

```
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/5

/home/nicole/Jupyter/JG3/Data/0.5/G/5
```

```
In [4]: ;ls

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 = 0.699
vG = 0.699
nIter = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG)
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
3407.690229 seconds (23.05 G allocations: 723.883 GB, 7.20% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 9.97086
 5.30722
```

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

```
Out[33]: 5.3072184798652495
```

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

```
Out[34]: 7.6390403452500895
```

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

```
Out[35]: 200-element Array{Float64,1}:
 -0.037111
  0.0649546
  0.0167568
  0.0301069
 -0.0391811
  0.139121
 -0.0262346
  0.0224267
  0.0405687
 -0.0715755
 -0.0452728
  0.15527
  0.212362
  ⋮
  0.119226
  0.0274639
 -0.017926
  0.10417
  0.132354
 -0.00846585
  0.0155656
 -0.0680205
 -0.0134622
  0.169335
 -0.071117
  0.00600105
```

```
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 = 0.917
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.973
```

```
Out[39]: 0.9173902082088676
```

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

```
Out[40]: 11.514132458333334
```

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

```
Out[41]: 1.5432699197870956
```

```
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 = 0.983
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.063
```

```
Out[42]: 0.9828139016644771
```

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

```
Out[43]: 12.736877111111111
```

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

```
Out[44]: 2.8015340518959437
```

```
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 = 0.961
```

```
Out[45]: 0.8766834674914437
```

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

```
Out[46]: 11.231960615384617
```

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

```
Out[47]: 1.252901273915823
```

```
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 = 0.704
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.868
```

```
Out[48]: 0.704267893741047
```

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

```
Out[49]: 10.187546249999999
```

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

```
Out[50]: 0.12145946578600805
```

```
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 = 0.776
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.986
```

```
Out[51]: 0.7756103496347929
```

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

```
Out[52]: 10.7345095
```

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

```
Out[53]: 0.7766062996659028
```

```
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 = 0.778
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.015
```

```
Out[54]: 0.7779129328859814
```

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

```
Out[55]: 11.27873
```

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

```
Out[56]: 1.3278710940207135
```

```
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 = 0.764
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.015
```

```
Out[57]: 0.763771795179957
```

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

```
Out[58]: 11.789662125
```

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

```
Out[59]: 1.832615173463413
```

```
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
JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.783
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.010
```

```
Out[60]: 0.7826191563239352
```

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

```
Out[61]: 12.30248425
```

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

```
Out[62]: 2.348537971651929
```

```
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
JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.981
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.061
```

```
Out[63]: 0.9808261510771289
```

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

```
Out[64]: 12.791862625000002
```

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

```
Out[65]: 2.852529514134608
```



```
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 )
JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.975
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.058
```

```
Out[66]: 0.9745233369922747
```

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

```
Out[67]: 11.279599999999999
```

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

```
Out[68]: 1.4599358440872876
```

```
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 )
JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.971
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.026
```

```
Out[69]: 0.9705935167960663
```

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

```
Out[70]: 11.827124999999997
```

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

```
Out[71]: 1.9485739238638713
```

```
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 = 0.975
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.043
```

```
Out[72]: 0.9753248033193407
```

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

```
Out[73]: 12.284759999999997
```

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

```
Out[74]: 2.368563867008886
```

```
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 = 0.971
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.060
```

```
Out[75]: 0.9705286184176921
```

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

```
Out[76]: 12.799939999999998
```

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

```
Out[77]: 2.8707787698902627
```

```
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 = 0.971

SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.066

Out[78]: 0.9708976885478496

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

Out[79]: 13.29354

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

Out[80]: 3.3199993650828725

```
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 = 0.981

SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.061

Out[81]: 0.9808261510771289

```
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]: 12.791862625000002

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

Out[85]: 2.852529514134608

```
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 = 0.683
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.870
```

```
Out[86]: 0.6832575096056187
```

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

```
Out[87]: 10.15954487179487
```

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

```
Out[88]: 0.08713955865007779
```

```
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 = 0.759
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[89]: 0.7585873098664176
```

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

```
Out[90]: 10.70649371794872
```

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

```
Out[91]: 0.7465558477633906
```

```
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 = 0.763
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.018
```

```
Out[92]: 0.7628284296247848
```

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

```
Out[93]: 11.252934358974361
```

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

```
Out[94]: 1.3011866639440937
```

```
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 = 0.747
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.018
```

```
Out[95]: 0.7472248275941438
```

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

```
Out[96]: 11.763757564102566
```

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

```
Out[97]: 1.8059955940678527
```

```
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 = 0.767
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.008
```

