```
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/9
```

```
/home/nicole/Jupyter/JG3/Data/0.5a0/M/9
```

```
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}:
  40755  2  2  0  0  2  0  1  1  1  1  …  2  2  0  2  1  1  2  0  0  1  2
         2
  40760  2  2  0  1  1  1  0  0  2  2     1  2  1  1  1  2  0  2  2  0  2
         0
  40799  1  1  0  1  1  1  1  2  1  1     1  1  1  1  1  1  1  1  1  1  2
         1
  40836  2  2  0  1  2  0  2  2  0  0     0  2  0  2  0  2  0  0  0  0  2
         2
  40837  1  1  0  1  1  1  1  2  1  1     1  1  1  1  1  1  1  1  1  1  2
         1
  40842  2  2  0  0  2  0  1  1  1  0  …  1  2  1  1  1  2  0  0  0  0  2
         2
  40849  2  1  0  1  1  1  1  0  2  2     2  2  1  2  2  2  0  0  0  0  2
         1
  40869  2  2  1  1  1  1  1  2  0  1     2  2  2  0  2  2  0  2  2  0  2
         0
  40930  2  2  0  0  2  0  1  1  1  1     0  1  1  2  0  0  1  0  0  1  1
         2
  40941  2  1  0  0  2  0  2  1  2  2     0  1  1  2  0  0  1  0  0  1  1
         2
  40982  2  1  0  1  1  1  1  1  2  1  …  1  2  0  2  0  1  0  0  0  1  1
         2
  40988  2  2  1  2  0  2  0  2  0  1     1  2  1  2  1  2  0  0  0  1  2
         1
  40989  2  2  1  1  1  1  1  2  1  0     0  1  0  2  0  1  1  0  0  1  2
         2
          ⋮              ⋮              ⋮  ⋱  ⋮                ⋮
          ⋮
  88710  2  0  0  0  2  0  2  1  2  2     2  2  1  2  1  2  0  0  0  0  2
         2
  88711  2  1  0  1  2  0  2  1  1  1     2  2  1  1  1  2  1  1  1  1  1
         1
  88712  2  0  0  0  2  0  2  0  2  2  …  1  2  2  1  1  1  0  1  1  0  1
         1
  88713  2  2  0  1  1  1  1  2  0  0     0  1  1  2  1  1  1  0  0  2  1
         2
  88714  2  1  0  0  2  0  1  1  2  2     1  1  0  2  0  1  2  0  0  1  1
         2
  88715  2  2  0  0  2  0  0  0  2  2     2  2  1  2  1  1  0  0  0  0  2
         2
  88716  2  2  0  1  1  1  0  1  2  1     2  2  1  1  2  1  0  1  1  0  2
         1
  88717  2  2  1  2  0  2  0  1  2  2  …  2  2  1  1  2  2  0  1  1  1  2
         0
  88718  2  1  0  0  2  0  1  1  2  2     0  2  1  2  0  1  1  0  0  0  1
         2
  88719  2  1  1  1  1  1  1  1  2  2     2  2  0  2  1  2  1  0  0  2  1
         1
  88720  2  2  1  2  0  2  0  1  1  1     2  2  1  1  2  1  0  1  1  0  2
         1
  88721  1  1  0  0  2  0  0  0  2  2     2  2  0  2  2  1  0  0  0  1  2
         1
```

