In [1]:
```julia
include("/home/nicole/Jupyter/SSBRnoJ/src/SSBR.jl")
using SSBR
```

In [2]:
```julia
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]:
```julia
; cd Data/0.5a0/M/8
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/8

In [4]:
```julia
;ls
```

MarNF.txt
PedAll.txt
Phe.txt
PheAll.txt

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

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

```
Out[6]: 9000x151 Array{Int64,2}:
 40755  0  2  1  1  1  1  1  1  1  1  …  1  1  1  0  2  1  1  1  1  1  2
        1
 40757  0  2  2  0  0  2  0  1  1  1     2  2  2  2  0  2  2  0  1  1  2
        1
 40762  0  2  1  0  0  2  0  2  1  1     2  1  2  2  1  1  1  1  1  1  2
        1
 40765  0  2  2  1  1  1  1  1  1  1     1  1  2  1  1  2  2  0  1  1  2
        0
 40902  0  2  2  0  0  2  0  2  2  0     2  2  2  2  0  2  2  0  2  0  2
        0
 40924  0  2  2  0  1  2  0  2  2  0  …  2  1  2  2  1  1  1  1  1  1  2
        1
 40935  1  2  2  0  2  0  2  0  0  2     1  1  2  1  1  2  2  0  1  0  2
        1
 40945  1  2  2  0  0  2  0  2  1  0     1  1  1  1  1  1  1  1  1  1  2
        1
 40991  0  2  2  0  0  2  0  0  0  2     0  1  2  0  2  1  2  0  0  1  2
        1
 41002  0  2  2  1  1  1  1  1  2  0     2  2  2  2  0  2  2  0  2  0  2
        0
 41005  0  2  1  1  2  1  1  1  1  0  …  2  1  2  1  1  2  1  0  1  0  2
        1
 41018  0  2  2  0  0  2  0  0  0  2     1  1  1  1  1  1  1  1  1  1  2
        1
 41019  0  1  1  0  1  1  1  1  2  0     2  2  2  2  0  2  2  0  2  0  2
        0
      ⋮              ⋮              ⋮  ⋱     ⋮                 ⋮
      ⋮
 88710  0  2  2  0  1  1  1  0  0  2     2  2  2  2  0  2  2  0  2  0  2
        0
 88711  0  2  2  0  2  0  2  0  1  1     2  2  2  2  0  2  2  0  2  0  2
        0
 88712  0  2  2  0  2  1  1  1  2  1  …  2  2  2  2  0  2  2  0  2  0  2
        0
 88713  0  2  2  1  2  0  2  0  1  2     1  2  2  0  1  2  2  0  1  1  2
        0
 88714  1  2  2  1  2  0  2  0  1  1     2  2  2  1  0  2  2  0  2  0  2
        0
 88715  0  2  1  1  2  0  2  0  0  1     2  2  2  2  0  2  2  0  2  0  2
        0
 88716  0  2  2  0  2  2  0  2  2  0     1  1  2  1  1  1  2  0  1  0  2
        1
 88717  0  2  2  0  2  0  2  0  2  1  …  2  2  2  2  1  2  2  0  1  0  2
        1
 88718  1  2  2  0  1  2  0  2  1  0     2  2  1  1  1  2  2  1  1  0  1
        0
 88719  0  2  2  0  2  0  2  0  0  2     2  2  2  2  0  2  2  0  2  0  2
        0
 88720  0  2  1  0  1  1  1  1  1  2     2  2  2  2  0  2  2  0  2  0  2
        0
 88721  1  2  2  1  2  0  2  0  1  2     2  2  2  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  1  1  1  1  1  1  1  1  2  0  0  …  1  1  1  0  2  1  1  1  1  1
         2  1
         0  2  2  0  0  2  0  1  1  1  1  1  1     2  2  2  2  0  2  2  0  1  1
         2  1
         0  2  1  0  0  2  0  2  1  1  1  1  0     2  1  2  2  1  1  1  1  1  1
         2  1
         0  2  2  1  1  1  1  1  1  1  1  1  2     1  1  2  1  1  2  2  0  1  1
         2  0
         0  2  2  0  0  2  0  2  2  0  0  0  2     2  2  2  2  0  2  2  0  2  0
         2  0
         0  2  2  0  1  2  0  2  2  0  0  0  2  …  2  1  2  2  1  1  1  1  1  1
         2  1
         1  2  2  0  2  0  2  0  0  2  2  2  1     1  1  2  1  1  2  2  0  1  0
         2  1
         1  2  2  0  0  2  0  2  1  0  0  0  1     1  1  1  1  1  1  1  1  1  1
         2  1
         0  2  2  0  0  2  0  0  0  2  2  1  0     0  1  2  0  2  1  2  0  0  1
         2  1
         0  2  2  1  1  1  1  1  2  0  1  0  1     2  2  2  2  0  2  2  0  2  0
         2  0
         0  2  1  1  2  1  1  1  1  0  0  0  1  …  2  1  2  1  1  2  1  0  1  0
         2  1
         0  2  2  0  0  2  0  0  0  2  2  1  0     1  1  1  1  1  1  1  1  1  1
         2  1
