

```
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/2

        /home/nicole/Jupyter/JG3/Data/0.5a0/G/2
```

```
In [4]: ;ls
        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
        all.ID
        genotype.ID
        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",calculateInbreeding)
nothing
df = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped); # with
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
nothing
```

```
In [31]: vRes = 0.323
vG = 0.323
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
2580.655119 seconds (23.07 G allocations: 724.447 GB, 7.60% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 2.57157
 0.769394
```

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

```
Out[33]: 0.7693940290118526
```

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

```
Out[34]: 1.6704807748079387
```

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

```
Out[35]: 200-element Array{Float64,1}:
 0.0200376
 0.0181662
-0.0992036
-0.00279797
 0.00711525
 0.142312
 0.0991294
 0.107175
 0.0020376
-0.0300703
-0.0112139
-0.029905
 0.00928008
  ⋮
 0.0131141
 0.0251551
 0.0418624
 0.0127407
-0.00446483
-0.0209726
 0.0135263
 0.0274267
 0.0221784
 0.0509634
 0.010404
 0.0102121
```

```
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 = 0.904
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.949
```

```
Out[39]: 0.9042256575140849
```

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

```
Out[40]: 3.6522895208333335
```

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

```
Out[41]: 1.0709009318797578
```

```
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 = 0.981
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.119
```

```
Out[42]: 0.9814046061784396
```

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

```
Out[43]: 4.515948888888889
```

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

```
Out[44]: 1.9437482100149654
```

```
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 = 0.857
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.912
```

```
Out[45]: 0.8565477857905578
```

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

```
Out[46]: 3.4529835128205124
```

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

```
Out[47]: 0.869474636925479
```

```
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 = 0.575
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.585
```

```
Out[48]: 0.5749185143147886
```

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

```
Out[49]: 2.760864875
```

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

```
Out[50]: 0.08603835686313431
```

```
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 = 0.775
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.953
```

```
Out[51]: 0.7745190308501868
```

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

```
Out[52]: 3.080259875
```

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

```
Out[53]: 0.5191162125675749
```

```
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 = 0.785
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.022
```

```
Out[54]: 0.7846196556571375
```

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

```
Out[55]: 3.481279124999999
```

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

```
Out[56]: 0.9314995446672378
```

```
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 = 0.775
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.046
```

```
Out[57]: 0.7752968509393889
```

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

```
Out[58]: 3.8310181249999995
```

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

```
Out[59]: 1.273447266034569
```

```
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 = 0.792
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.058
```

```
Out[60]: 0.7919808561245775
```

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

```
Out[61]: 4.203982375
```

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

```
Out[62]: 1.6358943407901556
```

```
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 = 0.979
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.116
```

```
Out[63]: 0.9786723806577317
```

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

```
Out[64]: 4.55633275
```

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

```
Out[65]: 1.9794098703558745
```



```
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
JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.980
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.140
```

```
Out[66]: 0.9798083296288502
```

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

```
Out[67]: 3.3919149999999996
```

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

```
Out[68]: 0.9743252862950058
```

```
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
JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.976
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.109
```

```
Out[69]: 0.9760889922675405
```

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

```
Out[70]: 3.9015649999999997
```

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

```
Out[71]: 1.391679609754888
```

```
In [72]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.976
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.076
```

```
Out[72]: 0.9755853764483574
```

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

```
Out[73]: 4.18399
```

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

```
Out[74]: 1.639065873559279
```

```
In [75]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.975
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.090
```

```
Out[75]: 0.9753716695447813
```

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

```
Out[76]: 4.5788999999999999
```

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

```
Out[77]: 1.9934585622229863
```

```
In [78]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.963
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.087
```

```
Out[78]: 0.9625816311768393
```

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

```
Out[79]: 4.9080200000000005
```

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

```
Out[80]: 2.2937453046062894
```

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
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 = 0.979
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.116
```

```
Out[81]: 0.9786723806577317
```

```
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]: 4.55633275
```

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

```
Out[85]: 1.9794098703558745
```

```
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 = 0.549
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.567
```

```
Out[86]: 0.5491309528346959
```

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

```
Out[87]: 2.7446841025641024
```

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

```
Out[88]: 0.06326176892898377
```

```
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 = 0.951
```

```
Out[89]: 0.7546268133608687
```

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

```
Out[90]: 3.0592007692307686
```

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

```
Out[91]: 0.4967427921268745
```

```
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 = 0.769
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.023
```

```
Out[92]: 0.7694876630016323
```

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

```
Out[93]: 3.463260897435897
```

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

```
Out[94]: 0.9133568182853905
```

```
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 = 0.758
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.045
```

