

```
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/0.5/M/9

/home/nicole/Jupyter/JG3/Data/0.5/M/9
```

```
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
MarNF.txt
PedAll.txt
Phe.txt
PheAll.txt
all.ID
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

```
In [5]: ;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

```
In [6]: ;awk '{print $1}' MarNF.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;wc G4.noGenotype.ID;wc G5.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("MarNF.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 = 0.547
vG = 0.547
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
2502.297541 seconds (23.06 G allocations: 724.247 GB, 7.74% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 10.0517
 -1.86575
```

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

```
Out[33]: -1.8657533990424824
```

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

```
Out[34]: 4.092972647714025
```

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

```
Out[35]: 150-element Array{Float64,1}:
 -0.104175
  0.109111
 -0.049439
  0.0202005
 -0.00807774
 -0.0049299
  0.00133049
 -0.00219056
 -0.0938181
 -0.0309313
 -0.0943782
 -0.223166
  0.00192602
  ⋮
  0.0671644
  0.198083
 -0.108555
 -0.0707761
 -0.0787729
 -0.00746078
 -0.0460399
  0.00673907
  0.0171455
  0.0871846
  0.060356
  0.0487798
```

```
In [36]: writedlm("alphaEstimatesJ",alphaHat)
```

```
In [37]: epsiHat
```

```
Out[37]: 45966-element Array{Float64,1}:
 -0.0858096
  0.384147
  0.234016
 -0.370648
 -0.198937
  0.523486
 -0.72457
 -1.39903
  0.071442
 -0.573748
 -0.462051
  0.374118
 -0.409972
  ⋮
 -0.333864
 -0.319746
 -0.318468
  0.38333
 -0.0313456
 -0.469817
 -0.440738
 -0.628966
  0.0772253
 -0.790695
  0.36636
  0.273148
```

```
In [38]: writedlm("epsiEstimatesJ",epsiHat)
```

```
In [39]: using DataFrames
```

```
In [40]: 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 [41]: 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 = 0.891
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.995
```

```
Out[41]: 0.890837377153245
```

```
In [42]: TBV = a[posAi]
         mean(TBV)
```

```
Out[42]: 11.428397729166667
```

```
In [43]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[43]: 1.3491258529688224
```

```
In [44]: 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)
         JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.783
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV =  0.991
```

```
Out[44]: 0.7832987439256746
```

```
In [45]: TBV = a[posAi]
         mean(TBV)
```

```
Out[45]: 12.488875555555556
```

```
In [46]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[46]: 2.3072694290044042
```

```
In [47]: 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)
         JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.864
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV =  0.956
```

```
Out[47]: 0.8637352621759612
```

```
In [48]: TBV = a[posAi]
         mean(TBV)
```

```
Out[48]: 11.183672076923077
```

```
In [49]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[49]: 1.1280157969606113
```

```
In [50]: 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 = 0.670
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.776
```

```
Out[50]: 0.6704722410963434
```

```
In [51]: TBV = a[posAi]
G0TBV=mean(TBV)
```

```
Out[51]: 10.275937750000002
```

```
In [52]: GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

```
Out[52]: 0.11026535811958497
```

```
In [53]: 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 = 0.763
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.970
```

```
Out[53]: 0.7626826200577279
```

```
In [54]: TBV = a[posAi]
G1TBV=mean(TBV)
```

```
Out[54]: 10.713453375
```

```
In [55]: GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

```
Out[55]: 0.7290871716966442
```

```
In [56]: 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 = 0.753
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.006
```

```
Out[56]: 0.752844028602273
```

```
In [57]: TBV = a[posAi]
G2TBV=mean(TBV)
```

```
Out[57]: 11.205781749999998
```

```
In [58]: GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

```
Out[58]: 1.2165651461775548
```

```
In [59]: 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 = 0.745
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.004
```

```
Out[59]: 0.7448373592575073
```

```
In [60]: TBV = a[posAi]
G3TBV=mean(TBV)
```

```
Out[60]: 11.694766500000002
```

```
In [61]: GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

```
Out[61]: 1.65791590989949
```



```
In [62]: 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 = 0.727
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.014
```

```
Out[62]: 0.7274550152375802
```

```
In [63]: TBV = a[posAi]
G4TBV=mean(TBV)
```

```
Out[63]: 12.144875125
```

```
In [64]: GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

```
Out[64]: 2.0441452615067828
```

```
In [65]: 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 = 0.759
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.944
```

