

```
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/M/50QTL  
  
/home/nicole/Jupyter/JG3/Data/0.5/M/50QTL
```

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

```
In [5]: using DataFrames
```

```
In [6]: MarNF = convert(Array,readtable("MarNF.txt",separator=' ',header=false))
```

```
Out[6]: 9000x151 Array{Int64,2}:
```

```
40742 1 2 0 2 2 1 1 0 0 1 ... 1 1 1 1 1 2 2 0 0 0 1 0
40750 0 2 0 2 2 0 0 0 0 0 1 1 1 2 1 1 1 0 1 1 1 2
40787 0 2 1 2 1 0 0 0 0 1 2 1 1 1 1 2 1 1 1 1 1 2
40825 0 1 1 2 2 1 1 1 1 1 2 1 1 1 1 1 1 0 1 1 0 2
40826 0 2 0 2 2 0 0 0 0 2 2 0 2 2 1 1 2 0 0 0 1 1
40846 0 2 0 2 2 0 0 0 0 0 ... 2 1 1 1 1 1 1 0 1 1 0 2
40872 0 2 1 2 1 0 0 0 0 2 2 1 1 1 1 2 2 1 0 0 2 2
40960 0 1 2 1 0 0 1 1 1 1 1 2 0 1 0 0 2 0 0 0 1 2
40965 1 2 1 2 1 1 1 1 1 1 2 1 1 2 0 1 2 0 0 0 1 1
40982 0 1 1 2 1 0 0 1 1 1 2 1 2 1 1 1 1 1 1 1 1 2
41023 0 2 0 2 2 0 0 0 0 2 ... 2 2 1 1 0 2 1 0 1 1 1 2
41026 0 1 1 2 2 1 1 1 1 0 1 2 0 0 0 1 2 0 0 0 0 1
41063 0 2 0 2 2 0 0 0 0 1 2 1 1 1 1 2 2 1 0 0 2 1
⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮
88710 0 1 2 2 1 1 1 1 1 1 2 0 2 2 2 2 1 0 1 1 1 2
88711 0 1 1 1 1 0 1 1 1 1 2 2 0 1 0 0 2 0 0 0 0 2
88712 0 2 1 2 1 0 0 0 1 1 ... 2 2 0 0 0 1 2 1 0 0 1 2
88713 0 2 0 2 2 2 2 2 1 0 2 0 2 2 2 2 1 0 1 1 0 2
88714 0 2 0 2 2 0 0 0 0 1 2 0 2 2 2 2 0 0 2 2 0 2
88715 0 2 1 2 1 1 1 1 1 1 2 1 2 1 1 2 1 0 1 1 1 1
88716 0 1 1 1 1 0 1 1 1 1 2 0 1 2 1 1 1 0 1 1 1 1
88717 0 2 0 2 2 0 1 1 1 1 ... 2 1 1 2 1 1 1 0 1 2 0 2
88718 0 2 1 2 1 0 0 0 0 2 2 1 2 1 1 2 2 0 0 0 2 1
88719 0 2 1 2 1 0 0 0 0 1 2 0 2 2 2 2 1 0 1 1 0 2
88720 0 2 0 2 2 0 1 1 1 0 2 0 2 2 2 2 0 0 2 2 0 2
88721 0 2 0 2 2 1 1 1 1 1 2 1 2 1 1 2 1 0 1 1 1 1
```

```
In [7]: MID = MarNF[:,1]
M = MarNF[:,2:end]
```

```
Out[7]: 9000x150 Array{Int64,2}:
```

```
 1  2  0  2  2  1  1  0  0  1  1  1  1  ...  1  1  1  1  1  2  2  0  0  0  1  0
 0  2  0  2  2  0  0  0  0  0  2  0  0      1  1  1  2  1  1  1  0  1  1  1  2
 0  2  1  2  1  0  0  0  0  1  2  0  1      2  1  1  1  1  2  1  1  1  1  1  2
 0  1  1  2  2  1  1  1  1  1  1  1  0      2  1  1  1  1  1  1  0  1  1  0  2
 0  2  0  2  2  0  0  0  0  2  0  2  0      2  0  2  2  1  1  2  0  0  0  1  1
 0  2  0  2  2  0  0  0  0  0  2  0  2  ...  2  1  1  1  1  1  1  0  1  1  0  2
 0  2  1  2  1  0  0  0  0  2  1  1  0      2  1  1  1  1  2  2  1  0  0  2  2
 0  1  2  1  0  0  1  1  1  1  2  0  0      1  2  0  1  0  0  2  0  0  0  1  2
 1  2  1  2  1  1  1  1  1  1  1  1  0      2  1  1  2  0  1  2  0  0  0  1  1
 0  1  1  2  1  0  0  1  1  1  2  1  2      2  1  2  1  1  1  1  1  1  1  1  2
 0  2  0  2  2  0  0  0  0  2  0  2  0  ...  2  2  1  1  0  2  1  0  1  1  1  2
 0  1  1  2  2  1  1  1  1  0  1  1  1      1  2  0  0  0  1  2  0  0  0  0  1
 0  2  0  2  2  0  0  0  0  1  1  1  0      2  1  1  1  1  2  2  1  0  0  2  1
 ⋮          ⋮          ⋮          ⋮          ⋮          ⋮
 0  1  2  2  1  1  1  1  1  1  2  0  0      2  0  2  2  2  2  1  0  1  1  1  2
 0  1  1  1  1  0  1  1  1  1  1  1  0      2  2  0  1  0  0  2  0  0  0  0  2
 0  2  1  2  1  0  0  0  1  1  0  2  0  ...  2  2  0  0  0  1  2  1  0  0  1  2
