

```
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/0.5a0/M/3

/home/nicole/Jupyter/JG3/Data/0.5a0/M/3
```

```
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
MarNF.txt
MarNFCenter.txt
PedAll.txt
Phe.txt
PheAll.txt
all.ID
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

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

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

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

```
40762 0 2 2 0 0 0 2 0 2 0 ... 2 0 0 1 0 2 1 0 1 0 0
2
40773 0 2 2 1 0 0 2 0 1 0 0 2 2 2 1 1 1 1 1 1 1
1
40799 0 1 2 2 1 1 1 1 1 2 2 0 1 2 1 2 1 2 0 0 0
2
40816 0 2 2 2 0 0 2 0 0 0 0 2 2 2 2 0 2 2 0 1 1
1
40898 0 2 2 2 1 1 1 1 1 2 1 1 1 2 1 1 1 2 0 1 1
1
40906 0 2 2 2 0 0 2 0 1 1 ... 2 0 1 1 0 2 0 1 1 0 0
2
40910 0 0 2 2 1 2 0 2 0 1 1 1 1 1 1 1 1 1 1 1 1
1
40915 0 2 2 2 0 0 2 0 2 2 0 2 2 2 2 0 2 2 0 2 2
0
40919 0 0 2 2 1 1 1 1 1 2 2 0 1 2 0 2 1 2 0 0 0
1
40931 0 2 2 2 0 0 2 0 2 2 1 1 1 1 1 1 1 1 1 1 1
1
40948 0 2 2 1 0 1 2 0 2 1 ... 2 0 1 2 0 2 0 2 0 0 0
2
40950 0 2 2 2 0 0 2 0 2 2 0 2 2 2 2 0 1 1 1 1 1
1
41011 1 1 2 2 0 1 1 1 1 0 2 1 0 2 1 2 1 2 0 0 0
2
      :           :           : \.      :           :
      :
88710 0 2 2 2 0 0 2 0 1 1 2 0 1 1 0 2 0 1 0 0 0
2
88711 0 2 2 1 0 0 2 0 1 0 2 1 0 2 1 2 1 2 0 0 0
2
88712 0 1 2 2 1 1 1 1 1 2 ... 2 1 0 2 1 2 0 1 1 0 0
2
88713 0 2 2 1 0 0 2 0 1 0 2 0 2 2 1 2 1 1 1 0 0
2
88714 0 1 2 1 0 0 2 0 2 1 2 0 0 1 0 2 0 1 1 0 0
2
88715 0 2 2 2 0 0 2 0 1 1 2 0 1 2 0 2 1 1 1 0 0
2
88716 0 2 2 2 0 0 2 0 1 1 2 0 1 2 0 1 1 2 0 1 1
1
88717 0 1 2 2 1 1 1 1 0 1 ... 2 1 0 2 1 2 0 1 1 0 0
2
88718 0 0 2 2 0 0 2 0 2 2 1 2 1 2 2 2 2 2 0 0 0
2
88719 0 1 2 2 1 0 2 0 2 2 2 1 1 2 1 2 1 1 0 0 0
2
88720 0 1 2 1 0 0 2 0 2 1 1 1 2 2 1 1 1 2 0 1 1
1
88721 0 2 2 2 0 0 2 0 0 0 2 0 1 2 1 2 1 2 0 0 0
2
```

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

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

