

```
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/7  
  
/home/nicole/Jupyter/JG3/Data/0.5/M/7
```

```
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 = 0.711
vG = 0.711
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
2457.673309 seconds (23.03 G allocations: 723.572 GB, 7.80% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 9.67153
-1.484
```

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

```
Out[33]: -1.4839985849905097
```

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

```
Out[34]: 4.093764442043283
```

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

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

```
-0.0581782
 0.095529
-0.128162
-0.00403827
 0.0353388
 0.134678
 0.0635776
-0.0711519
 0.0188629
 0.0120818
 0.0433457
-0.0467169
 0.0985414
 ⋮
 0.0832993
 0.206735
-0.1028
 0.140168
-0.0209545
 0.0373129
 0.00964946
 0.0497391
 0.0719851
 0.0471989
-0.00512002
 0.0132441
```

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

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

```
Out[37]: 45917-element Array{Float64,1}:
 -1.59704
  0.669871
 -0.155806
  0.688058
 -1.02885
  0.396585
 -0.145913
 -0.286174
  0.368901
 -0.715919
 -0.49512
 -0.925102
 -0.642128
  ⋮
 -0.0732655
  0.385724
 -0.510499
  1.23112
 -0.0559242
 -0.140248
 -0.26358
 -0.721304
 -0.000241511
 -0.249717
 -0.122975
  0.18491
```

```
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 = 0.894
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.996
```

```
Out[41]: 0.8942711232629328
```

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

```
Out[42]: 11.218311875
```

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

```
Out[43]: 1.5301512513484627
```

```
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)
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation =  0.793
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV =  0.959
```

```
Out[44]: 0.7925835554907248
```

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

```
Out[45]: 12.409567111111111
```

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

```
Out[46]: 2.6313125551437246
```

```
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)
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation =  0.868
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV =  0.968
```

```
Out[47]: 0.8683026882606537
```

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

```
Out[48]: 10.943406820512822
```

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

```
Out[49]: 1.2760371043187873
```

```
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
JCA11 = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.707
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.865
```

```
Out[50]: 0.706928504911758
```

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

```
Out[51]: 9.911972250000002
```

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

```
Out[52]: 0.12913658062484343
```

```
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
JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.764
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.996
```

```
Out[53]: 0.7636506880729776
```

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

```
Out[54]: 10.446048125
```

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

```
Out[55]: 0.8333999327444958
```

```
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 = 0.766
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.029
```

```
Out[56]: 0.7659357988890642
```

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

```
Out[57]: 10.958247499999999
```

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

```
Out[58]: 1.355591126915132
```

```
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 = 0.753
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.030
```

```
Out[59]: 0.7533893401514413
```

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

```
Out[60]: 11.531684875
```

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

```
Out[61]: 1.8918186680102393
```



```
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
JCA11 = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation = 0.740
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.024
```

```
Out[62]: 0.740003027353782
```

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

```
Out[63]: 11.999897374999996
```

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

```
Out[64]: 2.3036342245500756
```

```
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
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.770
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 0.916
```

```
Out[65]: 0.7702563668768909
```

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

```
Out[66]: 12.462021125
```

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

```
Out[67]: 2.6673269752459925
```

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

```
Out[68]: 2-element Array{Float64,1}:
 10.019
 0.915909
```

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

```
Out[69]: 0.39317985671058636
```

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

```
Out[70]: 0.555937045309398
```

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

```
Out[71]: 0.36011709172524
```

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

```
Out[72]: 0.9159093111687984
```

```
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 = 0.807
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.933
```

```
Out[73]: 0.8074910825308002
```

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

```
Out[74]: 10.996195
```

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

```
Out[75]: 1.6595536827256057
```

```
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 = 0.817
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.929
```

```
Out[76]: 0.8170688043284501
```

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

```
Out[77]: 11.449715
```

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

```
Out[78]: 1.948755936190145
```

```
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 = 0.796
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.946
```

```
Out[79]: 0.7955428827375542
```

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

```
Out[80]: 12.099385
```

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

```
Out[81]: 2.445036668859482
```

```
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 = 0.755
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.885
```

```
Out[82]: 0.7549003544252734
```

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

```
Out[83]: 12.470485000000002
```

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

```
Out[84]: 2.6728415197277853
```

```
In [85]: 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 = 0.657
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.704
```

```
Out[85]: 0.6573982025729751
```

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

```
Out[86]: 12.933895000000001
```

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

```
Out[87]: 2.989798164124912
```

```
In [88]: 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 = 0.770
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.916
```

```
Out[88]: 0.7702563668768909
```

```
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]: 12.462021125
```

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

```
Out[92]: 2.6673269752459925
```

```
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 = 0.691
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.887
```

```
Out[93]: 0.6907198687288756
```

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

```
Out[94]: 9.884171666666667
```

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

```
Out[95]: 0.08989511646841361
```

```
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 = 0.751
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.007
```

```
Out[96]: 0.751371577545173
```

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

```
Out[97]: 10.420313076923078
```

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

```
Out[98]: 0.8048010608612742
```

```
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 = 0.750
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.029
```

```
Out[99]: 0.7496299392797247
```

