

```
In [1]: include("/home/nicole/Jupyter/SSBRnoJ/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/0.5g2k/G/5  
  
/home/nicole/Jupyter/JG3/Data/0.5g2k/G/5
```

```
In [4]: ;ls  
  
GenNF.txt  
PedAll.txt  
Phe.txt  
PheAll.txt
```

```
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
        y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
        Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
        nothing
```

```
In [31]: vG      = 0.704
        vRes     = 0.704
        aHat3=SSBR.PBLUP(y_Vecs,Z_Mats,A_Mats,numSSBayes,vRes,vG);
```

```
In [32]: using DataFrames
```

```
In [33]: 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 [34]: IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false)
        posAi = getPos(ped,IDs)
        cor1 = cor(a[posAi],aHat3[posAi])[1,1]
        reg1 = linreg(aHat3[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 = 0.893
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.992
```

```
Out[34]: 0.8928671882537355
```

```
In [35]: TBV = a[posAi]
        mean(TBV)
```

```
Out[35]: 33.41670264583333
```

```
In [36]: EBV = aHat3[posAi]
        mean(EBV)
```

```
Out[36]: 1.44449143110824
```

```
In [37]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
        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 ) # 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 = 0.564
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.020
```

```
Out[37]: 0.564189640992863
```

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

```
Out[38]: 34.71152866666667
```

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

```
Out[39]: 2.7384163409294593
```

```
In [40]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # 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 = 0.881
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.986
```

```
Out[40]: 0.8813495956181576
```

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

```
Out[41]: 33.117896641025645
```

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

```
Out[42]: 1.145893374995651
```

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

```
SSBRJC from Gibbs - G0.ID : correlation = 0.710
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.877
```

```
Out[43]: 0.7095388602635634
```

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

```
Out[44]: 31.993005999999998
```

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

```
Out[45]: 0.0005564685228047559
```

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

```
SSBRJC from Gibbs - G1.ID : correlation =  0.782
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.998
```

```
Out[46]: 0.7824398567046458
```

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

```
Out[47]: 32.57758962499999
```

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

```
Out[48]: 0.6337907752291314
```

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

```
SSBRJC from Gibbs - G2.ID : correlation = 0.769
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 0.982
```

```
Out[49]: 0.7690815518591272
```

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

```
Out[50]: 33.18146625
```

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

```
Out[51]: 1.204598653307124
```

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

```
SSBRJC from Gibbs - G3.ID : correlation = 0.772
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.012
```

```
Out[52]: 0.771591881493912
```

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

```
Out[53]: 33.7279075
```

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

```
Out[54]: 1.7540235051932414
```

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

```
SSBRJC from Gibbs - G4.ID : correlation =  0.727
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.003
```

```
Out[55]: 0.7274530197601293
```

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

```
Out[56]: 34.251612
```

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

```
Out[57]: 2.2804104026733203
```

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

```
SSBRJC from Gibbs - G5.ID : correlation =  0.414
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.016
```

```
Out[58]: 0.4138115347303911
```



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

```
Out[59]: 34.768634500000005
```

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

```
Out[60]: 2.793568781723819
```

```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 =  0.904
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.009
```

```
Out[61]: 0.9035004779389788
```

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

```
Out[62]: 33.146454999999996
```

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

```
Out[63]: 1.2820018304482277
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # 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 = 0.927
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.962
```

```
Out[64]: 0.9273700272388709
```

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

```
Out[65]: 33.785545
```

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

```
Out[66]: 1.7670712980928855
```

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # 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 = 0.891
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.985
```

```
Out[67]: 0.8914357619867704
```

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

```
Out[68]: 34.282220000000001
```

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

```
Out[69]: 2.3144540861716654
```

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # 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 = 0.867
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.042
```

```
Out[70]: 0.8666953160663787
```

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

```
Out[71]: 34.79433
```

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

```
Out[72]: 2.8208030232762438
```

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # 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 = 0.500
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.034
```

```
Out[73]: 0.5000346479732581
```

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

```
Out[74]: 35.264860000000006
```

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

```
Out[75]: 3.3016538348838855
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # 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 = 0.414
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.016
```

```
Out[76]: 0.4138115347303911
```

```
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]: 34.768634500000005
```

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

```
Out[80]: 2.793568781723819
```

```
In [81]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # 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 = 0.688
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.871
```

```
Out[81]: 0.6875527283866962
```

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

```
Out[82]: 31.963430384615382
```

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

```
Out[83]: -0.03230110485989839
```

```
In [84]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
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 ) # 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 = 0.765
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.992
```

```
Out[84]: 0.7645327384661851
```

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

```
Out[85]: 32.5466164102564
```

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

```
Out[86]: 0.6047323002839071
```

```
In [87]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg15)
         JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.752
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[87]: 0.7517369189141418
```

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

```
Out[88]: 33.15324179487179
```

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

```
Out[89]: 1.176140821695213
```

```
In [90]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # with epsilon
         @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 = 0.757
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.012
```

```
Out[90]: 0.7565008579786607
```

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

```
Out[91]: 33.70056333333333
```

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

```
Out[92]: 1.726670184216754
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         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 ) # 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 =  0.715
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.003
```

```
Out[93]: 0.7148071778356189
```

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

```
Out[94]: 34.22563128205128
```

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

```
Out[95]: 2.25422467364228
```

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

```
Out[96]: SSBR.NumSSBayes(54875,45875,9000,40000,39000,1000,0)
```