```

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

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

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

```
Out[8]: 9000x150 Array{Float64,2}:
 -0.046  0.229  0.0688889 -1.42378 ... -0.377889 -0.388222  0.679
 -0.046  0.229  0.0688889 -0.423778  0.622111  0.611778 -0.321
 -0.046 -0.771  0.0688889  0.576222 -0.377889 -0.388222  0.679
 -0.046  0.229  0.0688889  0.576222  0.622111  0.611778 -0.321
 -0.046  0.229  0.0688889  0.576222  0.622111  0.611778 -0.321
 -0.046  0.229  0.0688889  0.576222 ... -0.377889 -0.388222  0.679
 -0.046 -1.771  0.0688889  0.576222  0.622111  0.611778 -0.321
 -0.046  0.229  0.0688889  0.576222  1.62211  1.61178 -1.321
 -0.046 -1.771  0.0688889  0.576222 -0.377889 -0.388222 -0.321
 -0.046  0.229  0.0688889  0.576222  0.622111  0.611778 -0.321
 -0.046  0.229  0.0688889 -0.423778 ... -0.377889 -0.388222  0.679
 -0.046  0.229  0.0688889  0.576222  0.622111  0.611778 -0.321
  0.954 -0.771  0.0688889  0.576222 -0.377889 -0.388222  0.679
  ⋮
 -0.046  0.229  0.0688889  0.576222 -0.377889 -0.388222  0.679
 -0.046  0.229  0.0688889 -0.423778 -0.377889 -0.388222  0.679
 -0.046 -0.771  0.0688889  0.576222 ... -0.377889 -0.388222  0.679
 -0.046  0.229  0.0688889 -0.423778 -0.377889 -0.388222  0.679
 -0.046 -0.771  0.0688889 -0.423778 -0.377889 -0.388222  0.679
 -0.046  0.229  0.0688889  0.576222 -0.377889 -0.388222  0.679
 -0.046  0.229  0.0688889  0.576222  0.622111  0.611778 -0.321
 -0.046 -0.771  0.0688889  0.576222 ... -0.377889 -0.388222  0.679
 -0.046 -1.771  0.0688889  0.576222 -0.377889 -0.388222  0.679
 -0.046 -0.771  0.0688889  0.576222 -0.377889 -0.388222  0.679
 -0.046 -0.771  0.0688889 -0.423778  0.622111  0.611778 -0.321
 -0.046  0.229  0.0688889  0.576222 -0.377889 -0.388222  0.679
```

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

```
Out[9]: 1x150 Array{Float64,2}:
 1.13489e-17 -6.71068e-17 -5.23038e-17 ... 1.46845e-16 -3.47376e-17
```

```
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.ID
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 G5.noGenotype.ID
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",calculateInbreedingCoefficients,calculatePedigree)
nothing
df = read_genotypes("MarNFCenter.txt",numSSBayes) # genotype file - centered
M_Mats = make_MMats(df,A_Mats,ped); # M file centered around mean
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 centering
nothing
```

```
In [39]: vRes = 0.328
vG = 0.328
nIter = 50000
@time aHat1,alphaHat,betaHat,epsiHat =
ssGibbs(M_Mats,y_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG,nIter,
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
3464.869934 seconds (23.02 G allocations: 723.198 GB, 7.41% gc time)
```

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

```
Out[40]: 1-element Array{Float64,1}:
1.10619
```

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

```
Out[41]: 150-element Array{Float64,1}:  
  0.0109256  
 -0.04652  
  0.028977  
 -0.0206436  
 -0.0772863  
  0.0569776  
  0.10789  
 -0.110568  
  0.054446  
 -0.0161738  
 -0.0503214  
  0.0753896  
 -0.0253271  
  ⋮  
  0.120215  
 -0.00280013  
 -0.0343141  
  0.197962  
  0.0164999  
  0.0338862  
 -0.0128959  
 -0.0172531  
  0.0048361  
 -0.00733909  
  0.026386  
 -0.0359655
```

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

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

```
Out[43]: 45891-element Array{Float64,1}:
 -1.08444
 -0.941493
 -0.170646
  0.344759
 -0.913278
 -0.622938
 -0.128685
 -0.225554
  0.35897
 -0.210025
 -0.582459
 -0.495326
 -0.166651
  ⋮
 -0.0421411
 -0.361097
 -0.119547
  0.278916
 -0.624863
 -0.155162
 -0.192736
 -0.235166
  0.329055
  0.042793
 -0.472427
 -1.16878
```

```
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 correlation
@printf("SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = %6.3f\n", reg1)
JCall = cor1
```

```
SSBRJC from Gibbs - all.ID : correlation = 0.801
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.348
```

```
Out[46]: 0.8013420154845958
```



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

```
Out[47]: -0.3017770742241423
```

```
In [48]: IDs = readtable("genotype.ID", eltypes =[UTF8String], separator = ' ',header=
         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 ) # 1
         @printf("SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = %6.3f\n", reg2)
         JCall = cor2
```

```
SSBRJC from Gibbs - genotype.ID : correlation = 0.664
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.283
```

```
Out[48]: 0.6638233124121523
```

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

```
Out[49]: -1.599871071170532e-7
```

```
In [50]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',header=
         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 ) ;
         @printf("SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = %6.3f\n", reg3)
         JCall = cor3
```

```
SSBRJC from Gibbs - noGenotype.ID : correlation = 0.817
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.190
```

```
Out[50]: 0.8169904504184137
```

