

```
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/10  
  
/home/nicole/Jupyter/JG3/Data/0.5g2k/G/10
```

```
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 [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      = 0.858
vRes     = 0.858
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 = 0.888
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.972
```

```
Out[34]: 0.8879010968062404
```

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

```
Out[35]: 34.115545895833336
```

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

```
Out[36]: 1.5124542808117378
```

```
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 = 0.546
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 0.948
```

```
Out[37]: 0.5460653215952119
```

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

```
Out[38]: 35.388306
```

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

```
Out[39]: 2.8473584308044755
```

```
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 = 0.878
```

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

```
Out[40]: 0.877623346479399
```

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

```
Out[41]: 33.82183202564103
```

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

```
Out[42]: 1.2043994769672601
```

```
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 = 0.750
```

```
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.957
```

```
Out[43]: 0.7497914760115664
```

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

```
Out[44]: 32.63486125
```

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

```
Out[45]: 0.0031618192450580947
```

```
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 =  0.774
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.988
```

```
Out[46]: 0.7741429501674518
```

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

```
Out[47]: 33.289144499999999
```

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

```
Out[48]: 0.6650633568516532
```

```
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 =  0.759
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.981
```

```
Out[49]: 0.7588523655714463
```

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

```
Out[50]: 33.902438499999999
```

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

```
Out[51]: 1.2951930174288553
```

```
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 =  0.746
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.976
```

```
Out[52]: 0.7456173640920641
```

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

```
Out[53]: 34.439698625
```



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

```
Out[54]: 1.8294877222402088
```

```
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 =  0.710
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.934
```

```
Out[55]: 0.7095563991308711
```

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

```
Out[56]: 34.985941625
```

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

```
Out[57]: 2.3784202877105343
```

```
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 =  0.399
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.927
```

```
Out[58]: 0.39855670359434564
```

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

```
Out[59]: 35.44119087500001
```

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

```
Out[60]: 2.903399481394118
```

```
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 =  0.894
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.986
```

```
Out[61]: 0.8939353910079378
```

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

```
Out[62]: 33.928745000000006
```

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

```
Out[63]: 1.3391377664672333
```

```
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 = 0.888
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.013
```

```
Out[64]: 0.8877044915201995
```

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

```
Out[65]: 34.4840300000000004
```

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

```
Out[66]: 1.9087599240183473
```

```
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 = 0.860
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.003
```

```
Out[67]: 0.8603468364495038
```

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

```
Out[68]: 34.975065
```

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

```
Out[69]: 2.3795101049289946
```

```
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 = 0.869
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.042
```

```
Out[70]: 0.8692298575923746
```

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

```
Out[71]: 35.536075000000004
```

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

```
Out[72]: 2.938886658027094
```

```
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 = 0.394
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.793
```

```
Out[73]: 0.394327344248327
```

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

```
Out[74]: 35.90222
```

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

```
Out[75]: 3.4288556769949827
```

```
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 =  0.399
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.927
```

```
Out[76]: 0.39855670359434564
```

```
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]: 35.44119087500001
```

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

```
Out[80]: 2.903399481394118
```

```
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 = 0.732
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.955
```

```
Out[81]: 0.73179157966684
```

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

```
Out[82]: 32.60168474358974
```

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

```
Out[83]: -0.031093974273459224
```

```
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 = 0.758
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.990
```

```
Out[84]: 0.7584004291866229
```

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

```
Out[85]: 33.25850641025641
```

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

```
Out[86]: 0.6331737012832764
```

```
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 = 0.744
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 0.980
```

```
Out[87]: 0.7443997521928087
```

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

```
Out[88]: 33.87493525641025
```

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

```
Out[89]: 1.2673900151852617
```

```
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 = 0.729
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 0.974
```

```
Out[90]: 0.7286060841102667
```

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

```
Out[91]: 34.411586410256405
```

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

```
Out[92]: 1.801041595681571
```

```
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)
         JCA11 = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.700
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.940
```

```
Out[93]: 0.6998950213281174
```

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

```
Out[94]: 34.962447307692315
```

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

```
Out[95]: 2.3514860469596512
```

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

```
Out[96]: SSBR.NumSSBayes(54904,45904,9000,40000,39000,1000,0)
```