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

Out[7]:  9000x150 Array{Int64,2}:
          2  2  0  0  2  0  1  1  1  1  1  0  1  …  2  2  0  2  1  1  2  0  0  1
          2  2
          2  2  0  1  1  1  0  0  2  2  0  2  1     1  2  1  1  1  2  0  2  2  0
          2  0
          1  1  0  1  1  1  1  2  1  1  1  0  1     1  1  1  1  1  1  1  1  1  1
          2  1
          2  2  0  1  2  0  2  2  0  0  2  0  2     0  2  0  2  0  2  0  0  0  0
          2  2
          1  1  0  1  1  1  1  2  1  1  1  0  1     1  1  1  1  1  1  1  1  1  1
          2  1
          2  2  0  0  2  0  1  1  1  0  2  1  1  …  1  2  1  1  1  2  0  0  0  0
          2  2
          2  1  0  1  1  1  1  0  2  2  0  1  0     2  2  1  2  2  2  0  0  0  0
          2  1
          2  2  1  1  1  1  1  2  0  1  1  0  1     2  2  2  0  2  2  0  2  2  0
          2  0
          2  2  0  0  2  0  1  1  1  1  1  1  1     0  1  1  2  0  0  1  0  0  1
          1  2
          2  1  0  0  2  0  2  1  2  2  0  0  0     0  1  1  2  0  0  1  0  0  1
          1  2
          2  1  0  1  1  1  1  1  2  1  1  1  0  …  1  2  0  2  0  1  0  0  0  1
          1  2
          2  2  1  2  0  2  0  2  0  1  1  1  0     1  2  1  2  1  2  0  0  0  1
          2  1
          2  2  1  1  1  1  1  2  1  0  2  0  1     0  1  0  2  0  1  1  0  0  1
          2  2
          ⋮                    ⋮                 ⋮           ⋱        ⋮                    ⋮

          2  0  0  0  2  0  2  1  2  2  0  0  0     2  2  1  2  1  2  0  0  0  0
          2  2
          2  1  0  1  2  0  2  1  1  1  1  0  1     2  2  1  1  1  2  1  1  1  1
          1  1
          2  0  0  0  2  0  2  0  2  2  0  0  0  …  1  2  2  1  1  1  0  1  1  0
          1  1
          2  2  0  1  1  1  1  2  0  0  2  0  1     0  1  1  2  1  1  1  0  0  2
          1  2
          2  1  0  0  2  0  1  1  2  2  0  1  0     1  1  0  2  0  1  2  0  0  1
          1  2
          2  2  0  0  2  0  0  0  2  2  0  0  0     2  2  1  2  1  1  0  0  0  0
          2  2
          2  2  0  1  1  1  0  1  2  1  1  1  1     2  2  1  1  2  1  0  1  1  0
          2  1
          2  2  1  2  0  2  0  1  2  2  1  1  0  …  2  2  1  1  2  2  0  1  1  1
          2  0
          2  1  0  0  2  0  1  1  2  2  0  1  0     0  2  1  2  0  1  1  0  0  0
          1  2
          2  1  1  1  1  1  1  1  2  2  0  0  0     2  2  0  2  1  2  1  0  0  2
          1  1
          2  2  1  2  0  2  0  1  1  1  1  1  0     2  2  1  1  2  1  0  1  1  0
          2  1
          1  1  0  0  2  0  0  0  2  2  0  0  0     2  2  0  2  2  1  0  0  0  1
          2  1
```

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

Out[8]: 9000x150 Array{Float64,2}:
```
  0.0861111    0.707889   -0.224556   …    0.269667    0.392889    0.774333
  0.0861111    0.707889   -0.224556       -0.730333    0.392889   -1.22567
 -0.913889    -0.292111   -0.224556        0.269667    0.392889   -0.225667
  0.0861111    0.707889   -0.224556       -0.730333    0.392889    0.774333
 -0.913889    -0.292111   -0.224556        0.269667    0.392889   -0.225667
  0.0861111    0.707889   -0.224556   …   -0.730333    0.392889    0.774333
  0.0861111   -0.292111   -0.224556       -0.730333    0.392889   -0.225667
  0.0861111    0.707889    0.775444       -0.730333    0.392889   -1.22567
  0.0861111    0.707889   -0.224556        0.269667   -0.607111    0.774333
  0.0861111   -0.292111   -0.224556        0.269667   -0.607111    0.774333
  0.0861111   -0.292111   -0.224556   …    0.269667   -0.607111    0.774333
  0.0861111    0.707889    0.775444        0.269667    0.392889   -0.225667
  0.0861111    0.707889    0.775444        0.269667    0.392889    0.774333
    ⋮                                  ⋱
  0.0861111   -1.29211    -0.224556       -0.730333    0.392889    0.774333
  0.0861111   -0.292111   -0.224556        0.269667   -0.607111   -0.225667
  0.0861111   -1.29211    -0.224556   …   -0.730333   -0.607111   -0.225667
  0.0861111    0.707889   -0.224556        1.26967    -0.607111    0.774333
  0.0861111   -0.292111   -0.224556        0.269667   -0.607111    0.774333
  0.0861111    0.707889   -0.224556       -0.730333    0.392889    0.774333
  0.0861111    0.707889   -0.224556       -0.730333    0.392889   -0.225667
  0.0861111    0.707889    0.775444   …    0.269667    0.392889   -1.22567
  0.0861111   -0.292111   -0.224556       -0.730333   -0.607111    0.774333
  0.0861111   -0.292111    0.775444        1.26967    -0.607111   -0.225667
  0.0861111    0.707889    0.775444       -0.730333    0.392889   -0.225667
 -0.913889    -0.292111   -0.224556        0.269667    0.392889   -0.225667
```

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

Out[9]: 1x150 Array{Float64,2}:
```
 -1.08555e-18  -3.09481e-16  -6.47383e-17  …  -3.94746e-17  -1.29477e-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 (
```