```
Out[95]: 0.7576635187674465
```

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

```
Out[96]: 3.8118416666666666
```

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

```
Out[97]: 1.2549854379271739
```

```
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 = 0.778
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.056
```

```
Out[98]: 0.7780179922328528
```

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

```
Out[99]: 4.185930128205128
```

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

```
Out[100]: 1.6190263673589727
```

```
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]: 4.185930128205128
```

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

```
Out[103]: 1.6190263673589727
```

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

```
Out[104]: SSBR.NumSSBayes(54954,45954,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45954x1 Array{Float64,2}:  
  -0.00117028  
  -0.5  
  -0.00117131  
  -0.887592  
  -0.503883  
  -0.501755  
  -0.526611  
  -0.81408  
  -0.752192  
  -0.772779  
  -0.0146162  
  -0.771036  
  -0.962707  
  ⋮  
  -0.961727  
  -0.962551  
  -0.00117234  
  -0.756725  
  -0.751795  
  -0.751936  
  -0.00233884  
  -0.962803  
  -0.503517  
  -0.890726  
  -0.878363  
  -0.0134321
```

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

```
Out[106]: 8001x1 Array{Float64,2}:  
  -0.990207  
  -0.985577  
  -0.985452  
  -0.98531  
  -0.984436  
  -0.98427  
  -0.982999  
  -0.982977  
  -0.982685  
  -0.982571  
  -0.981652  
  -0.981209  
  -0.981167  
  ⋮  
  5.54868e-17  
  5.55112e-17  
  5.55577e-17  
  5.556e-17  
  5.56436e-17  
  5.56574e-17  
  5.57709e-17  
  5.58152e-17  
  5.58206e-17  
  5.61454e-17  
  7.41042e-17  
  8.53373e-17
```



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

```
Out[107]: 45954x1 Array{Float64,2}:  
  -0.990207  
  -0.987007  
  -0.985912  
  -0.985806  
  -0.985626  
  -0.985577  
  -0.985452  
  -0.985448  
  -0.98531  
  -0.985263  
  -0.984879  
  -0.98461  
  -0.984436  
  ⋮  
  5.6874e-17  
  6.32693e-17  
  6.33331e-17  
  6.6688e-17  
  7.0995e-17  
  7.41042e-17  
  7.42296e-17  
  7.52177e-17  
  7.52508e-17  
  8.53373e-17  
  8.54678e-17  
  8.89738e-17
```

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

```
Out[108]: 43889x1 Array{Float64,2}:  
  -0.990207  
  -0.987007  
  -0.985912  
  -0.985806  
  -0.985626  
  -0.985577  
  -0.985452  
  -0.985448  
  -0.98531  
  -0.985263  
  -0.984879  
  -0.98461  
  -0.984436  
  ⋮  
  -7.2166e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.21238e-36  
  -7.21237e-36  
  -7.17242e-36  
  -6.64565e-36  
  -5.93075e-36  
  -5.78073e-36  
  -5.45576e-52  
  -1.36439e-65
```

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

```
Out[109]: 1335x1 Array{Float64,2}:
 8.03086e-52
 8.03086e-52
 8.05451e-52
 1.5926e-51
 1.60147e-51
 1.60241e-51
 1.60288e-51
 1.60335e-51
 1.60617e-51
 1.60806e-51
 1.6109e-51
 1.63329e-51
 2.1823e-51
 ⋮
 5.6874e-17
 6.32693e-17
 6.33331e-17
 6.6688e-17
 7.0995e-17
 7.41042e-17
 7.42296e-17
 7.52177e-17
 7.52508e-17
 8.53373e-17
 8.54678e-17
 8.89738e-17
```

```
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}:
 0.272778  1.75467  0.329667  1.97311  ...  1.181  0.598  1.87544  0.687556
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.12  1.725  0.455  1.93  1.75  0.44  ...  0.93  0.92  0.745  1.845  0.915
```

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

```
Out[113]: 1x200 Array{Float64,2}:
 0.18  1.735  0.395  1.965  1.84  0.645  ...  1.01  1.005  0.705  1.885  0.
865
```

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

```
Out[114]: 1x200 Array{Float64,2}:
 0.185  1.745  0.355  1.955  1.86  ...  0.37  1.19  1.18  0.6  1.855  0.655
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
  0.3  1.805  0.26  1.99  1.945  0.815  ...  1.2  1.195  0.565  1.895  0.69
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
  0.335  1.725  0.345  1.975  1.9  ...  0.31  1.26  1.26  0.57  1.875  0.61
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
  0.278875  1.75562  0.325625  1.97437  ...  1.18962  0.593125  1.876  0.680  
125
```

```
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)
```