 0  2  0  2  2  2  2  2  1  0  1  1  1      2  0  2  2  2  2  1  0  1  1  0  2
 0  2  0  2  2  0  0  0  0  1  1  1  1      2  0  2  2  2  2  0  0  2  2  0  2
 0  2  1  2  1  1  1  1  1  1  2  0  1      2  1  2  1  1  2  1  0  1  1  1  1
 0  1  1  1  1  0  1  1  1  1  1  1  0      2  0  1  2  1  1  1  0  1  1  1  1
 0  2  0  2  2  0  1  1  1  1  1  1  0  ...  2  1  1  2  1  1  1  0  1  2  0  2
 0  2  1  2  1  0  0  0  0  2  1  0  0      2  1  2  1  1  2  2  0  0  0  2  1
 0  2  1  2  1  0  0  0  0  1  2  0  0      2  0  2  2  2  2  1  0  1  1  0  2
 0  2  0  2  2  0  1  1  1  0  2  0  1      2  0  2  2  2  2  0  0  2  2  0  2
 0  2  0  2  2  1  1  1  1  1  0  2  0      2  1  2  1  1  2  1  0  1  1  1  1
```

```
In [8]: MC = M - ones(size(M,1))*mean(M,1)
```

```
Out[8]: 9000x150 Array{Float64,2}:
```

```
 0.875889  0.390889 -0.649  0.136222 ... -0.953222  0.462556 -1.81689
-0.124111  0.390889 -0.649  0.136222  0.0467778  0.462556  0.183111
-0.124111  0.390889  0.351  0.136222  0.0467778  0.462556  0.183111
-0.124111 -0.609111  0.351  0.136222  0.0467778 -0.537444  0.183111
-0.124111  0.390889 -0.649  0.136222 -0.953222  0.462556 -0.816889
-0.124111  0.390889 -0.649  0.136222 ... 0.0467778 -0.537444  0.183111
-0.124111  0.390889  0.351  0.136222 -0.953222  1.46256  0.183111
-0.124111 -0.609111  1.351 -0.863778 -0.953222  0.462556  0.183111
 0.875889  0.390889  0.351  0.136222 -0.953222  0.462556 -0.816889
-0.124111 -0.609111  0.351  0.136222  0.0467778  0.462556  0.183111
-0.124111  0.390889 -0.649  0.136222 ... 0.0467778  0.462556  0.183111
-0.124111 -0.609111  0.351  0.136222 -0.953222 -0.537444 -0.816889
-0.124111  0.390889 -0.649  0.136222 -0.953222  1.46256 -0.816889
  ⋮
-0.124111 -0.609111  1.351  0.136222  0.0467778  0.462556  0.183111
-0.124111 -0.609111  0.351 -0.863778 -0.953222 -0.537444  0.183111
-0.124111  0.390889  0.351  0.136222 ... -0.953222  0.462556  0.183111
-0.124111  0.390889 -0.649  0.136222  0.0467778 -0.537444  0.183111
-0.124111  0.390889 -0.649  0.136222  1.04678 -0.537444  0.183111
-0.124111  0.390889  0.351  0.136222  0.0467778  0.462556 -0.816889
-0.124111 -0.609111  0.351 -0.863778  0.0467778  0.462556 -0.816889
-0.124111  0.390889 -0.649  0.136222 ... 1.04678 -0.537444  0.183111
-0.124111  0.390889  0.351  0.136222 -0.953222  1.46256 -0.816889
-0.124111  0.390889  0.351  0.136222  0.0467778 -0.537444  0.183111
-0.124111  0.390889 -0.649  0.136222  1.04678 -0.537444  0.183111
-0.124111  0.390889 -0.649  0.136222  0.0467778  0.462556 -0.816889
```

```
In [9]: mean(MC,1)
```

```
Out[9]: 1x150 Array{Float64,2}:
```

```
-7.50017e-18 -2.84217e-17 -1.7053e-16 ... -1.10529e-16 -1.91452e-16
```

```
In [10]: MCstream=open("MarNFCenter.txt","w")
```

```
Out[10]: IOStream(<file MarNFCenter.txt>)
```

```
In [11]: for i in 1:size(MID,1)
        @printf(MCstream, "%19d", MID[i])
        for j in 1:size(MC,2)
            @printf(MCstream, "%10.6f", MC[i,j])
        end
        @printf(MCstream, "\n")
    end
```

```
In [12]: close(MCstream)
```

```
In [13]: ;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

