

```
In [1]: include("/home/nicole/Jupyter/SSBRnoJ/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/0.5a0/G/8

        /home/nicole/Jupyter/JG3/Data/0.5a0/G/8
```

```
In [4]: ;ls

G0.Genotype.ID
G0.ID
G0.noGenotype.ID
G1.Genotype.ID
G1.ID
G1.noGenotype.ID
G2.Genotype.ID
G2.ID
G2.noGenotype.ID
G3.Genotype.ID
G3.ID
G3.noGenotype.ID
G4.Genotype.ID
G4.ID
G4.noGenotype.ID
G5.Genotype.ID
G5.ID
G5.noGenotype.ID
GenNF.txt
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}' 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 [36]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[36]: 1.4360281566913307
```

```
In [37]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=
         posAi = getPos(ped,IDs)
         cor2 = cor(a[posAi],aHat3[posAi])[1,1]
         reg2 = linreg(aHat3[posAi], a[posAi])[2,1]
         @printf("SSBRJC from Gibbs - genotype.ID : correlation = %6.3f\n", cor2 ) # 1
         @printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3:
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.576
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.966
```

```
Out[37]: 0.576377365594253
```

```
In [38]: TBV = a[posAi]
         mean(TBV)
```

```
Out[38]: 5.430348888888889
```

```
In [39]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[39]: 2.7267177930100637
```

```
In [40]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',head
         posAi = getPos(ped,IDs)
         cor3 = cor(a[posAi],aHat3[posAi])[1,1]
         reg3 = linreg(aHat3[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 = 0.879
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.983
```

```
Out[40]: 0.8785033812906399
```

```
In [41]: TBV = a[posAi]
         mean(TBV)
```

```
Out[41]: 3.9158042307692305
```

```
In [42]: EBV = aHat3[posAi]
         mean(EBV)
```

```
Out[42]: 1.1381767021562386
```

```
In [43]: IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat3[posAi])[1,1]
reg4 = linreg(aHat3[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 =  0.713
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.896
```

```
Out[43]: 0.7128554854110432
```

```
In [44]: TBV = a[posAi]
mean(TBV)
```

```
Out[44]: 2.8020739999999997
```

```
In [45]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[45]: 0.001224704164246558
```

```
In [46]: IDs = readtable("G1.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat3[posAi])[1,1]
reg4 = linreg(aHat3[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 =  0.775
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.991
```

```
Out[46]: 0.7751880181125452
```

```
In [47]: TBV = a[posAi]
mean(TBV)
```

```
Out[47]: 3.3759308749999994
```

```
In [48]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[48]: 0.6186589939226499
```

```
In [49]: IDs = readtable("G2.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor5 = cor(a[posAi],aHat3[posAi])[1,1]
reg5 = linreg(aHat3[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 = 0.777
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.020
```

```
Out[49]: 0.7772520361459136
```

```
In [50]: TBV = a[posAi]
mean(TBV)
```

```
Out[50]: 3.9699628750000002
```

```
In [51]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[51]: 1.197176085931089
```

```
In [52]: IDs = readtable("G3.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor6 = cor(a[posAi],aHat3[posAi])[1,1]
reg6 = linreg(aHat3[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 = 0.752
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 0.984
```

```
Out[52]: 0.7517374448596913
```

```
In [53]: TBV = a[posAi]
mean(TBV)
```

```
Out[53]: 4.535933375
```

```
In [54]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[54]: 1.7535262900476227
```

```
In [55]: IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat3[posAi])[1,1]
reg7 = linreg(aHat3[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 =  0.716
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.939
```

```
Out[55]: 0.715887977788469
```

```
In [56]: TBV = a[posAi]
mean(TBV)
```

```
Out[56]: 5.0319438750000005
```

```
In [57]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[57]: 2.2627452562171344
```

```
In [58]: IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat3[posAi])[1,1]
reg8 = linreg(aHat3[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 =  0.427
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.957
```

```
Out[58]: 0.426668546745776
```

```
In [59]: TBV = a[posAi]
mean(TBV)
```

```
Out[59]: 5.482843125
```

```
In [60]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[60]: 2.782837609865241
```

```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat3[posAi])[1,1]
reg9 = linreg(aHat3[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 = 0.903
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.080
```

```
Out[61]: 0.9027152328148518
```

```
In [62]: TBV = a[posAi]
mean(TBV)
```

```
Out[62]: 3.9632150000000001
```

```
In [63]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[63]: 1.252143460227135
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat3[posAi])[1,1]
reg9 = linreg(aHat3[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 = 0.918
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.028
```

```
Out[64]: 0.9184102942737643
```

```
In [65]: TBV = a[posAi]
mean(TBV)
```

```
Out[65]: 4.5391800000000001
```

```
In [66]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[66]: 1.7627529293967004
```



```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
posAi = getPos(ped,IDs)
cor10 = cor(a[posAi],aHat3[posAi])[1,1]
reg10 = linreg(aHat3[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G2.Genotype.ID : correlation = %6.3f\n", cor10)
@printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg10)
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.868
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.997
```

```
Out[67]: 0.8684382041486678
```

