

```
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/7

        /home/nicole/Jupyter/JG3/Data/0.5/G/7
```

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

```
In [31]: vRes = 0.711
          vG = 0.711
          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
          5187.800292 seconds (23.05 G allocations: 723.937 GB, 6.17% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          9.70013
          5.39228
```

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

```
Out[33]: 5.39228091103539
```

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

```
Out[34]: 7.546205625783106
```

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

```
Out[35]: 200-element Array{Float64,1}:
 -0.0170947
  0.0764411
  0.0567359
  0.0167031
 -0.108765
  0.0107752
 -0.000857416
  0.0473979
  0.0106753
 -0.00906312
  0.0114032
  0.0324354
  0.0693975
  ⋮
 -0.00555584
 -0.0150388
  0.00242261
 -0.0173528
  0.202648
  0.0190213
  0.0125956
  0.0606878
  0.0597059
 -0.0271733
 -0.0286633
  0.12793
```

```
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 = 0.916
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.975
```

```
Out[39]: 0.9158058006175105
```

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

```
Out[40]: 11.218311875
```

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

```
Out[41]: 1.527217591179006
```

```
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 =  0.979
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV =  1.075
```

```
Out[42]: 0.9787137593683679
```

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

```
Out[43]: 12.409567111111111
```

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

```
Out[44]: 2.744617499861985
```

```
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 =  0.877
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV =  0.962
```

```
Out[45]: 0.877109112373594
```

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

```
Out[46]: 10.943406820512822
```

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

```
Out[47]: 1.2462791507137028
```

```
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 = 0.713
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.886
```

```
Out[48]: 0.7125061637704476
```

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

```
Out[49]: 9.911972250000002
```

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

```
Out[50]: 0.12178061940563695
```

```
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 = 0.995
```

```
Out[51]: 0.7793851889818092
```

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

```
Out[52]: 10.446048125
```

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

```
Out[53]: 0.7628174592397468
```

```
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 = 0.781
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.022
```

```
Out[54]: 0.7806525426759475
```

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

```
Out[55]: 10.958247499999999
```

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

```
Out[56]: 1.295166750876594
```

```
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 = 0.776
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.016
```

```
Out[57]: 0.7755116090616353
```

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

```
Out[58]: 11.531684875
```

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

```
Out[59]: 1.8625020078916126
```

```
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 = 0.783
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.016
```

```
Out[60]: 0.7832732281597123
```

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

```
Out[61]: 11.999897374999996
```

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

```
Out[62]: 2.3283338282094657
```

```
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 = 0.976
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.072
```

```
Out[63]: 0.976054233751346
```

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

```
Out[64]: 12.462021125
```

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

```
Out[65]: 2.792704881450979
```



```
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 = 0.976
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.059
```

```
Out[66]: 0.975677529193816
```

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

```
Out[67]: 10.996195
```

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

```
Out[68]: 1.4516927254892875
```

```
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 = 0.976
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.079
```

```
Out[69]: 0.9758032577211068
```

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

```
Out[70]: 11.449715
```

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

```
Out[71]: 1.8603300222146828
```

```
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 = 0.976
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.073
```

```
Out[72]: 0.976297424039526
```

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

```
Out[73]: 12.099385
```

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

```
Out[74]: 2.4609954117032418
```

```
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 = 0.969
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.061
```

```
Out[75]: 0.9692653445046291
```

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

```
Out[76]: 12.470485000000002
```

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

```
Out[77]: 2.8025562276935445
```

```
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 = 0.956
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.088
```

```
Out[78]: 0.9561893602268594
```

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

```
Out[79]: 12.933895000000001
```

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

```
Out[80]: 3.2240178486494115
```

```
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 = 0.976
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.072
```

```
Out[81]: 0.976054233751346
```

```
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]: 12.462021125
```

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

```
Out[85]: 2.792704881450979
```

```
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 = 0.692
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.889
```

```
Out[86]: 0.6917012563281101
```

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

```
Out[87]: 9.884171666666667
```

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

```
Out[88]: 0.08768030899323563
```

```
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 = 0.765
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.001
```

```
Out[89]: 0.7652852555892737
```

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

```
Out[90]: 10.420313076923078
```

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

```
Out[91]: 0.7346761114711587
```

```
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 = 0.762
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.025
```

```
Out[92]: 0.762364889772509
```

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

```
Out[93]: 10.928987564102563
```

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

```
Out[94]: 1.2652737082912955
```

```
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 = 0.762
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.016
```

```
Out[95]: 0.7615327925918483
```

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

```
Out[96]: 11.507613076923077
```