         0  1  1  0  1  1  1  1  2  0  1  1  1     2  2  2  2  0  2  2  0  2  0
         2  0
         ⋮                    ⋮                ⋱              ⋮                       ⋮
         0  2  2  0  1  1  1  0  0  2  1  2  0     2  2  2  2  0  2  2  0  2  0
         2  0
         0  2  2  0  2  0  2  0  1  1  1  0  1     2  2  2  2  0  2  2  0  2  0
         2  0
         0  2  2  0  2  1  1  1  2  1  0  1  1  …  2  2  2  2  0  2  2  0  2  0
         2  0
         0  2  2  1  2  0  2  0  1  2  0  1  0     1  2  2  0  1  2  2  0  1  1
         2  0
         1  2  2  1  2  0  2  0  1  1  0  1  0     2  2  2  1  0  2  2  0  2  0
         2  0
         0  2  1  1  2  0  2  0  0  1  0  1  0     2  2  2  2  0  2  2  0  2  0
         2  0
         0  2  2  0  2  2  0  2  2  0  0  0  2     1  1  2  1  1  1  2  0  1  0
         2  1
         0  2  2  0  2  0  2  0  2  1  0  2  0  …  2  2  2  2  1  2  2  0  1  0
         2  1
         1  2  2  0  1  2  0  2  1  0  0  0  1     2  2  1  1  1  2  2  1  1  0
         1  0
         0  2  2  0  2  0  2  0  0  2  0  2  0     2  2  2  2  0  2  2  0  2  0
         2  0
         0  2  1  0  1  1  1  1  1  2  1  1  0     2  2  2  2  0  2  2  0  2  0
         2  0
         1  2  2  1  2  0  2  0  1  2  1  1  0     2  2  2  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}:
        -0.292222   0.109333  -0.773333   0.588222  …   0.640222   0.119    0.575
        556
        -0.292222   0.109333   0.226667  -0.411778      0.640222   0.119    0.575
        556
        -0.292222   0.109333  -0.773333  -0.411778      0.640222   0.119    0.575
        556
        -0.292222   0.109333   0.226667   0.588222      0.640222   0.119   -0.424
        444
        -0.292222   0.109333   0.226667  -0.411778     -0.359778   0.119   -0.424
        444
        -0.292222   0.109333   0.226667  -0.411778  …   0.640222   0.119    0.575
        556
         0.707778   0.109333   0.226667  -0.411778     -0.359778   0.119    0.575
        556
         0.707778   0.109333   0.226667  -0.411778      0.640222   0.119    0.575
        556
        -0.292222   0.109333   0.226667  -0.411778      0.640222   0.119    0.575
        556
        -0.292222   0.109333   0.226667   0.588222     -0.359778   0.119   -0.424
        444
        -0.292222   0.109333  -0.773333   0.588222  …  -0.359778   0.119    0.575
        556
        -0.292222   0.109333   0.226667  -0.411778      0.640222   0.119    0.575
        556
        -0.292222  -0.890667  -0.773333  -0.411778     -0.359778   0.119   -0.424
        444
            ⋮                                      ⋱

        -0.292222   0.109333   0.226667  -0.411778     -0.359778   0.119   -0.424
        444
        -0.292222   0.109333   0.226667  -0.411778     -0.359778   0.119   -0.424
        444
        -0.292222   0.109333   0.226667  -0.411778  …  -0.359778   0.119   -0.424
        444
        -0.292222   0.109333   0.226667   0.588222      0.640222   0.119   -0.424
        444
         0.707778   0.109333   0.226667   0.588222     -0.359778   0.119   -0.424
        444
        -0.292222   0.109333  -0.773333   0.588222     -0.359778   0.119   -0.424
        444
        -0.292222   0.109333   0.226667  -0.411778     -0.359778   0.119    0.575
        556
        -0.292222   0.109333   0.226667  -0.411778  …  -0.359778   0.119    0.575
        556
         0.707778   0.109333   0.226667  -0.411778     -0.359778  -0.881   -0.424
        444
        -0.292222   0.109333   0.226667  -0.411778     -0.359778   0.119   -0.424
        444
        -0.292222   0.109333  -0.773333  -0.411778     -0.359778   0.119   -0.424
        444
         0.707778   0.109333   0.226667   0.588222     -0.359778   0.119   -0.424
        444
```

