

```
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/0.5a0/G/4

        /home/nicole/Jupyter/JG3/Data/0.5a0/G/4
```

```
In [4]: ;ls

Correlation.G5.G.C.txt
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
```

```
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);
      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)
      nothing
```

```
In [31]: vRes      = 1.991
          vG        = 1.991
          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
          2479.282270 seconds (23.04 G allocations: 723.703 GB, 7.43% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
          11.2428
           6.7908
```

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

```
Out[33]: 6.790802315211974
```

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

```
Out[34]: 9.016791175268683
```

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

```
Out[35]: 200-element Array{Float64,1}:
 0.20622
-0.0811429
 0.0699344
 0.000735114
 0.033495
 0.0096007
 0.084089
 0.0618065
-0.00157358
 0.0564638
 0.104238
 0.00277686
 0.0110458
  ⋮
-0.0882899
-0.0148638
-0.0145071
-0.0212031
-0.0264714
-0.0635804
 0.378582
-0.00202729
-0.0262598
 0.0424861
 0.0133169
 0.171687
```

```
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 = 0.930
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.996
```

```
Out[39]: 0.9296845512990747
```

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

```
Out[40]: 14.033610145833334
```

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

```
Out[41]: 2.8002411775039935
```

```
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 = 0.984
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.025
```

```
Out[42]: 0.9837775226702213
```

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

```
Out[43]: 16.113595555555556
```

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

```
Out[44]: 4.9254036947232045
```

```
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 = 0.898
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.000
```

```
Out[45]: 0.8981047423319389
```

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

```
Out[46]: 13.553613512820514
```

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

```
Out[47]: 2.3098190581457136
```

```
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 = 0.824
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.148
```

```
Out[48]: 0.8243213940382262
```

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

```
Out[49]: 11.54259725
```

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

```
Out[50]: 0.22994029141656364
```

```
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 = 0.771
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.010
```

```
Out[51]: 0.7712192583235902
```

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

```
Out[52]: 12.770068125
```

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

```
Out[53]: 1.540171454937509
```

```
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 = 0.773
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.025
```

```
Out[54]: 0.7726767089895201
```

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

```
Out[55]: 13.672560125
```

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

```
Out[56]: 2.4519715132974005
```

```
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 = 0.767
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.003
```

```
Out[57]: 0.7673391204172426
```

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

```
Out[58]: 14.580887250000002
```

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

```
Out[59]: 3.3626344063043336
```

```
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 = 0.781
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 0.992
```

```
Out[60]: 0.7811780129504153
```

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

```
Out[61]: 15.439914125
```

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

```
Out[62]: 4.211789434313727
```

```
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 = 0.982
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.025
```

```
Out[63]: 0.9820860559529762
```

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

```
Out[64]: 16.195634
```

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

```
Out[65]: 5.004939964754424
```



```
In [66]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G0.Genotype.ID : correlation = %6.3f\n", cor9 )
@printf("SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = %6
JCA11 = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.971
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.004
```

```
Out[66]: 0.9712944275979299
```

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

```
Out[67]: 14.014219999999998
```

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

```
Out[68]: 2.889994147760392
```

```
In [69]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G1.Genotype.ID : correlation = %6.3f\n", cor9 )
@printf("SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = %6
JCA11 = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.977
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.037
```

```
Out[69]: 0.9768035155944331
```

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

```
Out[70]: 14.530675
```

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

```
Out[71]: 3.398990972391852
```

```
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 = 0.979
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.017
```

```
Out[72]: 0.9793437122053731
```

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

```
Out[73]: 15.507835
```

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

```
Out[74]: 4.3346415586053
```

```
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 = 0.977
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.008
```

```
Out[75]: 0.9770773151638475
```

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

```
Out[76]: 16.290675000000004
```

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

```
Out[77]: 5.073522826168117
```

```
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 = 0.973
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.026
```

```
Out[78]: 0.9731813856677363
```

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

```
Out[79]: 16.943035000000002
```

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

```
Out[80]: 5.7484181674415495
```

```
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 = 0.982
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.025
```

```
Out[81]: 0.9820860559529762
```

```
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]: 16.195634
```

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

```
Out[85]: 5.004939964754424
```

```
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 = 0.809
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 1.199
```

```
Out[86]: 0.8091424096785176
```

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

```
Out[87]: 11.479222307692309
```

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

```
Out[88]: 0.16173378227954247
```

```
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 = 0.755
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.015
```

```
Out[89]: 0.7548442933912612
```

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

```
Out[90]: 12.72492435897436
```

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

```
Out[91]: 1.4925094160284234
```

```
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 = 0.755
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.031
```

```
Out[92]: 0.7552379616889389
```

