

```
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/5  
  
/home/nicole/Jupyter/JG3/Data/0.5/G/5
```

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

```
In [31]: vRes = 0.699
      vG = 0.699
      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 = 0.884
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.975
```

```
Out[34]: 0.8837159378609749
```

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

```
Out[35]: 11.514132458333334
```

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

```
Out[36]: 1.3608531455769752
```

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

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.549
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.971
```

```
Out[37]: 0.5487914932280055
```

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

```
Out[38]: 12.736877111111111
```

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

```
Out[39]: 2.6281006947094694
```

```
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 = 0.871
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[40]: 0.8709760496446026
```

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

```
Out[41]: 11.231960615384617
```

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

```
Out[42]: 1.0684114034694763
```

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

```
SSBRJC from Gibbs - G0.ID : correlation = 0.703
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.877
```

```
Out[43]: 0.7025869059763595
```

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

```
Out[44]: 10.187546249999999
```

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

```
Out[45]: -0.0012330787761268382
```

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

```
SSBRJC from Gibbs - G1.ID : correlation = 0.770
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 0.986
```

```
Out[46]: 0.7695038529551359
```

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

```
Out[47]: 10.7345095
```

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

```
Out[48]: 0.5933826959650165
```

```
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", re
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation =  0.770
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.008
```

```
Out[49]: 0.7698933888906929
```

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

```
Out[50]: 11.27873
```

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

```
Out[51]: 1.115851127843941
```

```
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", re
JCA11 = cor6
```

```
SSBRJC from Gibbs - G3.ID : correlation =  0.752
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.000
```

```
Out[52]: 0.7517874706985195
```

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

```
Out[53]: 11.789662125
```

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

```
Out[54]: 1.6209014121375802
```

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

```
SSBRJC from Gibbs - G4.ID : correlation =  0.726
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.975
```

```
Out[55]: 0.7260201658999998
```

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

```
Out[56]: 12.30248425
```

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

```
Out[57]: 2.1516343337973476
```

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

```
SSBRJC from Gibbs - G5.ID : correlation =  0.402
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.958
```

```
Out[58]: 0.4015215812384653
```

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

```
Out[59]: 12.791862625000002
```

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

```
Out[60]: 2.6845823824940918
```



```
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 = 0.886
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[61]: 0.8864881440255429
```

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

```
Out[62]: 11.279599999999999
```

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

```
Out[63]: 1.1994332438728719
```

```
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 = 0.880
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[64]: 0.8800984505023802
```

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

```
Out[65]: 11.827124999999997
```

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

```
Out[66]: 1.6604189877017697
```

```
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.
JCA11 = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.886
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 0.993
```

```
Out[67]: 0.8860873110479595
```

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

```
Out[68]: 12.284759999999997
```

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

```
Out[69]: 2.1217750695517226
```

```
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.
JCA11 = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.861
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.016
```

```
Out[70]: 0.8606697020077982
```

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

```
Out[71]: 12.799939999999998
```

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

```
Out[72]: 2.6805189121374697
```

```
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.
JCA11 = cor12
```

SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.412

SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.847

Out[73]: 0.41197431610069063

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

Out[74]: 13.29354

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

Out[75]: 3.219089748898632

```
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.
JCA11 = cor13
```

SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.402

SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 0.958

Out[76]: 0.4015215812384653

```
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]: 12.791862625000002

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

Out[80]: 2.6845823824940918

```
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 = 0.683
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.872
```

```
Out[81]: 0.682806542557785
```

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

```
Out[82]: 10.15954487179487
```

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

```
Out[83]: -0.03201939474148579
```

```
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 = 0.753
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.982
```

```
Out[84]: 0.7534989102649137
```

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

```
Out[85]: 10.70649371794872
```

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

```
Out[86]: 0.5660227910486897
```

```
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)
JCA11 = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation = 0.756
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.009
```

```
Out[87]: 0.7556524101668907
```

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

```
Out[88]: 11.252934358974361
```

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

```
Out[89]: 1.0900582062616901
```

```
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)
JCA11 = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation = 0.736
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.004
```

```
Out[90]: 0.736167290567994
```

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

```
Out[91]: 11.763757564102566
```

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

```
Out[92]: 1.5937317326504032
```

```
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 = 0.714
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 0.981
```

```
Out[93]: 0.7140784999955377
```

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

```
Out[94]: 12.277072564102564
```

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

```
Out[95]: 2.1242636821280843
```

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

```
Out[96]: SSBR.NumSSBayes(54913,45913,9000,40000,39000,1000,0)
```