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

```
Out[51]: -0.371417900586535
```

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

```
SSBRJC from Gibbs - G0.ID : correlation = 0.558
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.602
```

```
Out[52]: 0.5584345066312205
```

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

```
Out[53]: -0.7894772404109408
```

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

```
SSBRJC from Gibbs - G1.ID : correlation =  0.737
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.016
```

```
Out[54]: 0.7371393883163025
```

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

```
Out[55]: -0.6667530442000814
```

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

```
SSBRJC from Gibbs - G2.ID : correlation =  0.743
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.083
```

```
Out[56]: 0.7428929092234313
```

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

```
Out[57]: -0.3712609880390502
```

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

```
SSBRJC from Gibbs - G3.ID : correlation =  0.739
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.136
```

```
Out[58]: 0.7391579760040599
```

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

```
Out[59]: -0.09743228742897964
```

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

```
SSBRJC from Gibbs - G4.ID : correlation = 0.701
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = 1.182
```

```
Out[60]: 0.7007713720749298
```

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

```
Out[61]: 0.10255236163143593
```

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

```
SSBRJC from Gibbs - G5.ID : correlation = 0.642
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = 1.183
```

```
Out[62]: 0.6415327638769064
```

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

```
Out[63]: 0.011708753102762388
```

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

```
Out[64]: 0.6784617973028438
```

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

```
Out[65]: 5-element Array{Float64,1}:
          -0.666753
          -0.371261
          -0.0974323
           0.102552
           0.0117088
```

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

```
Out[66]: 2-element Array{Float64,1}:
 1.91656
 1.18261
```

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

```
Out[67]: 0.09331002283549161
```

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

```
Out[68]: 0.31708352413037566
```

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

```
Out[69]: 0.1103493621813649
```

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

```
Out[70]: 1.1826099579453984
```

```
In [71]: IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 )
@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 = 0.743
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.235
```

```
Out[71]: 0.7429926823557168
```

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

```
Out[72]: -0.43712980487566144
```

```
In [73]: IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head=1)
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 )
@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 = 0.730
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.046
```

```
Out[73]: 0.7296213808133606
```

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

```
Out[74]: -0.1743008646946716
```

```
In [75]: IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=1,
         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)
         @printf("SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg10)
         JCall = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation = 0.709
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.187
```

```
Out[75]: 0.7087314736667882
```

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

```
Out[76]: -0.03821707431328081
```

```
In [77]: IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=1,
         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)
         @printf("SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg11)
         JCall = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation = 0.561
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 0.946
```

```
Out[77]: 0.5609550420948556
```

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

```
Out[78]: 0.09044055373828189
```

```
In [79]: IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ', head=1,
         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)
         @printf("SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg12)
         JCall = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation = 0.543
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 0.900
```

```
Out[79]: 0.5433240074928971
```

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

```
Out[80]: 0.09084986661501641
```

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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)
         @printf("SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = %6.3f\n", reg13)
         JCall = cor13
```

```
SSBRJC from Gibbs - G5.Genotype.ID : correlation = 0.642
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.183
```

```
Out[81]: 0.6415327638769064
```

```
In [82]: writedlm("Correlation.G5.M.C*.txt",cor13)
```

```
In [83]: writedlm("Regression.G5.M.C*.txt",reg13)
```

```
In [84]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

```
Out[84]: 0.011708753102762388
```

```
In [85]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
         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)
         @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 = 0.550
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.584
```

```
Out[85]: 0.549692632518869
```

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

```
Out[86]: -0.7985117900400506
```

```
In [87]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.725
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 0.987
```

```
Out[87]: 0.7251436001427324
```

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

```
Out[88]: -0.6793800231617585
```

```
In [89]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.738
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.057
```

```
Out[89]: 0.7376479039932632
```

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

```
Out[90]: -0.3798005755704802
```

```
In [91]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1,
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)
@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 = 0.745
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.116
```

```
Out[91]: 0.7448306909231324
```

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

```
Out[92]: -0.10224953976660174
```

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ', header = 1)
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)
@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 = 0.725
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.189
```

```
Out[93]: 0.724878904093405
```

```
In [94]: GEBV = aHat1[posAi]
mean(GEBV)
```

```
Out[94]: 0.1028524256062159
```

```
In [95]: numSSBayes
```

```
Out[95]: SSBR.NumSSBayes(54891,45891,9000,40000,39000,1000,150)
```