

```
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/0.5g2k/G/9  
  
/home/nicole/Jupyter/JG3/Data/0.5g2k/G/9
```

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

```
Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.txt
G0.Genotype.ID
G0.ID
G0.noGenotype.ID
G1.Genotype.ID
G1.ID
G1.noGenotype.ID
G2.Genotype.ID
G2.ID
G2.noGenotype.ID
G3.Genotype.ID
G3.ID
G3.noGenotype.ID
G4.Genotype.ID
G4.ID
G4.noGenotype.ID
G5.Genotype.ID
G5.ID
G5.noGenotype.ID
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.JC.txt
Regression.G5.G.PBLUP.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
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      = 0.682
         vRes     = 0.682
         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
         7142.653798 seconds (23.87 G allocations: 737.342 GB, 2.63% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          30.1215
           3.10701
```

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

```
Out[33]: 3.1070113469072127
```

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

```
Out[34]: 16.614270801950003
```

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

```
Out[35]: 2000-element Array{Float64,1}:
 0.00856269
-0.00594836
-0.00377762
-0.0130578
 0.00266958
 0.00459507
 0.0150309
 0.0147903
-0.00198133
 0.00255856
 0.00512402
 0.00058171
-0.000984673
  ⋮
 0.00772571
-0.00339567
 0.000838497
 0.00805105
-0.00856725
 0.00850079
 0.0300827
 0.0259277
-0.00683255
-0.029652
 0.0174637
 0.00748029
```

```
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 = 0.920
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.996
```

```
Out[39]: 0.9201688022498467
```

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

```
Out[40]: 31.740460895833337
```

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

```
Out[41]: 1.6144770576788532
```

```
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 = 0.920
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.097
```

```
Out[42]: 0.9204657148075781
```

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

```
Out[43]: 33.07933477777778
```

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

```
Out[44]: 2.9380093344571687
```

```
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 = 0.886
```

```
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.979
```

```
Out[45]: 0.8862145129354484
```

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

```
Out[46]: 31.431490000000004
```

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

```
Out[47]: 1.309046532268473
```

```
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 = 0.709
```

```
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.860
```

```
Out[48]: 0.7087210563559156
```



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

```
Out[49]: 30.3241715
```

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

```
Out[50]: 0.12199482883315713
```

```
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 =  0.781
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.002
```

```
Out[51]: 0.7813734094934683
```

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

```
Out[52]: 30.86662312499999
```

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

```
Out[53]: 0.7795558012323243
```

```
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 = 0.774
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.025
```

```
Out[54]: 0.7735672257826245
```

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

```
Out[55]: 31.47034175
```

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

```
Out[56]: 1.3889571975344588
```

```
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 = 0.774
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.055
```

```
Out[57]: 0.7735695217649319
```

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

```
Out[58]: 32.05523775
```

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

```
Out[59]: 1.943943036899923
```

```
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 = 0.786
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.061
```

```
Out[60]: 0.7862330097910585
```

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

```
Out[61]: 32.58414175000001
```

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

```
Out[62]: 2.4592423263967222
```

```
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 = 0.903
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.087
```

```
Out[63]: 0.9032637872360373
```

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

```
Out[64]: 33.142249500000005
```

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

```
Out[65]: 2.9931691551765356
```

```
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 =  0.943
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.078
```

```
Out[66]: 0.9430858653483376
```

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

```
Out[67]: 31.40948
```

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

```
Out[68]: 1.5025476532901214
```

```
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 = 0.935
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.063
```

```
Out[69]: 0.9351187525715774
```

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

```
Out[70]: 32.04329
```

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

```
Out[71]: 2.0353917330709503
```

```
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 = 0.930
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.077
```

```
Out[72]: 0.9302540939291033
```

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

```
Out[73]: 32.625765
```

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

```
Out[74]: 2.514480825961023
```

```
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 = 0.935
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.081
```

```
Out[75]: 0.9347361151576645
```

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

```
Out[76]: 33.108585
```

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

```
Out[77]: 2.9536695605540575
```

```
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 = 0.887
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.039
```

```
Out[78]: 0.886855484377185
```

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

```
Out[79]: 33.692964999999994
```

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

```
Out[80]: 3.4775640706350104
```

```
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 =  0.903
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.087
```

```
Out[81]: 0.9032637872360373
```

```
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]: 33.142249500000005
```

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

```
Out[85]: 2.9931691551765356
```

```
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 =  0.688
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.864
```

```
Out[86]: 0.6883728306826176
```

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

```
Out[87]: 30.29634307692307
```

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

```
Out[88]: 0.08659603846246575
```

```
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 =  0.764
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.009
```

```
Out[89]: 0.7639883122556765
```

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

```
Out[90]: 30.836452179487175
```



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

```
Out[91]: 0.7473548799031287
```

```
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 = 0.755
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.024
```

```
Out[92]: 0.755317027077706
```

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

```
Out[93]: 31.44071551282051
```

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

```
Out[94]: 1.3600976173183932
```

```
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 = 0.757
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.056
```

```
Out[95]: 0.7571356558435793
```

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

```
Out[96]: 32.02822884615385
```

