

```
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/0.5/G/10  
  
/home/nicole/Jupyter/JG3/Data/0.5/G/10
```

In [4]: ;ls

```
Correlation.G5.G.C.txt
Correlation.G5.G.J.txt
Correlation.G5.G.JC.txt
Correlation.G5.G.N.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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.G.C.txt
Regression.G5.G.J.txt
Regression.G5.G.JC.txt
Regression.G5.G.N.txt
all.ID
alphaEstimates
genotype.ID
meanOfSNPGAll
meanOfSNPGG0
meanOfSNPGG1
meanOfSNPGG2
meanOfSNPGG3
meanOfSNPGG4
meanOfSNPGG5
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 [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
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
nothing
```

```
In [31]: vRes    = 0.583
vG       = 0.583
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 = ' ',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 [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 e
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n",
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.889
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.993
```

```
Out[34]: 0.8894286427966482
```

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

```
Out[35]: 9.817296166666667
```

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

```
Out[36]: 1.2936662935245997
```

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

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.573
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.032
```

```
Out[37]: 0.5731395404790167
```

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

```
Out[38]: 10.998993111111111
```

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

```
Out[39]: 2.466262805771759
```

```
In [40]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
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 = 0.874
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.985
```

```
Out[40]: 0.8743091919044534
```

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

```
Out[41]: 9.544596871794871
```

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

```
Out[42]: 1.0230670983906398
```

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

```
SSBRJC from Gibbs - G0.ID : correlation = 0.679
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.816
```

```
Out[43]: 0.6788080155962495
```

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

```
Out[44]: 8.537600375
```

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

```
Out[45]: -0.001899501667626823
```

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

```
SSBRJC from Gibbs - G1.ID : correlation = 0.769
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.969
```

```
Out[46]: 0.7689947124010899
```

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

```
Out[47]: 9.044070624999998
```

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

```
Out[48]: 0.5483683709510622
```

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

```
SSBRJC from Gibbs - G2.ID : correlation = 0.759
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.004
```

```
Out[49]: 0.7592064624988186
```

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

```
Out[50]: 9.610254000000001
```

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

```
Out[51]: 1.087050487630855
```

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

```
SSBRJC from Gibbs - G3.ID : correlation = 0.770
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.048
```

```
Out[52]: 0.7696959468368674
```

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

```
Out[53]: 10.094816125000001
```

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

```
Out[54]: 1.5745966221371754
```

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

```
SSBRJC from Gibbs - G4.ID : correlation = 0.744
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.039
```

```
Out[55]: 0.7437708495789795
```

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

```
Out[56]: 10.564574125
```

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

```
Out[57]: 2.036946040928878
```

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

```
SSBRJC from Gibbs - G5.ID : correlation = 0.421
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.024
```

```
Out[58]: 0.4205978950699461
```

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

```
Out[59]: 11.052461749999999
```

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

```
Out[60]: 2.5169357411672535
```



```
In [61]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor9
```

```
SSBRJC from Gibbs - G0.Genotype.ID : correlation = 0.905
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.976
```

```
Out[61]: 0.9054657406484298
```

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

```
Out[62]: 9.537889999999999
```

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

```
Out[63]: 1.1175629284733881
```

```
In [64]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor9
```

```
SSBRJC from Gibbs - G1.Genotype.ID : correlation = 0.861
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.947
```

```
Out[64]: 0.8609832880429119
```

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

```
Out[65]: 10.16994
```

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

```
Out[66]: 1.6241137786094937
```

```
In [67]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor10
```

SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.900

SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.088

Out[67]: 0.89999993650532498

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

Out[68]: 10.58867

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

Out[69]: 2.064114649039866

```
In [70]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor11
```

SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.883

SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.033

Out[70]: 0.8831881301484668

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

Out[71]: 11.03682

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

Out[72]: 2.4971344615418034

```
In [73]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.521
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.042
```

```
Out[73]: 0.5206038669110643
```

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

```
Out[74]: 11.5229
```

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

```
Out[75]: 3.0014707953744537
```

```
In [76]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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.
JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.421
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.024
```

```
Out[76]: 0.4205978950699461
```

```
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]: 11.052461749999999
```

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

```
Out[80]: 2.5169357411672535
```

```
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 = 0.656
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.806
```

```
Out[81]: 0.6563593376095247
```

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

```
Out[82]: 8.511951923076923
```

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

```
Out[83]: -0.030603666543037464
```

```
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 = 0.750
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.962
```

```
Out[84]: 0.7497908573555194
```

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

```
Out[85]: 9.01520217948718
```

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

```
Out[86]: 0.5207851553700767
```

```
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", JCall = cor15)
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.742
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[87]: 0.7417326601675827
```

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

```
Out[88]: 9.585166410256411
```

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

```
Out[89]: 1.0619975604152394
```

```
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", JCall = cor16)
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.755
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.050
```

```
Out[90]: 0.7554637786097405
```

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

```
Out[91]: 10.07066217948718
```

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

```
Out[92]: 1.550941805742185
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
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 = %
JCall = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation = 0.731
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.044
```

```
Out[93]: 0.7310333464869863
```

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

```
Out[94]: 10.540001666666667
```

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

```
Out[95]: 2.012214636968735
```

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

```
Out[96]: SSBR.NumSSBayes(54932,45932,9000,40000,39000,1000,0)
```