```
  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
```

```
 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",calculateInbreedi
         nothing
         df      = read_genotypes("MarNFCenter.txt",numSSBayes)  # genotype file - cen
         M_Mats = make_MMats(df,A_Mats,ped);                      # M file centered alr
         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
         nothing
```

```
In [39]: vRes   = 0.594
         vG     = 0.594
         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
3854.785322 seconds (23.05 G allocations: 724.038 GB, 7.19% gc time)
```

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

```
Out[40]: 1-element Array{Float64,1}:
          2.83092
```

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

```
Out[41]: 150-element Array{Float64,1}:
           0.14579
          -0.103479
           0.00766101
           0.0173134
           0.0102773
          -0.0192771
           0.0239512
          -0.0419942
          -0.0885634
          -0.0100519
          -0.0574127
          -0.0647198
          -0.0466234
           ⋮
           0.108541
           0.130917
           0.048822
          -0.0219776
          -0.0167258
           0.0461088
           0.000785081
          -0.0974686
          -0.0347406
          -0.0176702
          -0.0149486
          -0.0146495
```

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

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

```
Out[43]: 45952-element Array{Float64,1}:
         -1.20248
         -1.05199
         -0.471857
         -0.679482
         -0.369207
         -0.693876
         -0.740306
         -0.60695
         -1.03117
         -1.16502
         -0.234264
          0.0739742
         -0.809451
          ⋮
          0.631489
          0.343196
          0.147644
          0.2372
          0.266294
         -0.569384
         -0.945555
          0.0494626
         -0.371777
          0.347841
         -0.472566
         -0.972237
```

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

```
In [45]: df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',hea
         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
         @printf("SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV = %6.3f\n",
         JCAll = cor1

         SSBRJC from Gibbs - all.ID : correlation =   0.823
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =   1.438
```

```
Out[46]: 0.8226193618909772
```

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

Out[47]: -0.40063574434538546

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

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.600
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.168
```

Out[48]: 0.6001434726340046

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

Out[49]: 4.234986986438748e-8

```
In [50]: IDs = readtable("noGenotype.ID", eltypes =[UTF8String], separator = ' ',heade
         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
         JCAll = cor3
```

```
         SSBRJC from Gibbs - noGenotype.ID : correlation =  0.847
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.293
```

Out[50]: 0.8471079101855561

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

Out[51]: -0.4930901566596752

```
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", re
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G0.ID : correlation =  0.662
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.816
```

Out[52]: 0.6620087726829252

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

Out[53]: -1.0870904156977559

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

```
SSBRJC from Gibbs - G1.ID : correlation =   0.755
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =   1.070
```

Out[54]: 0.7545750526900606

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

Out[55]: -0.8783487729578742

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

```
SSBRJC from Gibbs - G2.ID : correlation =   0.729
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =   1.079
```

