

```
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/0.3/G/3

        /home/nicole/Jupyter/JG3/Data/0.3/G/3
```

```
In [4]: ;ls

Correlation.G5.G.JC.txt
Correlation.G5.G.PBLUP.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
```

```
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
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 G
7800 7800 46800 G0.noGenotype.ID
7800 7800 46800 G1.noGenotype.ID
7800 7800 46800 G2.noGenotype.ID
7800 7800 46800 G3.noGenotype.ID
7800 7800 46800 G4.noGenotype.ID
0 0 0 G5.noGenotype.ID
```

```
In [30]: ped,A_Mats,numSSBayes = calc_Ai("PedAll.txt","genotype.ID",calculateInbreeding=false)
nothing
df      = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);           # without centering
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 J
nothing
```

```
In [31]: vG      = 0.505
vRes     = 1.180
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,nIter, outFreq=5000);
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
2516.171060 seconds (23.05 G allocations: 723.883 GB, 7.61% gc time)
```

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

```
Out[32]: 2-element Array{Float64,1}:
 10.1827
  4.60714
```

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

```
Out[33]: 4.6071368842349
```

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

```
Out[34]: 7.394894207513142
```

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

```
Out[35]: 200-element Array{Float64,1}:
```

```
 0.023631
 0.0740686
-0.0530611
 0.120263
 0.146857
 0.00270796
-0.0202537
-0.0286254
-0.0563802
 0.0506446
 0.0551852
-0.041836
-0.0218718
  ⋮
 0.0312366
 0.156772
-0.0182944
-0.00636091
 0.051936
 0.101435
-0.020036
 0.0202341
 0.0250874
-0.0144323
 0.00315539
 0.0295882
```

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

```
In [37]: using DataFrames
```

```
In [38]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',header=false)
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 epsilon
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.879
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.978
```

```
Out[39]: 0.8785657675967928
```

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

```
Out[40]: 11.403961104166665
```

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

```
Out[41]: 1.2217732849499299
```

```
In [42]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.974
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.085
```

```
Out[42]: 0.9736633608035205
```

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

```
Out[43]: 12.325620777777777
```

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

```
Out[44]: 2.1762716392499457
```

```
In [45]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg3)
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.824
```

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

```
Out[45]: 0.8237515153988133
```

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

```
Out[46]: 11.19127041025641
```

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

```
Out[47]: 1.001504433957618
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCall = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.641
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 1.021
```

```
Out[48]: 0.6409086325041278
```

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

```
Out[49]: 10.388020375
```

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

```
Out[50]: 0.0969924794940673
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = %6.3f\n", reg4)
JCall = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.690
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.021
```

```
Out[51]: 0.6896477222314276
```

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

```
Out[52]: 10.811168499999999
```



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

```
Out[53]: 0.6299877313444049
```

```
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 epsilon
         @printf("SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = %6.3f\n", reg5)
         JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.700
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.023
```

```
Out[54]: 0.6999035594963923
```

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

```
Out[55]: 11.223220624999998
```

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

```
Out[56]: 1.0641168673311525
```

```
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 epsilon
         @printf("SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = %6.3f\n", reg6)
         JCA11 = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation = 0.699
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.038
```

```
Out[57]: 0.6989843358409952
```

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

```
Out[58]: 11.6114015
```

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

```
Out[59]: 1.4585740065187685
```

```
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 epsilon
        @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", reg7)
        JCall = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.735
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.070
```

```
Out[60]: 0.7353045314959988
```

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

```
Out[61]: 12.023300125000002
```

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

```
Out[62]: 1.8668581687792516
```

```
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 epsilon
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", reg8)
JCall = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.971
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.085
```

```
Out[63]: 0.9714918571236583
```

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

```
Out[64]: 12.3666555
```

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

```
Out[65]: 2.2141104562319325
```

```
In [66]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 = 0.964
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.066
```

```
Out[66]: 0.9639677580967436
```

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

```
Out[67]: 11.23138
```

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

```
Out[68]: 1.1878562310358722
```

```
In [69]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 = 0.964
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.052
```

```
Out[69]: 0.963771090191681
```

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

```
Out[70]: 11.604315
```

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

```
Out[71]: 1.5082830412869848
```

```
In [72]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 = 0.967
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.070
```

```
Out[72]: 0.9670437958291723
```

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

```
Out[73]: 11.992505000000001
```

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

```
Out[74]: 1.863562215005351
```

```
In [75]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.967
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.074
```

```
Out[75]: 0.9665204634076595
```

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

```
Out[76]: 12.446694999999998
```

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

```
Out[77]: 2.279613625998218
```

```
In [78]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg12)
JCA11 = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.969
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.079
```

```
Out[78]: 0.9685175666622846
```

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

```
Out[79]: 12.711820000000003
```

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

```
Out[80]: 2.5284904036438243
```

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg13)
JCA11 = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.971
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.085
```

```
Out[81]: 0.9714918571236583
```

```
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]: 12.3666555
```

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

```
Out[85]: 2.2141104562319325
```

```
In [86]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.620
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  1.066
```

```
Out[86]: 0.6198389047226037
```

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

```
Out[87]: 10.366395769230772
```

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

```
Out[88]: 0.06902161406991845
```

```
In [89]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.669
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.033
```

```
Out[89]: 0.668986565658629
```

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