```
Out[65]: 0.7587727467595493
```

```
In [66]: TBV = a[posAi]
G5TBV=mean(TBV)
```

```
Out[66]: 12.535571875
```

```
In [67]: GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

```
Out[67]: 2.336776270412877
```

```
In [68]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[68]: 2-element Array{Float64,1}:
 10.3301
 0.943816
```

```
In [69]: VarGEBV=var(aHat1[posAi])
```

```
Out[69]: 0.2581250340291712
```

```
In [70]: VarTBV=var(a[posAi])
```

```
Out[70]: 0.39937518948266976
```

```
In [71]: Cov=cov(aHat1[posAi], a[posAi])
```

```
Out[71]: 0.24362246191159925
```

```
In [72]: b=Cov/VarGEBV
```

```
Out[72]: 0.9438157086463261
```

```
In [73]: 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 = 0.823
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.964
```

```
Out[73]: 0.823085582598434
```

```
In [74]: TBV = a[posAi]
mean(TBV)
```

```
Out[74]: 11.166174999999999
```

```
In [75]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[75]: 1.4708285672032977
```

```
In [76]: 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 = 0.769
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.844
```

```
Out[76]: 0.7690867217573529
```

```
In [77]: TBV = a[posAi]
mean(TBV)
```

```
Out[77]: 11.69979
```

```
In [78]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[78]: 1.7880909572232875
```

```
In [79]: 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)
         JCall = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.761
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.837
```

```
Out[79]: 0.7613262940791566
```

```
In [80]: TBV = a[posAi]
         mean(TBV)
```

```
Out[80]: 12.181799999999999
```

```
In [81]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[81]: 2.108933284708022
```

```
In [82]: 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)
         JCall = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.710
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.757
```

```
Out[82]: 0.7098761316656894
```

```
In [83]: TBV = a[posAi]
         mean(TBV)
```

```
Out[83]: 12.595339999999998
```

```
In [84]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[84]: 2.3797819896480497
```

```
In [85]: 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 = 0.675

SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.778

Out[85]: 0.67501625039172

```
In [86]: TBV = a[posAi]
mean(TBV)
```

Out[86]: 12.933420000000002

```
In [87]: GEBV = aHat1[posAi]
mean(GEBV)
```

Out[87]: 2.6084386899004515

```
In [88]: 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 = 0.759

SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.944

Out[88]: 0.7587727467595493

```
In [89]: writedlm("Correlation.G5.M.J.txt",cor13)
```

```
In [90]: writedlm("Regression.G5.M.J.txt",reg13)
```

```
In [91]: TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[91]: 12.535571875