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

```
Out[68]: 5.082269999999999
```

```
In [69]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[69]: 2.2933978002202684
```

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=10)
posAi = getPos(ped,IDs)
cor11 = cor(a[posAi],aHat3[posAi])[1,1]
reg11 = linreg(aHat3[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G3.Genotype.ID : correlation = %6.3f\n", cor11)
@printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg11)
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.864
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[70]: 0.8639118791509449
```

```
In [71]: TBV = a[posAi]
mean(TBV)
```

```
Out[71]: 5.5289
```

```
In [72]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[72]: 2.7750779074757967
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=1,
posAi = getPos(ped,IDs)
cor12 = cor(a[posAi],aHat3[posAi])[1,1]
reg12 = linreg(aHat3[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 = 0.545
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.015
```

```
Out[73]: 0.5451725942105462
```

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

```
Out[74]: 5.9384100000000001
```

```
In [75]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[75]: 3.3054241935232884
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=1,
posAi = getPos(ped,IDs)
cor13 = cor(a[posAi],aHat3[posAi])[1,1]
reg13 = linreg(aHat3[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 = 0.427
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.957
```

```
Out[76]: 0.426668546745776
```

```
In [77]: writedlm("Correlation.G5.G.PBLUP.txt",cor13)
```

```
In [78]: writedlm("Regression.G5.G.PBLUP.txt",reg13)
```

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

```
Out[79]: 5.482843125
```

```
In [80]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[80]: 2.782837609865241
```

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat3[posAi])[1,1]
reg14 = linreg(aHat3[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 = 0.692
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.890
```

```
Out[81]: 0.6922583111263111
```

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

```
Out[82]: 2.7723011538461537
```

```
In [83]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[83]: -0.03085013573480187
```

```
In [84]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat3[posAi])[1,1]
reg14 = linreg(aHat3[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 = 0.757
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.988
```

```
Out[84]: 0.7572728267223393
```

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

```
Out[85]: 3.3461039743589738
```

```
In [86]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[86]: 0.5893232519874178
```

```
In [87]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
posAi = getPos(ped,IDs)
cor15 = cor(a[posAi],aHat3[posAi])[1,1]
reg15 = linreg(aHat3[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : correlation = %6.3f\n", cor15)
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg15)
JCall = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.763
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.021
```

```
Out[87]: 0.7627115921532942
```

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

```
Out[88]: 3.941442179487179
```

```
In [89]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[89]: 1.169067836846751
```

```
In [90]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
posAi = getPos(ped,IDs)
cor16 = cor(a[posAi],aHat3[posAi])[1,1]
reg16 = linreg(aHat3[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 = 0.737
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.984
```

```
Out[90]: 0.736586652624187
```

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

```
Out[91]: 4.510472692307693
```

```
In [92]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[92]: 1.7273326588315154
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
posAi = getPos(ped,IDs)
cor17 = cor(a[posAi],aHat3[posAi])[1,1]
reg17 = linreg(aHat3[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 = 0.704
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.945
```

```
Out[93]: 0.7039342667128198
```

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

```
Out[94]: 5.008701153846155
```

```
In [95]: EBV = aHat3[posAi]
mean(EBV)
```

```
Out[95]: 2.2360098988503094
```

```
In [96]: numSSBayes
```

```
Out[96]: SSBR.NumSSBayes(54922,45922,9000,40000,39000,1000,0)
```