.195  1.82  1.445
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
 0.07025  1.88763  0.625125  1.95575  ...  0.315625  1.16613  1.8075  1.43788
```

```
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)
```