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

```
Out[97]: 1.838398053537717
```

```
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 = 0.770
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.013
```

```
Out[98]: 0.7703206286428688
```

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

```
Out[99]: 11.975948717948715
```

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

```
Out[100]: 2.3053675712751076
```

```
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]: 11.975948717948715
```

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

```
Out[103]: 2.3053675712751076
```

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

```
Out[104]: SSBR.NumSSBayes(54917,45917,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45917x1 Array{Float64,2}:  
  -0.168084  
  -0.00350809  
   3.90161e-19  
  -0.887661  
  -0.503514  
  -0.502671  
   0.0  
  -0.752156  
  -0.752184  
  -0.753424  
  -0.00231388  
  -0.815662  
  -0.962573  
   ⋮  
  -0.971951  
  -0.00117033  
  -0.854178  
  -0.753751  
  -0.752204  
  -0.00231016  
  -0.962551  
  -0.503514  
  -0.890363  
  -0.87827  
  -0.00117165  
  -0.25701
```

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

```
Out[106]: 8001x1 Array{Float64,2}:  
  -0.981325  
  -0.981294  
  -0.981267  
  -0.981241  
  -0.981173  
  -0.981142  
  -0.980858  
  -0.980804  
  -0.980797  
  -0.979775  
  -0.979548  
  -0.979536  
  -0.979227  
  ⋮  
  5.56159e-17  
  5.58444e-17  
  5.5891e-17  
  5.59013e-17  
  5.59142e-17  
  5.61862e-17  
  5.62307e-17  
  5.65449e-17  
  5.86647e-17  
  6.10506e-17  
  8.51031e-17  
  8.89559e-17
```



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

```
Out[107]: 45917x1 Array{Float64,2}:  
  -0.986868  
  -0.985718  
  -0.985549  
  -0.985507  
  -0.985337  
  -0.98531  
  -0.98449  
  -0.983869  
  -0.983768  
  -0.983758  
  -0.983587  
  -0.983232  
  -0.982671  
  ⋮  
  7.40483e-17  
  7.42043e-17  
  7.42098e-17  
  7.4361e-17  
  8.51031e-17  
  8.51031e-17  
  8.61278e-17  
  8.89559e-17  
  1.02969e-16  
  1.11022e-16  
  1.11095e-16  
  1.11274e-16
```

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

```
Out[108]: 43998x1 Array{Float64,2}:  
  -0.986868  
  -0.985718  
  -0.985549  
  -0.985507  
  -0.985337  
  -0.98531  
  -0.98449  
  -0.983869  
  -0.983768  
  -0.983758  
  -0.983587  
  -0.983232  
  -0.982671  
  ⋮  
  -7.34107e-36  
  -7.23782e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.21449e-36  
  -7.00015e-66  
  -3.56334e-67  
  -3.55597e-67  
  -1.78167e-67  
  -1.77903e-67  
  -1.77799e-67  
  -8.89515e-68
```

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

```
Out[109]: 1315x1 Array{Float64,2}:
 1.97512e-83
 3.94792e-83
 3.9561e-83
 3.87655e-66
 8.01203e-52
 8.01203e-52
 8.03559e-52
 8.03559e-52
 1.60147e-51
 1.60194e-51
 1.60241e-51
 1.60241e-51
 1.60479e-51
 ⋮
 7.40483e-17
 7.42043e-17
 7.42098e-17
 7.4361e-17
 8.51031e-17
 8.51031e-17
 8.61278e-17
 8.89559e-17
 1.02969e-16
 1.11022e-16
 1.11095e-16
 1.11274e-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}:
 0.107556  1.773  0.631778  1.91978  1.54767  ...  0.720889  1.69067  1.085
56
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.105  1.69  0.605  1.905  1.64  0.285  ...  0.805  0.805  0.64  1.715  1.
035
```

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

```
Out[113]: 1x200 Array{Float64,2}:
 0.16  1.705  0.595  1.905  1.625  0.24  ...  0.775  0.775  0.68  1.72  1.0
95
```

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

```
Out[114]: 1x200 Array{Float64,2}:
 0.12  1.76  0.64  1.905  1.535  0.265  ...  0.835  0.835  0.695  1.68  1.0
2
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
  0.095  1.805  0.625  1.935  1.55  0.24  ...  0.36  0.77  0.77  0.7  1.705  
  1.1
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
  0.11  1.805  0.635  1.94  1.54  0.26  ...  0.835  0.835  0.725  1.68  1.09  
  5
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
  0.10625  1.7755  0.63325  1.92  1.54388  ...  0.802125  0.725  1.6895  1.0  
  8763
```

```
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)
```