

```
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/5  
  
/home/nicole/Jupyter/JG3/Data/0.5a0/M/5
```

```
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}:
 40775  0  2  2  0  2  1  1  1  2  1  ...  0  1  1  0  2  1  2  0  0  0  2
2
 40819  0  2  2  0  1  1  1  0  1  2      2  1  2  2  1  2  2  0  1  1  2
1
 40858  0  1  1  1  2  2  2  0  2  2      2  1  1  2  1  1  1  0  1  1  1
1
 40860  0  2  1  0  1  0  0  2  2  1      2  2  2  2  0  2  2  0  2  0  2
0
 40866  0  2  2  0  1  1  1  0  1  2      1  1  1  2  1  1  1  1  1  1  2
1
 40895  0  0  2  2  2  2  2  0  2  0  ...  0  2  0  0  2  1  2  1  1  1  1
1
 40903  0  2  2  0  0  0  0  2  2  0      2  2  2  2  0  2  2  0  2  0  2
0
 40912  0  1  1  0  1  1  1  1  0  2      1  2  1  2  1  1  2  0  1  0  1
1
 40958  0  1  2  1  2  2  2  0  1  1      0  0  0  2  2  0  1  1  0  1  1
2
 40970  0  2  2  0  1  1  1  0  1  2      2  2  1  2  1  2  2  0  1  1  1
1
 40985  0  1  1  1  2  2  2  0  2  2  ...  0  1  1  0  2  1  2  0  0  0  2
2
 41025  1  2  2  1  1  1  1  1  2  0      2  2  2  2  0  1  1  1  1  1  2
1
 41077  1  2  2  0  1  1  1  0  0  2      1  2  1  1  1  2  2  0  1  1  2
0
      :          :          :  \  :          :
      :
88710  0  1  2  1  1  1  1  0  1  1      2  2  1  2  0  2  2  0  2  0  2
0
88711  0  0  1  0  2  2  2  0  1  2      2  2  2  2  0  2  2  0  2  0  2
0
88712  0  1  2  1  2  2  2  0  1  2  ...  2  1  2  2  1  2  2  0  1  1  2
1
88713  0  0  1  2  2  2  2  0  1  0      2  2  2  2  0  2  2  0  2  0  2
0
88714  1  1  2  1  2  2  2  0  1  1      2  2  1  1  1  1  2  0  1  0  2
1
88715  0  1  2  0  1  1  1  1  1  1      2  2  1  2  1  2  2  1  1  0  1
0
88716  1  1  1  2  2  2  2  0  1  0      2  1  1  2  0  2  2  0  2  0  2
1
88717  0  0  2  1  2  2  2  0  1  1  ...  2  2  2  2  0  2  2  0  2  0  2
0
88718  0  0  2  1  2  2  2  0  1  1      1  2  1  1  1  1  1  0  1  0  2
1
88719  0  1  1  0  1  1  1  0  1  2      2  2  2  2  0  2  2  0  2  0  2
0
88720  0  1  1  0  0  0  0  2  1  1      2  2  1  2  0  2  2  0  2  0  2
0
88721  0  0  0  1  2  2  2  0  1  1      2  2  1  2  0  2  2  0  2  0  2
0
```

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

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

```

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

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

```
Out[8]: 9000x150 Array{Float64,2}:
-0.137333  0.910333  0.520444 ... -0.356444  0.162889  1.41656
-0.137333  0.910333  0.520444      0.643556  0.162889  0.416556
-0.137333 -0.089667 -0.479556      0.643556 -0.837111  0.416556
-0.137333  0.910333 -0.479556     -0.356444  0.162889 -0.583444
-0.137333  0.910333  0.520444      0.643556  0.162889  0.416556
-0.137333 -1.08967  0.520444 ...  0.643556 -0.837111  0.416556
-0.137333  0.910333  0.520444     -0.356444  0.162889 -0.583444
-0.137333 -0.089667 -0.479556     -0.356444 -0.837111  0.416556
-0.137333 -0.089667  0.520444      0.643556 -0.837111  1.41656
-0.137333  0.910333  0.520444      0.643556 -0.837111  0.416556
-0.137333 -0.089667 -0.479556 ... -0.356444  0.162889  1.41656
 0.862667  0.910333  0.520444      0.643556  0.162889  0.416556
 0.862667  0.910333  0.520444      0.643556  0.162889 -0.583444
 ⋮
-0.137333 -0.089667  0.520444     -0.356444  0.162889 -0.583444
-0.137333 -1.08967 -0.479556     -0.356444  0.162889 -0.583444
-0.137333 -0.089667  0.520444 ...  0.643556  0.162889  0.416556
-0.137333 -1.08967 -0.479556     -0.356444  0.162889 -0.583444
 0.862667 -0.089667  0.520444     -0.356444  0.162889  0.416556
-0.137333 -0.089667  0.520444     -0.356444 -0.837111 -0.583444
 0.862667 -0.089667 -0.479556     -0.356444  0.162889  0.416556
-0.137333 -1.08967  0.520444 ... -0.356444  0.162889 -0.583444
-0.137333 -1.08967  0.520444     -0.356444  0.162889  0.416556
-0.137333 -0.089667 -0.479556     -0.356444  0.162889 -0.583444
-0.137333 -0.089667 -0.479556     -0.356444  0.162889 -0.583444
-0.137333 -1.08967 -1.47956      -0.356444  0.162889 -0.583444
```

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