Out[56]: 0.7285072145066849

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

Out[57]: -0.5045415081474772

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

```
SSBRJC from Gibbs - G3.ID : correlation =   0.730
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =   1.133
```

Out[58]: 0.7299442095544401

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

```
Out[59]: -0.11482512489683265
```

```
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", re
         JCAll = cor7
```

```
         SSBRJC from Gibbs - G4.ID : correlation =  0.689
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.164
```

```
Out[60]: 0.6893645095206947
```

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

```
Out[61]: 0.16659036861103343
```

```
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", re
         JCAll = cor8
```

```
         SSBRJC from Gibbs - G5.ID : correlation =  0.573
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.061
```

```
Out[62]: 0.5727726649827654
```

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

```
Out[63]: 0.014400987016593288
```

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

```
Out[64]: 0.8927497599744675
```

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

```
Out[65]: 5-element Array{Float64,1}:
          -0.878349
          -0.504542
          -0.114825
           0.16659
           0.014401
```

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

Out[66]: 2-element Array{Float64,1}:
          3.94232
          1.0613

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

Out[67]: 0.15032990607550595

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

Out[68]: 0.5161265434921708

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

Out[69]: 0.1595449542870027

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

Out[70]: 1.0612988356878792

In [71]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCAll = cor9
```

        SSBRJC from Gibbs - G0.Genotype.ID : correlation =   0.702
        SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =   1.070

Out[71]: 0.7015008089725682

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

Out[72]: -0.48149425068647483

In [73]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCAll = cor9
```

        SSBRJC from Gibbs - G1.Genotype.ID : correlation =   0.649
        SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =   0.981

Out[73]: 0.6493877459981111

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

Out[74]: -0.273242792794381

In [75]:
```
IDs = readtable("G2.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCAll = cor10
```

```
SSBRJC from Gibbs - G2.Genotype.ID : correlation =   0.637
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.067
```

Out[75]: 0.637167058659616

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

Out[76]: -0.03581612687238648

In [77]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCAll = cor11
```

```
SSBRJC from Gibbs - G3.Genotype.ID : correlation =   0.503
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   0.961
```

Out[77]: 0.5029828493549052

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

Out[78]: 0.10421660878279126

In [79]:
```
IDs = readtable("G4.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
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
JCAll = cor12
```

```
SSBRJC from Gibbs - G4.Genotype.ID : correlation =   0.502
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.793
```

Out[79]: 0.5018541902868825

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

Out[80]: 0.11029898665086327

```
In [81]: IDs = readtable("G5.Genotype.ID", eltypes =[UTF8String], separator = ' ',head
         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
         JCAll = cor13
```

```
         SSBRJC from Gibbs - G5.Genotype.ID : correlation =   0.573
         SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   1.061
```

Out[81]: 0.5727726649827654

```
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]: 0.014400987016593288

```
In [85]: IDs = readtable("G0.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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 = %
         JCAll = cor14
```

```
         SSBRJC from Gibbs - G0.noGenotype.ID : correlation =   0.651
         SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.791
```

Out[85]: 0.651138613006726

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

Out[86]: -1.102618522492917

```
In [87]: IDs = readtable("G1.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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 = 9
         JCAll = cor14
```

```
         SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.746
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.043
```

Out[87]: 0.7463029639871404

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

Out[88]: -0.8938643109107842

```
In [89]: IDs = readtable("G2.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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 = 9
         JCAll = cor15
```

```
         SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.723
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.049
```

Out[89]: 0.7228411956345145

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

Out[90]: -0.5165601076673514

```
In [91]: IDs = readtable("G3.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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 = 9
         JCAll = cor16
```

```
         SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.740
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.113
```

Out[91]: 0.7396798724979243

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

Out[92]: -0.12044157960656658

```
In [93]: IDs = readtable("G4.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
         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", cor1
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =
         JCAll = cor17
```

```
         SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.714
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.178
```

Out[93]: 0.7142885424361788

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

Out[94]: 0.16803373737924288

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

Out[95]: SSBR.NumSSBayes(54952,45952,9000,40000,39000,1000,150)