

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

```
In [4]: ;ls  
  
Correlation.G5.M.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  
MarNF.txt  
PedAll.txt  
Phe.txt  
PheAll.txt  
Regression.G5.M.JC.txt  
all.ID  
alphaEstimatesJC  
epsiEstimatesJC  
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 G
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
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",calculateInbreedin
nothing
df      = read_genotypes("MarNF.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    = 0.699
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
4701.794923 seconds (23.03 G allocations: 723.518 GB, 6.85% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 9.95098
-1.15995
```

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

```
Out[33]: -1.1599455652573654
```

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

```
Out[34]: 4.3955174649173205
```

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

```
Out[35]: 150-element Array{Float64,1}:
```

```
-0.110102
 0.118041
 0.0419282
 0.0426303
-0.0784881
 0.00385742
 0.0517974
-0.03961
-0.149467
-0.24246
-0.0282451
 0.078937
-0.0841968
 ⋮
-0.188948
-0.0743323
 0.0127268
 0.00136938
 0.115818
 0.119884
 0.0133802
 0.0496737
-0.188538
-0.165604
-0.117118
-0.0267716
```

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

In [37]: `epsiHat`

```
Out[37]: 45913-element Array{Float64,1}:
 0.256009
-0.0454292
-0.468176
 0.204721
-0.692048
-0.115924
 0.13012
-0.0848879
 0.800042
-0.116656
-0.254454
 0.267562
 0.300983
  ⋮
-0.119091
-0.0269054
-1.01075
 0.789401
-0.749157
 0.670989
 0.126385
 0.646879
-0.462373
-0.287627
-0.580671
-0.137645
```

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

In [39]: `using DataFrames`

```
In [40]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',head
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 e
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.902
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.992
```

Out[41]: 0.9019192808162164

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

```
Out[42]: 11.514132458333334
```

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

```
Out[43]: 1.542501799226296
```

```
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 ) # w
         @printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.849
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.018
```

```
Out[44]: 0.8492648369627428
```

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

```
Out[45]: 12.736877111111111
```

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

```
Out[46]: 2.7071135369388033
```

```
In [47]: IDs = readtable("noGenotype.ID", eltypes=[UTF8String], separator = ' ',heade
         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.
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.870
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.966
```

```
Out[47]: 0.8702487764119992
```

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

```
Out[48]: 11.231960615384617
```

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

```
Out[49]: 1.273745244369563
```

```
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 ex
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.700
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.854
```

```
Out[50]: 0.7004421767308988
```

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

```
Out[51]: 10.187546249999999
```

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

```
Out[52]: 0.1265848391839888
```

```
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 ex
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.764
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.982
```

```
Out[53]: 0.7643911640044709
```

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

```
Out[54]: 10.7345095
```

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

```
Out[55]: 0.8241578957658535
```

```
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 ex
@printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.762
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.010
```

```
Out[56]: 0.7615687859096476
```

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

```
Out[57]: 11.27873
```

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

```
Out[58]: 1.3721213909881036
```

```
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 ex
@printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.748
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.025
```

```
Out[59]: 0.7481240541581864
```

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

```
Out[60]: 11.789662125
```

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

```
Out[61]: 1.854949572486124
```



```
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 ex
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.753
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.033
```

```
Out[62]: 0.7527702823827508
```

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

```
Out[63]: 12.30248425
```

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

```
Out[64]: 2.3284726703655894
```

```
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 ex
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.832
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.990
```

```
Out[65]: 0.8315771165051925
```

```
In [66]: writedlm("Correlation.G5.M.J.txt",cor13)
```

```
LoadError: UndefVarError: cor13 not defined
while loading In[66], in expression starting on line 1
```

```
In [67]: writedlm("Regression.G5.M.J.txt",reg13)
```

```
LoadError: UndefVarError: reg13 not defined
while loading In[67], in expression starting on line 1
```

```
In [68]: TBV = a[posAi]
G5TBV=mean(TBV)
```

```
Out[68]: 12.791862625000002
```

```
In [69]: GEBV = aHat1[posAi]
        G5GEBV=mean(GEBV)
```

```
Out[69]: 2.748724426568116
```

```
In [70]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[70]: 2-element Array{Float64,1}:
         10.0719
          0.989545
```

```
In [71]: VarGEBV=var(aHat1[posAi])
```

```
Out[71]: 0.39012033615247643
```

```
In [72]: VarTBV=var(a[posAi])
```

```
Out[72]: 0.5524134329322257
```

```
In [73]: Cov=cov(aHat1[posAi], a[posAi])
```

```
Out[73]: 0.3860414516514
```

```
In [74]: b=Cov/VarGEBV
```

```
Out[74]: 0.9895445478661686
```

```
In [75]: 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 = 0.836
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.938
```

```
Out[75]: 0.835525313851702
```