```
In [92]: GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[92]: 2.336776270412877

```
In [93]: 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 = 0.652
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.788
```

```
Out[93]: 0.6523023242229558
```

```
In [94]: TBV = a[posAi]
mean(TBV)
```

```
Out[94]: 10.253111153846152
```

```
In [95]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[95]: 0.07537912198923336
```

```
In [96]: 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 = 0.748
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.976
```

```
Out[96]: 0.7479074805599061
```

```
In [97]: TBV = a[posAi]
mean(TBV)
```

```
Out[97]: 10.688162692307694
```

```
In [98]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[98]: 0.7019332284780124
```

```
In [99]: 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 = 0.737
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[99]: 0.7370327319986033
```

```
In [100]: TBV = a[posAi]
mean(TBV)
```

```
Out[100]: 11.180755641025641
```

```
In [101]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[101]: 1.1936839118562608
```

```
In [102]: 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 = 0.732
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.994
```

```
Out[102]: 0.732055180846771
```

```
In [103]: TBV = a[posAi]
mean(TBV)
```

```
Out[103]: 11.671674871794874
```

```
In [104]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[104]: 1.6394065232392705
```

```
In [105]: 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 = 0.717
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[105]: 0.7172630424884755
```

```
In [106]: TBV = a[posAi]
mean(TBV)
```

```
Out[106]: 12.124656025641027
```

```
In [107]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[107]: 2.0296761992402788
```

```
In [108]: numSSBayes
```

```
Out[108]: SSBR.NumSSBayes(54966,45966,9000,40000,39000,1000,150)
```

```
In [109]: J_Vecs.J1
```

```
Out[109]: 45966x1 Array{Float64,2}:
-0.013436
-0.5
-0.00349581
-0.913858
-0.503951
-0.503889
-0.00116959
-0.817037
-0.752156
-0.752192
-0.00233987
-0.751899
-0.962571
⋮
-0.94522
-0.962573
-0.756471
-0.752339
-0.751903
1.86707e-17
-0.966064
-0.504107
-0.887683
-0.878393
-0.168172
6.49633e-20
```

```
In [110]: sortrows(J_Vecs.J1[end-8000:end,:])
```

```
Out[110]: 8001x1 Array{Float64,2}:  
  -0.990145  
  -0.984727  
  -0.983551  
  -0.981443  
  -0.981314  
  -0.981147  
  -0.981132  
  -0.98088  
  -0.980876  
  -0.980848  
  -0.980847  
  -0.980837  
  -0.980808  
  ⋮  
  5.56389e-17  
  5.56598e-17  
  5.56907e-17  
  5.57473e-17  
  5.57627e-17  
  5.58374e-17  
  5.63186e-17  
  5.65768e-17  
  6.61924e-17  
  7.14323e-17  
  8.88178e-17  
  1.2259e-16
```



```
In [111]: J1 = sortrows(J_Vecs.J1)
```

```
Out[111]: 45966x1 Array{Float64,2}:  
  -0.990145  
  -0.986216  
  -0.985984  
  -0.985915  
  -0.985665  
  -0.985546  
  -0.985536  
  -0.985405  
  -0.985217  
  -0.984727  
  -0.984479  
  -0.984386  
  -0.983639  
  ⋮  
  6.76027e-17  
  7.10931e-17  
  7.14323e-17  
  7.52907e-17  
  7.54313e-17  
  7.75322e-17  
  7.92816e-17  
  8.88178e-17  
  9.02541e-17  
  9.40576e-17  
  9.99201e-17  
  1.2259e-16
```

```
In [112]: J1[J1 .< 0.0,:]
```

```
Out[112]: 43930x1 Array{Float64,2}:  
  -0.990145  
  -0.986216  
  -0.985984  
  -0.985915  
  -0.985665  
  -0.985546  
  -0.985536  
  -0.985405  
  -0.985217  
  -0.984727  
  -0.984479  
  -0.984386  
  -0.983639  
  ⋮  
  -7.22508e-36  
  -7.2166e-36  
  -7.2166e-36  
  -4.91411e-36  
  -7.60646e-65  
  -3.80323e-65  
  -2.34411e-65  
  -1.17206e-65  
  -9.00332e-67  
  -4.50166e-67  
  -3.55912e-67  
  -3.55912e-67
```

```
In [113]: J1[J1 .> 0.0,:]
```

```
Out[113]: 1367x1 Array{Float64,2}:
 2.60249e-81
 8.44487e-81
 1.60289e-51
 1.60289e-51
 1.61185e-51
 3.07671e-51
 3.20102e-51
 3.20294e-51
 3.20577e-51
 3.95084e-51
 4.05474e-51
 4.05474e-51
 4.6261e-51
 ⋮
 6.76027e-17
 7.10931e-17
 7.14323e-17
 7.52907e-17
 7.54313e-17
 7.75322e-17
 7.92816e-17
 8.88178e-17
 9.02541e-17
 9.40576e-17
 9.99201e-17
 1.2259e-16
```

```
In [114]: G = convert(Array,readtable("MarNF.txt", separator = ' ',header=false));
```

```
In [115]: GAll=mean(G[:,2:end],1)
```

```
Out[115]: 1x150 Array{Float64,2}:
 0.443  1.97044  1.63533  0.210222  ...  0.486222  1.13878  1.76722  1.1695
 6
```

```
In [116]: GG0=mean(G[1:200,2:end],1)
```

```
Out[116]: 1x150 Array{Float64,2}:
 0.46  1.955  1.66  0.24  0.53  0.53  ...  0.595  0.595  0.915  1.835  1.15
 5
```

```
In [117]: GG1=mean(G[201:400,2:end],1)
```

```
Out[117]: 1x150 Array{Float64,2}:
 0.41  1.945  1.665  0.2  0.38  0.38  ...  0.505  0.505  1.04  1.77  1.145
```

```
In [118]: GG2=mean(G[401:600,2:end],1)
```

```
Out[118]: 1x150 Array{Float64,2}:
 0.41  1.97  1.66  0.205  0.375  ...  1.42  0.53  0.53  1.095  1.79  1.12
```

```
In [119]: GG3=mean(G[601:800,2:end],1)
```

```
Out[119]: 1x150 Array{Float64,2}:  
  0.4  1.97  1.675  0.21  0.355  0.355  ...  0.455  0.455  1.155  1.725  1.2  
  15
```

```
In [120]: GG4=mean(G[801:1000,2:end],1)
```

```
Out[120]: 1x150 Array{Float64,2}:  
  0.475  1.985  1.595  0.21  0.315  0.315  ...  0.485  0.485  1.185  1.775  
  1.15
```

```
In [121]: GG5=mean(G[1001:9000,2:end],1)
```

```
Out[121]: 1x150 Array{Float64,2}:  
  0.4445  1.97113  1.63338  0.209875  ...  0.48275  1.14637  1.76575  1.1711  
  2
```

```
In [122]: writedlm("meanOfSNPMAll",GAll)
```

```
In [123]: writedlm("meanOfSNPMG0",GG0)
```

```
In [124]: writedlm("meanOfSNPMG1",GG1)
```

```
In [125]: writedlm("meanOfSNPMG2",GG2)
```

```
In [126]: writedlm("meanOfSNPMG3",GG3)
```

```
In [127]: writedlm("meanOfSNPMG4",GG4)
```

```
In [128]: writedlm("meanOfSNPMG5",GG5)
```