```
In [14]: ;awk '{print $1}' MarNFCenter.txt | sort -b > genotype.ID
```

```
In [15]: ;join -v1 all.ID genotype.ID > noGenotype.ID
```

```
In [16]: ;awk '{print $1,$2}' Phe.txt > sim.phenotype
```

```
In [17]: ;awk '{print $1,$3}' PheAll.txt > sim.bv
```

```
In [18]: ; awk 'NR >=1 && NR <=8000 {print $1}' PedAll.txt | sort -b > G0.ID
```

```
In [19]: ; awk 'NR >=8001 && NR <=16000 {print $1}' PedAll.txt | sort -b > G1.ID
```

```
In [20]: ; awk 'NR >=16001 && NR <=24000 {print $1}' PedAll.txt | sort -b > G2.ID
```

```
In [21]: ; awk 'NR >=24001 && NR <=32000 {print $1}' PedAll.txt | sort -b > G3.ID
```

```
In [22]: ; awk 'NR >=32001 && NR <=40000 {print $1}' PedAll.txt | sort -b > G4.ID
```

```
In [23]: ; awk 'NR >=40001 && NR <=48000 {print $1}' PedAll.txt | sort -b > G5.ID
```

```
In [24]: ;join G0.ID genotype.ID > G0.Genotype.ID
```

```
In [25]: ;join G1.ID genotype.ID > G1.Genotype.ID
```

```
In [26]: ;join G2.ID genotype.ID > G2.Genotype.ID
```

```
In [27]: ;join G3.ID genotype.ID > G3.Genotype.ID
```

```
In [28]: ;join G4.ID genotype.ID > G4.Genotype.ID
```

```
In [29]: ;join G5.ID genotype.ID > G5.Genotype.ID
```

```
In [30]: ;join -v1 G0.ID genotype.ID > G0.noGenotype.ID
```

```
In [31]: ;join -v1 G1.ID genotype.ID > G1.noGenotype.ID
```

```
In [32]: ;join -v1 G2.ID genotype.ID > G2.noGenotype.ID
```

```
In [33]: ;join -v1 G3.ID genotype.ID > G3.noGenotype.ID
```

```
In [34]: ;join -v1 G4.ID genotype.ID > G4.noGenotype.ID
```

```
In [35]: ;join -v1 G5.ID genotype.ID > G5.noGenotype.ID
```

```
In [36]: ;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 [37]: ;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 [38]: ped,A_Mats,numSSBayes = calc_Ai("PedAll.txt","genotype.ID",calculateInbreeding=false)
nothing
df      = read_genotypes("MarNFCenter.txt",numSSBayes)  # genotype file - centered already
M_Mats = make_MMats(df,A_Mats,ped);                    # M file centered already
y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes);
Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
X_Mats, W_Mats = make_XWMats(Z_Mats,M_Mats,numSSBayes)      # no J
nothing
```

```
In [39]: vRes    = 0.668
vG       = 0.668
nIter    = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter, outFreq=5000);
nothing
```

```
This is iteration 5000
This is iteration 10000
This is iteration 15000
This is iteration 20000
This is iteration 25000
This is iteration 30000
This is iteration 35000
This is iteration 40000
This is iteration 45000
This is iteration 50000
4782.224179 seconds (23.02 G allocations: 723.404 GB, 6.92% gc time)
```