```
Out[90]: 10.790831410256411
```

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

```
Out[91]: 0.6074673387817746
```

```
In [92]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # with epsilon
@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 =  0.681
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.026
```

```
Out[92]: 0.68089863203803
```

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

```
Out[93]: 11.203495384615383
```



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

```
Out[94]: 1.0436182686728395
```

```
In [95]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.678
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.039
```

```
Out[95]: 0.6782529329782059
```

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

```
Out[96]: 11.589983717948718
```

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

```
Out[97]: 1.437521708583398
```

```
In [98]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.722
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.071
```

```
Out[98]: 0.7221737544423779
```

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

```
Out[99]: 12.005645769230771
```

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

```
Out[100]: 1.84989323968016
```

```
In [101]: IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
          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 ) # with epsilon
          @printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg18)
          JCall = cor17
```

```
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]: 12.005645769230771
```

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

```
Out[103]: 1.84989323968016
```

```
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}:
```

```
-0.0910514  
-0.0460233  
-0.00117096  
-0.887588  
-0.504094  
-0.512636  
-0.00234055  
-0.75832  
-0.834378  
-0.753569  
-0.00234194  
-0.820407  
-0.962573  
:  
-0.962788  
2.59784e-19  
-0.756621  
-0.814019  
-0.751913  
-0.00205434  
-0.962612  
-0.511041  
-0.925089  
-0.878362  
7.86776e-17  
-0.00730704
```

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

```
Out[106]: 8001x1 Array{Float64,2}:
```

```
-0.987848  
-0.983122  
-0.983022  
-0.983021  
-0.982014  
-0.981669  
-0.981265  
-0.981231  
-0.981221  
-0.981167  
-0.981154  
-0.981152  
-0.981142  
:  
5.5571e-17  
5.56415e-17  
5.58937e-17  
5.62775e-17  
5.69801e-17  
5.85748e-17  
5.98616e-17  
6.08857e-17  
7.59165e-17  
7.86776e-17  
8.84953e-17  
8.85164e-17
```

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

```
Out[107]: 45913x1 Array{Float64,2}:  
  -0.987848  
  -0.98775  
  -0.986976  
  -0.986972  
  -0.985598  
  -0.985569  
  -0.985307  
  -0.984234  
  -0.984219  
  -0.984073  
  -0.983729  
  -0.983606  
  -0.983122  
  ⋮  
  6.67104e-17  
  6.70633e-17  
  7.24466e-17  
  7.40484e-17  
  7.47331e-17  
  7.59165e-17  
  7.86776e-17  
  8.84953e-17  
  8.85164e-17  
  8.85362e-17  
  8.88309e-17  
  1.11342e-16
```

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

```
Out[108]: 43908x1 Array{Float64,2}:  
  -0.987848  
  -0.98775  
  -0.986976  
  -0.986972  
  -0.985598  
  -0.985569  
  -0.985307  
  -0.984234  
  -0.984219  
  -0.984073  
  -0.983729  
  -0.983606  
  -0.983122  
  ⋮  
  -7.21449e-36  
  -7.21449e-36  
  -7.21238e-36  
  -7.21238e-36  
  -7.21235e-36  
  -7.20816e-36  
  -7.11812e-36  
  -6.75383e-36  
  -4.91411e-36  
  -3.55911e-67  
  -1.77955e-67  
  -1.77799e-67
```

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

```
Out[109]: 1363x1 Array{Float64,2}:
 8.00735e-52
 8.31907e-52
 1.58054e-51
 1.60053e-51
 1.60146e-51
 1.60147e-51
 1.60147e-51
 1.60194e-51
 1.60194e-51
 1.60194e-51
 1.60241e-51
 1.60241e-51
 1.60241e-51
 ⋮
 6.67104e-17
 6.70633e-17
 7.24466e-17
 7.40484e-17
 7.47331e-17
 7.59165e-17
 7.86776e-17
 8.84953e-17
 8.85164e-17
 8.85362e-17
 8.88309e-17
 1.11342e-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}:
 0.221111  1.69789  0.413889  1.98533  1.86344  ...  0.561889  1.71633  1.23789
```

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

```
Out[112]: 1x200 Array{Float64,2}:
 0.145  1.69  0.535  1.95  1.705  0.31  ...  0.32  0.7  0.7  0.625  1.745  1.16
```

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

```
Out[113]: 1x200 Array{Float64,2}:  
  0.285  1.705  0.46  1.97  1.805  0.405  ...  0.715  0.72  0.6  1.725  1.16
```

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

```
Out[114]: 1x200 Array{Float64,2}:  
  0.21  1.72  0.435  1.98  1.82  0.415  ...  0.695  0.695  0.63  1.75  1.25
```

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

```
Out[115]: 1x200 Array{Float64,2}:  
  0.255  1.67  0.425  1.985  1.88  0.415  ...  0.705  0.705  0.555  1.74  1.185
```

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

```
Out[116]: 1x200 Array{Float64,2}:  
  0.2  1.725  0.365  2.0  1.9  0.455  0.91  ...  0.68  0.68  0.535  1.685  1.31
```

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

```
Out[117]: 1x200 Array{Float64,2}:  
  0.221375  1.69738  0.410125  1.98638  ...  0.697  0.5585  1.71475  1.241
```

```
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)
```