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

```
Out[100]: 10.928987564102563
```

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

```
Out[101]: 1.3276566258396358
```

```
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 = 0.742
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.024
```

```
Out[102]: 0.7424322753540883
```

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

```
Out[103]: 11.507613076923077
```

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

```
Out[104]: 1.8717924410431228
```

```
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 = 0.731
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.017
```

```
Out[105]: 0.7309994646259389
```

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

```
Out[106]: 11.975948717948715
```

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

```
Out[107]: 2.28604027738149
```

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

```
Out[108]: SSBR.NumSSBayes(54917,45917,9000,40000,39000,1000,150)
```

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

```
Out[109]: 45917x1 Array{Float64,2}:
-0.168084
-0.00350809
3.90161e-19
-0.887661
-0.503514
-0.502671
0.0
-0.752156
-0.752184
-0.753424
-0.00231388
-0.815662
-0.962573
⋮
-0.971951
-0.00117033
-0.854178
-0.753751
-0.752204
-0.00231016
-0.962551
-0.503514
-0.890363
-0.87827
-0.00117165
-0.25701
```

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

```
Out[110]: 8001x1 Array{Float64,2}:  
  -0.981325  
  -0.981294  
  -0.981267  
  -0.981241  
  -0.981173  
  -0.981142  
  -0.980858  
  -0.980804  
  -0.980797  
  -0.979775  
  -0.979548  
  -0.979536  
  -0.979227  
  ⋮  
  5.56159e-17  
  5.58444e-17  
  5.5891e-17  
  5.59013e-17  
  5.59142e-17  
  5.61862e-17  
  5.62307e-17  
  5.65449e-17  
  5.86647e-17  
  6.10506e-17  
  8.51031e-17  
  8.89559e-17
```



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

```
Out[111]: 45917x1 Array{Float64,2}:  
  -0.986868  
  -0.985718  
  -0.985549  
  -0.985507  
  -0.985337  
  -0.98531  
  -0.98449  
  -0.983869  
  -0.983768  
  -0.983758  
  -0.983587  
  -0.983232  
  -0.982671  
  ⋮  
  7.40483e-17  
  7.42043e-17  
  7.42098e-17  
  7.4361e-17  
  8.51031e-17  
  8.51031e-17  
  8.61278e-17  
  8.89559e-17  
  1.02969e-16  
  1.11022e-16  
  1.11095e-16  
  1.11274e-16
```

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

```
Out[112]: 43998x1 Array{Float64,2}:  
  -0.986868  
  -0.985718  
  -0.985549  
  -0.985507  
  -0.985337  
  -0.98531  
  -0.98449  
  -0.983869  
  -0.983768  
  -0.983758  
  -0.983587  
  -0.983232  
  -0.982671  
  ⋮  
  -7.34107e-36  
  -7.23782e-36  
  -7.2166e-36  
  -7.2166e-36  
  -7.21449e-36  
  -7.00015e-66  
  -3.56334e-67  
  -3.55597e-67  
  -1.78167e-67  
  -1.77903e-67  
  -1.77799e-67  
  -8.89515e-68
```

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

```
Out[113]: 1315x1 Array{Float64,2}:
 1.97512e-83
 3.94792e-83
 3.9561e-83
 3.87655e-66
 8.01203e-52
 8.01203e-52
 8.03559e-52
 8.03559e-52
 1.60147e-51
 1.60194e-51
 1.60241e-51
 1.60241e-51
 1.60479e-51
 ⋮
 7.40483e-17
 7.42043e-17
 7.42098e-17
 7.4361e-17
 8.51031e-17
 8.51031e-17
 8.61278e-17
 8.89559e-17
 1.02969e-16
 1.11022e-16
 1.11095e-16
 1.11274e-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}:
 0.107556  1.91978  1.54767  0.257111  ...  0.802556  0.720889  1.69067
```

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

```
Out[116]: 1x150 Array{Float64,2}:
 0.105  1.905  1.64  0.285  0.63  0.625  ...  1.625  0.36  0.805  0.64  1.7
15
```

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

```
Out[117]: 1x150 Array{Float64,2}:
 0.16  1.905  1.625  0.24  0.635  0.64  ...  1.635  0.385  0.775  0.68  1.7
2
```

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

```
Out[118]: 1x150 Array{Float64,2}:
 0.12  1.905  1.535  0.265  0.64  0.635  ...  1.67  0.365  0.835  0.695  1.
68
```

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

```
Out[119]: 1x150 Array{Float64,2}:  
  0.095  1.935  1.55  0.24  0.58  0.58  ...  1.25  1.66  0.36  0.77  0.7  1.  
 705
```

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

```
Out[120]: 1x150 Array{Float64,2}:  
  0.11  1.94  1.54  0.26  0.6  0.595  ...  1.715  0.395  0.835  0.725  1.68
```

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

```
Out[121]: 1x150 Array{Float64,2}:  
  0.10625  1.92  1.54388  0.257  0.59825  ...  0.37725  0.802375  0.725  1.6  
 895
```

```
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)
```