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

```
Out[97]: 1.9180526132164835
```

```
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 =  0.771
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.059
```

```
Out[98]: 0.7706407361158232
```

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

```
Out[99]: 32.555710384615395
```

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

```
Out[100]: 2.4331315124418937
```

```
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]: 32.555710384615395
```

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

```
Out[103]: 2.4331315124418937
```

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

```
Out[104]: SSBR.NumSSBayes(54936,45936,9000,40000,39000,1000,2000)
```

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

```
Out[105]: 45936x1 Array{Float64,2}:  
  -0.167106  
  -0.0483071  
    0.0  
  -0.925161  
  -0.545749  
  -0.626371  
  -0.753427  
  -0.752202  
  -0.753965  
   -0.5  
  -0.962529  
  -0.50173  
  -0.943794  
    ⋮  
  -0.96261  
    7.16982e-49  
  -0.756591  
  -0.751902  
  -0.752051  
  -0.00117096  
  -0.971937  
  -0.66877  
  -0.897145  
  -0.878291  
  -0.00117027  
  -0.00412824
```

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

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

```
-0.990025  
-0.984489  
-0.981342  
-0.981236  
-0.981184  
-0.980943  
-0.980803  
-0.980258  
-0.979676  
-0.97966  
-0.979455  
-0.97943  
-0.979409  
:  
5.53044e-17  
5.5487e-17  
5.55598e-17  
5.55601e-17  
5.55606e-17  
5.56086e-17  
5.56821e-17  
5.5706e-17  
5.58446e-17  
6.142e-17  
8.55174e-17  
8.87784e-17
```

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

```
Out[107]: 45936x1 Array{Float64,2}:  
  -0.990025  
  -0.98809  
  -0.987366  
  -0.987008  
  -0.985663  
  -0.98563  
  -0.985531  
  -0.985516  
  -0.985507  
  -0.985263  
  -0.984489  
  -0.98443  
  -0.984282  
  ⋮  
  7.40761e-17  
  7.41998e-17  
  7.42328e-17  
  7.43279e-17  
  7.62382e-17  
  7.92937e-17  
  8.55174e-17  
  8.87784e-17  
  8.8823e-17  
  8.88974e-17  
  9.11936e-17  
  1.11387e-16
```

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

```
Out[108]: 43959x1 Array{Float64,2}:
```

```
-0.990025  
-0.98809  
-0.987366  
-0.987008  
-0.985663  
-0.98563  
-0.985531  
-0.985516  
-0.985507  
-0.985263  
-0.984489  
-0.98443  
-0.984282  
:  
-1.08281e-35  
-7.25056e-36  
-7.22085e-36  
-7.2166e-36  
-6.62143e-36  
-6.61108e-36  
-5.53453e-36  
-2.1823e-51  
-2.75916e-65  
-1.37958e-65  
-3.55494e-67  
-1.7874e-67
```

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

```
Out[109]: 1280x1 Array{Float64,2}:  
 8.04974e-52  
 1.22891e-51  
 1.47025e-51  
 1.601e-51  
 1.60995e-51  
 3.20059e-51  
 3.202e-51  
 4.51394e-51  
 4.8016e-51  
 4.80598e-51  
 4.81189e-51  
 7.71331e-51  
 1.4673e-50  
 ⋮  
 7.40761e-17  
 7.41998e-17  
 7.42328e-17  
 7.43279e-17  
 7.62382e-17  
 7.92937e-17  
 8.55174e-17  
 8.87784e-17  
 8.8823e-17  
 8.88974e-17  
 9.11936e-17  
 1.11387e-16
```

```
In [110]: G = convert(Array,readtable("GenNF.txt", separator = ' ',header=false));
```

```
In [111]: GAll=mean(G[:,2:end],1)
```

```
Out[111]: 1x2000 Array{Float64,2}:  
 0.172333  1.67578  0.499333  1.88289  ...  0.405444  1.04078  0.683222
```

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

```
Out[112]: 1x2000 Array{Float64,2}:  
 0.12  1.72  0.485  1.92  1.74  0.26  ...  1.49  0.565  0.53  1.045  0.695
```



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

```
Out[113]: 1x2000 Array{Float64,2}:  
 0.155  1.735  0.455  1.94  1.755  ...  1.555  1.56  0.67  0.45  1.04  0.69
```

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

```
Out[114]: 1x2000 Array{Float64,2}:  
 0.16  1.725  0.445  1.915  1.775  0.26  ...  1.62  0.68  0.385  1.055  0.665
```

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

```
Out[115]: 1x2000 Array{Float64,2}:  
 0.135  1.685  0.51  1.89  1.725  0.245  ...  1.625  0.72  0.395  1.035  0.69
```

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

```
Out[116]: 1x2000 Array{Float64,2}:  
 0.21  1.62  0.53  1.85  1.735  0.31  0.845  ...  1.625  0.7  0.38  1.035  0.69
```

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

```
Out[117]: 1x2000 Array{Float64,2}:  
 0.174375  1.67312  0.501125  1.88038  ...  0.402625  1.04062  0.682875
```

```
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)
```