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

```
Out[93]: 13.625501794871795
```

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

```
Out[94]: 2.4036979223920696
```

```
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 = 0.750
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[95]: 0.7497478105313863
```

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

```
Out[96]: 14.53704653846154
```

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

```
Out[97]: 3.3187654724616724
```

```
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 = 0.769
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[98]: 0.7685619194498452
```

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

```
Out[99]: 15.40137256410256
```

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

```
Out[100]: 4.17238869756686
```

```
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]: 15.40137256410256
```

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

```
Out[103]: 4.17238869756686
```

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

```
Out[104]: SSBR.NumSSBayes(54900,45900,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45900x1 Array{Float64,2}:  
  3.43407e-19  
 -0.00118274  
  0.0  
 -0.915703  
 -0.504089  
 -0.501463  
 -0.0520833  
 -0.752198  
 -0.753422  
 -0.772599  
  1.30003e-19  
 -0.834809  
 -0.962637  
  ⋮  
 -0.943794  
 -0.962573  
 -0.00116242  
 -0.816504  
 -0.755551  
 -0.753421  
 -0.00117096  
 -0.96261  
 -0.639481  
 -0.88787  
 -0.502629  
 -0.000586168
```

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

```
Out[106]: 8001x1 Array{Float64,2}:
-0.986889
-0.985957
-0.985613
-0.985433
-0.984121
-0.98379
-0.983431
-0.983277
-0.983135
-0.983008
-0.981245
-0.981129
-0.98081
⋮
5.5582e-17
5.55843e-17
5.56167e-17
5.56388e-17
5.56396e-17
5.56412e-17
5.5704e-17
5.58111e-17
5.58769e-17
5.60402e-17
5.84724e-17
6.81721e-17
```



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

```
Out[107]: 45900x1 Array{Float64,2}:  
  -1.00243  
  -0.988969  
  -0.986889  
  -0.986202  
  -0.985957  
  -0.985613  
  -0.985452  
  -0.985433  
  -0.985377  
  -0.985375  
  -0.985203  
  -0.984978  
  -0.984763  
  ⋮  
  6.48833e-17  
  6.52495e-17  
  6.6039e-17  
  6.62586e-17  
  6.66651e-17  
  6.81721e-17  
  7.40486e-17  
  8.89238e-17  
  8.91103e-17  
  8.9262e-17  
  9.99488e-17  
  1.29767e-16
```

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

```
Out[108]: 43906x1 Array{Float64,2}:  
  -1.00243  
  -0.988969  
  -0.986889  
  -0.986202  
  -0.985957  
  -0.985613  
  -0.985452  
  -0.985433  
  -0.985377  
  -0.985375  
  -0.985203  
  -0.984978  
  -0.984763  
  ⋮  
  -7.27634e-36  
  -7.25083e-36  
  -7.25083e-36  
  -7.22083e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.21128e-36  
  -7.05063e-36  
  -2.42284e-67  
  -1.79376e-67  
  -1.77772e-67  
  -8.88859e-68
```

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

```
Out[109]: 1320x1 Array{Float64,2}:
 8.00613e-52
 8.07836e-52
 1.60123e-51
 1.60241e-51
 1.60335e-51
 1.61001e-51
 1.61001e-51
 1.61567e-51
 1.62435e-51
 2.1823e-51
 2.38745e-51
 4.43215e-51
 4.64621e-51
 ⋮
 6.48833e-17
 6.52495e-17
 6.6039e-17
 6.62586e-17
 6.6651e-17
 6.81721e-17
 7.40486e-17
 8.89238e-17
 8.91103e-17
 8.9262e-17
 9.99488e-17
 1.29767e-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}:
 0.235111  1.27278  0.939778  1.81044  ...  0.535333  1.19756  1.828  1.376
 44
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.175  1.52  0.735  1.885  1.625  ...  0.635  0.635  0.965  1.815  1.255
```

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

```
Out[113]: 1x200 Array{Float64,2}:
 0.185  1.465  0.76  1.855  1.625  0.42  ...  0.59  0.595  1.11  1.785  1.2
 55
```

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

```
Out[114]: 1x200 Array{Float64,2}:
 0.18  1.33  0.94  1.825  1.54  0.47  ...  0.925  0.59  0.59  1.1  1.81  1.
 305
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
  0.23  1.2  0.99  1.78  1.6  0.525  1.17  ...  0.505  0.505  1.23  1.845  
  1.43
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
  0.28  1.215  1.005  1.805  1.565  0.58  ...  0.48  0.48  1.295  1.83  1.44  
  5
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
  0.23825  1.26362  0.9465  1.808  ...  0.532125  1.20475  1.82937  1.38125
```

```
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)
```