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

```
Out[76]: 11.279599999999999
```

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

```
Out[77]: 1.6008321266015906
```

```
In [78]: 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 = 0.802
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.845
```

```
Out[78]: 0.8017220896367915
```

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

```
Out[79]: 11.827124999999997
```

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

```
Out[80]: 2.0137780432068224
```

```
In [81]: 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.
JCall = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.810
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.890
```

```
Out[81]: 0.8103898238207096
```

```
In [82]: TBV = a[posAi]
mean(TBV)
```

```
Out[82]: 12.284759999999997
```

```
In [83]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[83]: 2.365393125763648
```

```
In [84]: 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.
JCall = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.805
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.942
```

```
Out[84]: 0.8054613911490673
```

```
In [85]: TBV = a[posAi]
mean(TBV)
```

```
Out[85]: 12.799939999999998
```

```
In [86]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[86]: 2.7674163525479516
```

```
In [87]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor12 = cor(a[posAi],aHat1[posAi])[1,1]
reg12 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.Genotype.ID : correlation = %6.3f\n", cor12 )
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.
JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.769
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.870
```

```
Out[87]: 0.7689978635029012
```

```
In [88]: TBV = a[posAi]
mean(TBV)
```

```
Out[88]: 13.29354
```

```
In [89]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[89]: 3.1237124514015253
```

```
In [90]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
posAi = getPos(ped,IDs)
cor13 = cor(a[posAi],aHat1[posAi])[1,1]
reg13 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.Genotype.ID : correlation = %6.3f\n", cor13 )
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.
JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.832
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[90]: 0.8315771165051925
```

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

```
Out[91]: 12.791862625000002
```

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

```
Out[92]: 2.748724426568116
```

```
In [93]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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 = %
JCall = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation = 0.682
```

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

```
Out[93]: 0.6821648901144679
```

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

```
Out[94]: 10.15954487179487
```

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

```
Out[95]: 0.08878362668610158
```

```
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 = 0.750
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[96]: 0.749566210427723
```

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

```
Out[97]: 10.70649371794872
```

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

```
Out[98]: 0.7936548150622389
```

```
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 = 0.748
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.012
```

```
Out[99]: 0.7480027015266804
```

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

```
Out[100]: 11.252934358974361
```

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

```
Out[101]: 1.3466528849682176
```

```
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)
JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.733
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.021
```

```
Out[102]: 0.7332399684716727
```

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

```
Out[103]: 11.763757564102566
```

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

```
Out[104]: 1.8315529883819748
```

```
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)
JCA11 = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.739
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.024
```

```
Out[105]: 0.7394401480486559
```

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

```
Out[106]: 12.277072564102564
```

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

```
Out[107]: 2.308081906749283
```

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

```
Out[108]: SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,150)
```

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

```
Out[109]: 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 [110]: sortrows(J_Vecs.J1[end-8000:end,:])
```

```
Out[110]: 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 [111]: J1 = sortrows(J_Vecs.J1)
```

```
Out[111]: 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 [112]: J1[J1 .< 0.0,:]
```

```
Out[112]: 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 [113]: J1[J1 .> 0.0,:]
```

```
Out[113]: 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 [114]: G = convert(Array,readtable("MarNF.txt", separator = ' ',header=false));
```

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

```
Out[115]: 1x150 Array{Float64,2}:
 0.0557778  1.85733  0.350667  1.95511  ...  0.468444  1.68667  1.10989
```

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

```
Out[116]: 1x150 Array{Float64,2}:
 0.075  1.72  0.555  1.905  1.64  0.505  ...  0.385  0.775  0.77  1.79  1.0
 1
```

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

```
Out[117]: 1x150 Array{Float64,2}:
 0.075  1.81  0.465  1.94  1.67  0.45  ...  0.35  0.59  0.575  1.775  1.055
```

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

```
Out[118]: 1x150 Array{Float64,2}:
 0.07  1.82  0.425  1.95  1.715  0.375  ...  0.34  0.58  0.575  1.775  1.03
```

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

```
Out[119]: 1x150 Array{Float64,2}:  
 0.055  1.885  0.295  1.975  1.805  ...  0.285  0.475  0.465  1.645  1.09
```

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

```
Out[120]: 1x150 Array{Float64,2}:  
 0.04  1.875  0.325  1.955  1.765  0.3  ...  0.31  0.405  0.38  1.655  1.16
```

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

```
Out[121]: 1x150 Array{Float64,2}:  
 0.054875  1.86175  0.342875  1.95637  ...  0.477625  0.457875  1.6815  1.1  
15
```

```
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)
```