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

```
Out[9]: 1x150 Array{Float64,2}:
        7.10543e-18  -1.42109e-17  -9.4739e-17  …  -9.43443e-17  3.63166e-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 G
```
```
  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   = 0.741
vG     = 0.741
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
2424.906474 seconds (23.03 G allocations: 723.625 GB, 7.61% gc time)
```

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

Out[40]:
```
1-element Array{Float64,1}:
 4.44476
```

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

Out[41]:
```
150-element Array{Float64,1}:
   0.0173199
  -0.0589574
  -0.0379911
   0.131532
   0.129797
  -0.0517794
   0.0515505
   0.0565082
   0.0703079
   0.0532508
   0.00932283
   0.0997719
   0.166304
   ⋮
  -0.0715782
   0.0154376
   0.0843185
   0.0272765
   0.0540832
   0.0776098
   0.0558417
   0.108856
   0.00859784
  -0.00973744
   0.025147
  -0.118309
```

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

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

```
Out[43]: 45922-element Array{Float64,1}:
            0.146655
           -1.10948
            0.136854
            0.115198
           -0.942523
           -0.415231
           -0.954261
            0.27848
           -0.0418059
           -0.262689
           -1.52537
            0.0836332
            0.00592196
            ⋮
            0.275469
           -0.00169451
           -0.467988
           -0.824285
           -0.346424
           -0.504082
           -1.33455
            0.171699
           -0.154436
            0.262784
            0.300095
           -0.559764
```

```
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 =  0.836
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.397
```

```
Out[46]: 0.8357093836311597
```

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

Out[47]: -0.41762818690862735

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

```
         SSBRJC from Gibbs - genotype.ID : correlation =  0.696
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.227
```

Out[48]: 0.6958529061888855

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

Out[49]: 1.8639738170773195e-7

```
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 =  0.849
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.271
```

Out[50]: 0.8485055752903037

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

Out[51]: -0.5140039653638602

```
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 e₁
         @printf("SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor4
```

```
         SSBRJC from Gibbs - G0.ID : correlation =  0.688
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.900
```

Out[52]: 0.6882460961295744

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

Out[53]: -1.1479693232668597

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

```
          SSBRJC from Gibbs - G1.ID : correlation =  0.753
          SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.051
```

Out[54]: 0.7530364730074725

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

Out[55]: -0.920576896525742

```
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", re
          JCAll = cor5
```

```
          SSBRJC from Gibbs - G2.ID : correlation =  0.754
          SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.107
```

Out[56]: 0.7544038883326388

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

Out[57]: -0.5099443740530993

```
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", re
          JCAll = cor6
```

```
          SSBRJC from Gibbs - G3.ID : correlation =  0.722
          SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.067
```

Out[58]: 0.7217266709832914

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

Out[59]: -0.10772897054557108

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 =   0.690
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.069
```

Out[60]: 0.6901790057574884

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

Out[61]: 0.16517567532930835

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 =   0.674
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.144
```

Out[62]: 0.6738256640254439

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

Out[63]: 0.015274767610199542

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

Out[64]: 0.9358516641359416

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

Out[65]:
```
5-element Array{Float64,1}:
 -0.920577
 -0.509944
 -0.107729
  0.165176
  0.0152748
```

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

```
Out[66]: 2-element Array{Float64,1}:
          5.46537
          1.14364
```

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

```
Out[67]: 0.1717475697682244
```

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

```
Out[68]: 0.49473813778245723
```

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

```
Out[69]: 0.19641766470232952
```

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

```
Out[70]: 1.1436415954379893
```

```
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 =  0.763
         SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.234
```

```
Out[71]: 0.7631639369860604
```

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

```
Out[72]: -0.5761730459093127
```

```
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 =  0.781
         SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.252
```

```
Out[73]: 0.7810236667116829
```

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

Out[74]: -0.2702126446223156

```
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 =  0.691
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.057
```

Out[75]: 0.6913137477416891

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

Out[76]: -0.0334800122187983

```
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 =  0.618
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.949
```

Out[77]: 0.617670862410895

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

Out[78]: 0.14550343772317223

```
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 =  0.652
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.034
```

Out[79]: 0.6523574236213361

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

Out[80]: 0.1233799485014499

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 =  0.674
SSBRJC from Gibbs – G5.Genotype.ID : regression of TBV on GEBV =  1.144
```

Out[81]: 0.6738256640254439

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]: 0.015274767610199542

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 =  0.680
SSBRJC from Gibbs – G0.noGenotype.ID : regression of TBV on GEBV =  0.874
```

Out[85]: 0.6798970081272689

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

Out[86]: −1.1626307662760273

```
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 =  0.743
SSBRJC from Gibbs – G1.noGenotype.ID : regression of TBV on GEBV =  1.023
```

Out[87]: 0.7428312096328469

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

Out[88]: -0.9372529029848043

```
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 =  0.750
SSBRJC from Gibbs – G2.noGenotype.ID : regression of TBV on GEBV =  1.084
```

Out[89]: 0.7501115048052822

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

Out[90]: -0.5221614089719275

```
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 =  0.725
SSBRJC from Gibbs – G3.noGenotype.ID : regression of TBV on GEBV =  1.050
```

Out[91]: 0.7247705884469544

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

Out[92]: -0.1142221092191286

```
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 =  0.708
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.075
```

Out[93]: 0.7082497680392534

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

Out[94]: 0.1662473606325868

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

Out[95]: SSBR.NumSSBayes(54922,45922,9000,40000,39000,1000,150)