```
In [40]: betaHat
```

```
Out[40]: 1-element Array{Float64,1}:
 11.6054
```

```
In [41]: alphaHat
```

```
Out[41]: 150-element Array{Float64,1}:
```

```
-0.0272535  
-0.0799801  
 0.0364017  
-0.0494421  
 0.0548077  
-0.0993445  
-0.0449977  
-0.00152377  
 0.0725806  
 0.0230241  
 0.00341329  
 0.0182465  
-0.0199399  
  ⋮  
-0.00542091  
 0.0547699  
 0.0866035  
 0.104659  
 0.0232834  
 0.0444456  
-0.0700246  
-0.0813918  
 0.00248491  
-0.0966177  
-0.0195873  
-0.117207
```

```
In [42]: writedlm("alphaEstimatesLeggaraC",alphaHat)
```



```
In [43]: epsiHat
```

```
Out[43]: 45906-element Array{Float64,1}:
 -0.427383
 -1.49184
  0.438004
 -1.59582
 -0.473623
 -0.841677
 -0.310152
  0.403212
 -1.18813
  0.20926
 -1.48443
  0.483905
 -0.810377
  ⋮
  0.348677
  0.474242
 -0.00284592
 -0.135246
  0.38145
 -0.866893
 -0.633613
  0.329362
 -0.2064
 -0.140329
  0.184708
 -2.56447
```

```
In [44]: writedlm("epsiEstimatesLeggaraC",epsiHat)
```

```
In [45]: 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 [46]: IDs = readtable("all.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor1 = cor(a[posAi],aHat1[posAi])[1,1]
reg1 = linreg(aHat1[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)
JCA11 = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.819
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.361
```

```
Out[46]: 0.8190961794666928
```

```
In [47]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[47]: -0.3760673978945322
```

```
In [48]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor2 = cor(a[posAi],aHat1[posAi])[1,1]
reg2 = linreg(aHat1[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)
JCA11 = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.618
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.141
```

```
Out[48]: 0.6183647178526069
```

```
In [49]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[49]: -2.6268322571038675e-7
```

```
In [50]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor3 = cor(a[posAi],aHat1[posAi])[1,1]
reg3 = linreg(aHat1[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)
JCA11 = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.838
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.240
```

```
Out[50]: 0.8379504463916551
```

```
In [51]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[51]: -0.4628521214048336
```

```
In [52]: IDs = readtable("G0.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat1[posAi])[1,1]
reg4 = linreg(aHat1[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)
JCA11 = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation = 0.685
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.868
```

```
Out[52]: 0.6848310055024557
```

```
In [53]: GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

```
Out[53]: -1.0438502473992322
```

```
In [54]: IDs = readtable("G1.ID", eltypes=[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor4 = cor(a[posAi],aHat1[posAi])[1,1]
reg4 = linreg(aHat1[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)
JCA11 = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation = 0.753
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV = 1.052
```

```
Out[54]: 0.7532548086186739
```

```
In [55]: GEBV = aHat1[posAi]
G1GEBV=mean(GEBV)
```

```
Out[55]: -0.8247988043505209
```

```
In [56]: IDs = readtable("G2.ID", eltypes=[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor5 = cor(a[posAi],aHat1[posAi])[1,1]
reg5 = linreg(aHat1[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)
JCA11 = cor5
```

```
SSBRJC from Gibbs - G2.ID : correlation = 0.732
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV = 1.047
```

```
Out[56]: 0.7318375965777343
```

```
In [57]: GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

```
Out[57]: -0.4537099757902055
```

```
In [58]: IDs = readtable("G3.ID", eltypes=[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor6 = cor(a[posAi],aHat1[posAi])[1,1]
reg6 = linreg(aHat1[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 = 0.718
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV = 1.052
```

```
Out[58]: 0.7183104229318484
```

```
In [59]: GEBV = aHat1[posAi]
G3GEBV=mean(GEBV)
```

```
Out[59]: -0.08898208396336263
```

```
In [60]: IDs = readtable("G4.ID", eltypes=[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat1[posAi])[1,1]
reg7 = linreg(aHat1[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 = 0.696
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.096
```

```
Out[60]: 0.6958302768867441
```

```
In [61]: GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

```
Out[61]: 0.14257512104062967
```

```
In [62]: IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat1[posAi])[1,1]
reg8 = linreg(aHat1[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)
JCA11 = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation = 0.592
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.056
```

```
Out[62]: 0.5915344925230578
```

```
In [63]: GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

