

```
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/0.1/G/3

/home/nicole/Jupyter/JG3/Data/0.1/G/3
```

```
In [4]: ;ls

Correlation.G5.G.JC.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
```

```
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      = 0.865
          vG        = 7.792
          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
          2561.635857 seconds (23.06 G allocations: 724.047 GB, 7.33% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          8.94794
          1.46823
```

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

```
Out[33]: 1.4682345483565278
```

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

```
Out[34]: 5.208089102694675
```

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

```
Out[35]: 200-element Array{Float64,1}:
 0.0889997
-0.101093
 0.235661
 0.110802
 0.169854
 0.387839
 0.215116
 0.221275
 0.0609287
-0.326826
 0.32077
 0.0728246
-0.0728705
  ⋮
-0.126005
-0.223166
 0.0203274
-0.0487472
 0.244383
 0.0518122
 0.00127904
-0.204371
-0.108773
-0.187492
 0.00336207
-0.0246237
```

```
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",
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.540
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.258
```

```
Out[39]: 0.5403656667108959
```

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

```
Out[40]: 10.273093
```

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

```
Out[41]: 1.5722708627320634
```

```
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 = 0.877
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.819
```

```
Out[42]: 0.8769012195116113
```

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

```
Out[43]: 11.030237777777776
```

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

```
Out[44]: 3.624189021536428
```

```
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 = 0.437
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.208
```

```
Out[45]: 0.4372004552383708
```

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

```
Out[46]: 10.098367282051282
```

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

```
Out[47]: 1.0987512876233643
```

```
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 = 0.696
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.525
```

```
Out[48]: 0.6964635088170991
```

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

```
Out[49]: 9.244850249999999
```

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

```
Out[50]: 0.19586811510341567
```

```
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 = 0.338
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.130
```

```
Out[51]: 0.33755546020822463
```

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

```
Out[52]: 9.896761625
```

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

```
Out[53]: 0.9273968596057541
```

```
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 = 0.351
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.140
```

```
Out[54]: 0.3511197545286474
```

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

```
Out[55]: 10.160266124999998
```

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

```
Out[56]: 1.1674667521590123
```

```
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 = 0.331
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.128
```

```
Out[57]: 0.33124857460516177
```

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

```
Out[58]: 10.491404249999999
```

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

```
Out[59]: 1.546643873269591
```

```
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 = 0.344
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.130
```

```
Out[60]: 0.3442492762761398
```

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

```
Out[61]: 10.792163
```

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

```
Out[62]: 1.942619632521748
```

```
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 = 0.873
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.816
```

```
Out[63]: 0.8729442992048853
```

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

```
Out[64]: 11.053112749999999
```

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

```
Out[65]: 3.653629943732861
```



```
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 = 0.868
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.774
```

```
Out[66]: 0.8677885279335632
```

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

```
Out[67]: 10.552165
```

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

```
Out[68]: 2.9552368821201793
```

```
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 = 0.901
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.891
```

```
Out[69]: 0.9013991538251714
```

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

```
Out[70]: 10.432319999999999
```

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

```
Out[71]: 2.9594760161654228
```

```
In [72]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.878
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.842
```

```
Out[72]: 0.8777267985294123
```

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

```
Out[73]: 10.804575000000002
```

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

```
Out[74]: 3.3496917737697998
```

```
In [75]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.898
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.860
```

```
Out[75]: 0.8981563489528517
```

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

```
Out[76]: 11.123205
```

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

```
Out[77]: 3.672436514543165
```

```
In [78]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.861
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.872
```

```
Out[78]: 0.8614105812033063
```

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

```
Out[79]: 11.323925
```

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

```
Out[80]: 4.006467033226243
```

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.873
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.816
```

```
Out[81]: 0.8729442992048853
```

```
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]: 11.053112749999999
```

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

```
Out[85]: 3.653629943732861
```

```
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 = 0.675
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.530
```

```
Out[86]: 0.674645113932315
```

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

```
Out[87]: 9.21132935897436
```

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

```
Out[88]: 0.1251150697952935
```

```
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 = 0.324
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.124
```

```
Out[89]: 0.32367266858942306
```

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

```
Out[90]: 9.883029358974357
```

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

```
Out[91]: 0.875292265847814
```

```
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 = 0.337
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.134
```

```
Out[92]: 0.33661697768150345
```

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

```
Out[93]: 10.143745384615382
```

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

```
Out[94]: 1.1115122644254023
```

```
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 = 0.316
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.122
```

```
Out[95]: 0.3162994840759935
```

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

```
Out[96]: 10.47520423076923
```

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