```
Out[98]: 0.7668692525304325
```

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

```
Out[99]: 12.277072564102564
```

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

```
Out[100]: 2.3236287051536997
```

```
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]: 12.277072564102564
```

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

```
Out[103]: 2.3236287051536997
```

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

```
Out[104]: SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45913x1 Array{Float64,2}:  
  -0.498354  
  -0.00116993  
  -0.00117096  
  -0.888089  
  -0.503731  
  -0.502045  
  -0.39986  
  -0.752347  
  -0.772497  
  -0.751902  
  -0.168081  
  -0.770897  
  -0.971974  
  ⋮  
  -0.962625  
  -0.00117578  
  -0.756697  
  -0.772504  
  -0.751901  
  -0.00117096  
  -0.962588  
  -0.553488  
  -0.887606  
  -0.888444  
  -0.00359712  
  1.00343e-19
```

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

```
Out[106]: 8001x1 Array{Float64,2}:  
  -0.985679  
  -0.984432  
  -0.98307  
  -0.98224  
  -0.981641  
  -0.981288  
  -0.981255  
  -0.981241  
  -0.981053  
  -0.980935  
  -0.980847  
  -0.980823  
  -0.980769  
  ⋮  
   5.54868e-17  
   5.55095e-17  
   5.55112e-17  
   5.55598e-17  
   5.5563e-17  
   5.56896e-17  
   5.58118e-17  
   5.61177e-17  
   5.63927e-17  
   5.72229e-17  
   5.76048e-17  
   1.03621e-16
```



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

```
Out[107]: 45913x1 Array{Float64,2}:  
  -1.00043  
  -0.985971  
  -0.985679  
  -0.985673  
  -0.985559  
  -0.985515  
  -0.985433  
  -0.985336  
  -0.984686  
  -0.984432  
  -0.984228  
  -0.984108  
  -0.984089  
  ⋮  
  6.48111e-17  
  6.52054e-17  
  6.63179e-17  
  6.93627e-17  
  7.27749e-17  
  7.41413e-17  
  7.42107e-17  
  1.03621e-16  
  1.10998e-16  
  1.11071e-16  
  1.11477e-16  
  1.16402e-16
```

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

```
Out[108]: 43945x1 Array{Float64,2}:  
  -1.00043  
  -0.985971  
  -0.985679  
  -0.985673  
  -0.985559  
  -0.985515  
  -0.985433  
  -0.985336  
  -0.984686  
  -0.984432  
  -0.984228  
  -0.984108  
  -0.984089  
  ⋮  
  -7.2166e-36  
  -7.2166e-36  
  -7.21448e-36  
  -7.21447e-36  
  -7.20922e-36  
  -7.20922e-36  
  -7.20808e-36  
  -2.1823e-51  
  -7.62092e-65  
  -3.81046e-65  
  -2.55514e-65  
  -3.56081e-67
```

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

```
Out[109]: 1285x1 Array{Float64,2}:
 8.46092e-81
 8.00384e-52
 1.60051e-51
 1.60077e-51
 1.60077e-51
 1.60193e-51
 1.60194e-51
 1.60241e-51
 1.60365e-51
 1.60365e-51
 1.60382e-51
 1.60429e-51
 2.1823e-51
 ⋮
 6.48111e-17
 6.52054e-17
 6.63179e-17
 6.93627e-17
 7.27749e-17
 7.41413e-17
 7.42107e-17
 1.03621e-16
 1.10998e-16
 1.11071e-16
 1.11477e-16
 1.16402e-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}:
 0.0557778  1.85733  0.350667  1.95511  ...  0.468444  1.191  1.68667  1.10
 989
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.075  1.72  0.555  1.905  1.64  0.24  ...  0.775  0.77  0.85  1.79  1.01
```

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

```
Out[113]: 1x200 Array{Float64,2}:
 0.075  1.81  0.465  1.94  1.67  0.21  ...  0.59  0.575  0.98  1.775  1.055
```

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

```
Out[114]: 1x200 Array{Float64,2}:
 0.07  1.82  0.425  1.95  1.715  0.17  ...  0.58  0.575  1.09  1.775  1.03
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
 0.055  1.885  0.295  1.975  1.805  ...  0.475  0.465  1.205  1.645  1.09
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
 0.04  1.875  0.325  1.955  1.765  0.135  ...  0.405  0.38  1.305  1.655  
 1.16
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
 0.054875  1.86175  0.342875  1.95637  ...  0.457875  1.20413  1.6815  1.11  
 5
```

```
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)
```