```
Out[63]: 0.012361603095498575
```

```
In [64]: GEBVG5G1=G5GEBV-G1GEBV
```

```
Out[64]: 0.8371604074460195
```

```
In [65]: GEBVG1G5=[G1GEBV;G2GEBV;G3GEBV;G4GEBV;G5GEBV]
```

```
Out[65]: 5-element Array{Float64,1}:
-0.824799
-0.45371
-0.0889821
0.142575
0.0123616
```

```
In [66]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[66]: 2-element Array{Float64,1}:
12.5608
1.05591
```

```
In [67]: VarGEBV=var(aHat1[posAi])
```

```
Out[67]: 0.14807282889447843
```

```
In [68]: VarTBV=var(a[posAi])
```

```
Out[68]: 0.4718144954888738
```

```
In [69]: Cov=cov(aHat1[posAi], a[posAi])
```

```
Out[69]: 0.15635198527587013
```

```
In [70]: b=Cov/VarGEBV
```

```
Out[70]: 1.0559127318847383
```

```
In [71]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[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 = 0.764
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.160
```

```
Out[71]: 0.764200414227757
```

```
In [72]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[72]: -0.47729718184354475
```

```
In [73]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor9 = cor(a[posAi],aHat1[posAi])[1,1]
reg9 = linreg(aHat1[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 = 0.725
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.111
```

```
Out[73]: 0.72467695354905
```

```
In [74]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[74]: -0.22632103096470269
```

```
In [75]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor10 = cor(a[posAi],aHat1[posAi])[1,1]
         reg10 = linreg(aHat1[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 =  0.675
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.100
```

```
Out[75]: 0.6749761352036453
```

```
In [76]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[76]: 0.008417328949620018
```

```
In [77]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
         posAi = getPos(ped,IDs)
         cor11 = cor(a[posAi],aHat1[posAi])[1,1]
         reg11 = linreg(aHat1[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 =  0.609
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.049
```

```
Out[77]: 0.6088007217507496
```

```
In [78]: GEBV = aHat1[posAi]
         mean(GEBV)
```

```
Out[78]: 0.09305060419196148
```



```
In [79]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor12 = cor(a[posAi],aHat1[posAi])[1,1]
reg12 = linreg(aHat1[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 =  0.436
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.656
```

```
Out[79]: 0.43607578896492827
```

```
In [80]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[80]: 0.10767433510156613
```

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor13 = cor(a[posAi],aHat1[posAi])[1,1]
reg13 = linreg(aHat1[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 =  0.592
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.056
```

```
Out[81]: 0.5915344925230578
```

```
In [82]: GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

```
Out[82]: 0.012361603095498575
```

```
In [83]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat1[posAi])[1,1]
reg14 = linreg(aHat1[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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.676
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.846
```

```
Out[83]: 0.6758527913122219
```

```
In [84]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[84]: -1.058377249080147
```

```
In [85]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor14 = cor(a[posAi],aHat1[posAi])[1,1]
reg14 = linreg(aHat1[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)
JCA11 = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.745
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.027
```

```
Out[85]: 0.7447866615331429
```

```
In [86]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[86]: -0.8401443882834906
```

```
In [87]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor15 = cor(a[posAi],aHat1[posAi])[1,1]
reg15 = linreg(aHat1[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 =  0.726
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.021
```

```
Out[87]: 0.7262268313214282
```

```
In [88]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[88]: -0.46555939386045747
```

```
In [89]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
posAi = getPos(ped,IDs)
cor16 = cor(a[posAi],aHat1[posAi])[1,1]
reg16 = linreg(aHat1[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 =  0.725
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.037
```

```
Out[89]: 0.7249189232339429
```

```
In [90]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[90]: -0.0936495887878581
```

```
In [91]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=false)
        posAi = getPos(ped,IDs)
        cor17 = cor(a[posAi],aHat1[posAi])[1,1]
        reg17 = linreg(aHat1[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 =  1.106
```

```
Out[91]: 0.7150904056059288
```

```
In [92]: GEBV = aHat1[posAi]
        mean(GEBV)
```

```
Out[92]: 0.14347001298778514
```

```
In [93]: numSSBayes
```

```
Out[93]: SSBR.NumSSBayes(54906,45906,9000,40000,39000,1000,150)
```