```
Out[97]: 1.4921363696471917
```

```
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 = 0.332
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.125
```

```
Out[98]: 0.3322855996775347
```

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

```
Out[99]: 10.778528076923077
```

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

```
Out[100]: 1.88970046840112
```

```
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]: 10.778528076923077
```

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

```
Out[103]: 1.88970046840112
```

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

```
Out[104]: SSBR.NumSSBayes(54925,45925,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45925x1 Array{Float64,2}:  
  -0.00351127  
  -0.88779  
  -0.515213  
  -0.503732  
  -0.00234055  
  -0.752192  
  -0.751902  
  -0.751756  
  -0.00117028  
  -0.752311  
  -0.962595  
  -0.501463  
  -0.943826  
  ⋮  
  -0.943827  
  -0.962573  
  -0.00117096  
  -0.757162  
  -0.757761  
  -0.770001  
  -0.500439  
  -0.971862  
  -0.504093  
  -0.88779  
  -0.878488  
  -0.00117096
```

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

```
Out[106]: 8001x1 Array{Float64,2}:  
  -0.982252  
  -0.981408  
  -0.981388  
  -0.981248  
  -0.981212  
  -0.981152  
  -0.981146  
  -0.980864  
  -0.980837  
  -0.980797  
  -0.98078  
  -0.980755  
  -0.980747  
  ⋮  
  5.55842e-17  
  5.55843e-17  
  5.55846e-17  
  5.56168e-17  
  5.56346e-17  
  5.56576e-17  
  5.58194e-17  
  5.61715e-17  
  5.62624e-17  
  5.81617e-17  
  6.11258e-17  
  7.5085e-17
```



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

```
Out[107]: 45925x1 Array{Float64,2}:  
  -0.986533  
  -0.985645  
  -0.985623  
  -0.985619  
  -0.985597  
  -0.985302  
  -0.985283  
  -0.984749  
  -0.984482  
  -0.984458  
  -0.984087  
  -0.983828  
  -0.983065  
  ⋮  
  6.11258e-17  
  6.20241e-17  
  6.42309e-17  
  6.56163e-17  
  6.76734e-17  
  7.46666e-17  
  7.5085e-17  
  7.55122e-17  
  7.94764e-17  
  8.8797e-17  
  1.00747e-16  
  1.11193e-16
```

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

```
Out[108]: 43891x1 Array{Float64,2}:  
  -0.986533  
  -0.985645  
  -0.985623  
  -0.985619  
  -0.985597  
  -0.985302  
  -0.985283  
  -0.984749  
  -0.984482  
  -0.984458  
  -0.984087  
  -0.983828  
  -0.983065  
  ⋮  
  -7.2166e-36  
  -7.2166e-36  
  -7.21477e-36  
  -7.21477e-36  
  -7.2124e-36  
  -7.21238e-36  
  -7.20807e-36  
  -2.79335e-49  
  -2.79335e-49  
  -1.79591e-67  
  -1.79591e-67  
  -1.77799e-67
```

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

```
Out[109]: 1334x1 Array{Float64,2}:
 8.00737e-52
 8.01203e-52
 8.02378e-52
 8.02378e-52
 8.04974e-52
 8.08804e-52
 8.08804e-52
 1.60051e-51
 1.60147e-51
 1.602e-51
 1.60241e-51
 1.60241e-51
 1.60241e-51
 ⋮
 6.11258e-17
 6.20241e-17
 6.42309e-17
 6.56163e-17
 6.76734e-17
 7.46666e-17
 7.5085e-17
 7.55122e-17
 7.94764e-17
 8.8797e-17
 1.00747e-16
 1.11193e-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}:
 0.209333  1.20333  0.986111  1.85578  ...  1.00722  0.591778  1.80378  0.8
75
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.215  1.38  0.805  1.865  1.72  ...  0.4  0.895  0.9  0.735  1.78  0.93
```

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

```
Out[113]: 1x200 Array{Float64,2}:
 0.205  1.44  0.77  1.855  1.71  0.44  ...  0.96  0.965  0.63  1.845  0.91
```

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

```
Out[114]: 1x200 Array{Float64,2}:
 0.24  1.24  0.955  1.825  1.685  0.585  ...  0.955  0.955  0.62  1.84  0.9
15
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
 0.27  1.195  0.985  1.865  1.745  0.71  ...  1.015  1.015  0.57  1.845  0.  
85
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
 0.19  1.12  1.08  1.86  1.71  0.74  1.34  ...  1.045  1.05  0.575  1.775  
0.83
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
 0.2075  1.19437  0.9945  1.856  1.71962  ...  1.011  0.5875  1.80212  0.87  
35
```

```
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)
```