```
Out[9]: 1x150 Array{Float64,2}:
 1.47043e-17 -3.15797e-17 -3.13428e-16 ... -1.06976e-16  1.18424e-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.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 the 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 = 0.767
vG = 0.767
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
2430.214491 seconds (23.03 G allocations: 723.652 GB, 7.80% gc time)
```

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

```
Out[40]: 1-element Array{Float64,1}:
5.20748
```

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

```
Out[41]: 150-element Array{Float64,1}:  
  0.0607493  
 -0.171779  
 -0.0657885  
  0.0874743  
  0.165166  
 -0.0122797  
 -0.0337685  
  0.0644786  
  0.000846859  
  0.0640041  
 -0.0346518  
  0.0566241  
 -0.0110126  
  ⋮  
  0.0236621  
  0.050747  
  0.0164414  
  0.0882174  
 -0.0413914  
  0.0722652  
 -0.00161623  
 -0.0671163  
 -0.0680782  
 -0.0414581  
 -0.0187912  
  0.0848449
```

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

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

```
Out[43]: 45924-element Array{Float64,1}:
-1.5565
-0.71428
-0.114331
-1.69622
-0.265613
-0.0940516
-0.226407
-0.701594
-0.789421
-0.234228
-0.130494
 0.142427
-0.920294
  ⋮
 0.639713
 0.091782
-0.394234
-0.290409
 0.209311
-0.436015
-0.0121064
-0.00562029
-0.0893244
-0.51577
-0.294424
-1.56303
```

```
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 = 0.828
SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 1.388
```

```
Out[46]: 0.8282427860879481
```



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

```
Out[47]: -0.4166995055918444
```

```
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 = 0.744
SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV = 1.381
```

```
Out[48]: 0.7435517399222451
```

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

```
Out[49]: 2.3280634711871547e-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 = 0.833
SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV = 1.244
```

```
Out[50]: 0.8328817385950238
```

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

```
Out[51]: -0.5128609836837347
```

```
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 = 0.692
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = 0.909
```

```
Out[52]: 0.6921915340276842
```

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

```
Out[53]: -1.0876577746290728
```

```
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 =  0.749
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.038
```

```
Out[54]: 0.7490986405655673
```

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

```
Out[55]: -0.8816461583113846
```

```
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 =  0.741
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.063
```

```
Out[56]: 0.7414688430117318
```

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

```
Out[57]: -0.51044446297901
```

```
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 =  0.727
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.092
```

```
Out[58]: 0.726805291280291
```

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

```
Out[59]: -0.1476049692271557
```

```
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 =  0.679
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.067
```

```
Out[60]: 0.6791114028545111
```

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

```
Out[61]: 0.11034997777529416
```

```
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 =  0.724
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.309
```

```
Out[62]: 0.7241116747554375
```

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

```
Out[63]: 0.016806353820263062
```

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

```
Out[64]: 0.8984525121316477
```

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

```
Out[65]: 5-element Array{Float64,1}:
          -0.881646
          -0.510444
          -0.147605
           0.11035
           0.0168064
```

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

```
Out[66]: 2-element Array{Float64,1}:
 6.18753
 1.30861
```

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

```
Out[67]: 0.151110758044321
```

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

```
Out[68]: 0.49352325556280474
```

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

```
Out[69]: 0.1977457019443951
```

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

```
Out[70]: 1.3086143204072607
```

```
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 = 0.756
```

```
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.109
```

```
Out[71]: 0.7562448105192418
```

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

```
Out[72]: -0.5787043389937309
```

```
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 = 0.806
```

```
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.249
```

```
Out[73]: 0.8064920472387429
```

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

```
Out[74]: -0.2841582293280516
```

```
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 = 0.781
```

```
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV = 1.358
```

```
Out[75]: 0.7809296546320171
```

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

```
Out[76]: -0.0814789554407
```

```
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 = 0.652
```

```
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV = 1.075
```

```
Out[77]: 0.6518279319439744
```

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

```
Out[78]: 0.12097420395094485
```

```
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 = 0.674
```

```
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV = 1.065
```

```
Out[79]: 0.6736909070801199
```

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

```
Out[80]: 0.1511236432866366
```

```
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 = 0.724
```

```
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV = 1.309
```

```
Out[81]: 0.7241116747554375
```

```
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]: 0.016806353820263062
```

```
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 = 0.686
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 0.889
```

```
Out[85]: 0.6859623821345643
```

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

```
Out[86]: -1.1007078627222866
```

```
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 = 0.740
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 1.013
```

```
Out[87]: 0.740129258961589
```

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

```
Out[88]: -0.8969663616186496
```

```
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 = 0.737
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = 1.039
```

```
Out[89]: 0.736546082516953
```

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

```
Out[90]: -0.5214435785569154
```

```
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 = 0.728
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = 1.074
```

```
Out[91]: 0.7283750134734635
```

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

```
Out[92]: -0.15449161469326084
```

```
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 = 0.693
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 1.062
```

```
Out[93]: 0.6932152425280866
```

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

```
Out[94]: 0.1093044991724392
```

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

```
Out[95]: SSBR.NumSSBayes(54924,45924,9000,40000,39000,1000,150)
```