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/10
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/10

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

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

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

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

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

40742	0	1	1	2	2	2	2	1	1	1	…	2	1	1	1	1	1	1	1	1	1	1
40793	0	1	1	2	2	0	0	0	1	1		2	0	2	2	1	2	1	2	0	0	2
																						1
40797	0	2	0	2	2	0	0	0	0	0		2	1	2	1	0	2	2	1	1	0	1
																						2
40799	0	2	0	2	2	2	2	2	0	2		2	2	0	0	0	2	0	0	1	0	2
																						2
40818	0	1	2	1	0	1	1	1	1	1		2	2	1	0	2	1	2	2	0	1	1
																						1
40835	0	1	1	2	2	1	1	1	1	1	…	2	2	0	0	1	2	0	1	2	0	2
																						2
40853	0	2	0	2	2	1	1	0	2	2		2	0	2	2	2	0	2	2	0	2	0
																						0
40858	0	1	1	2	2	2	2	1	1	1		2	0	2	2	2	0	2	2	0	2	0
																						0
40862	0	1	1	2	2	1	1	1	0	0		2	1	1	1	1	1	1	1	1	1	1
																						1
40863	0	2	1	2	1	0	0	0	1	0		2	1	1	1	1	1	2	2	0	2	0
																						0
40869	0	2	0	2	2	1	1	1	0	1	…	2	1	1	1	1	1	1	2	0	1	0
																						1
40889	0	2	1	2	1	1	1	1	1	0		2	0	2	2	2	0	2	2	0	2	0
																						0
40918	0	2	0	2	2	0	0	0	1	1		2	2	0	0	0	2	1	2	0	1	0
																						1
⋮			⋮				⋮	⋱		⋮					⋮						
⋮																						
88710	0	1	1	2	2	2	2	2	0	2		2	2	0	0	0	2	0	0	2	0	2
																						2
88711	1	2	0	2	2	2	2	2	0	1		2	1	2	1	1	1	2	2	0	1	0
																						1
88712	1	2	0	2	1	2	2	2	0	1	…	2	2	1	0	0	2	1	1	1	0	1
																						2
88713	0	2	0	2	2	1	1	1	0	1		2	2	0	0	0	2	0	2	0	0	0
																						2
88714	0	2	1	2	1	0	0	0	2	1		1	1	2	1	1	1	1	2	1	1	1
																						1
88715	1	2	0	2	2	0	0	0	2	1		2	1	1	1	1	1	1	1	1	1	1
																						1
88716	0	1	1	2	2	1	1	1	0	1		2	1	2	0	0	2	1	1	0	0	0
																						2
88717	0	1	1	2	2	1	1	1	1	2	…	2	2	1	0	0	2	0	0	1	0	1
																						2
88718	0	1	2	1	0	1	1	1	1	1		2	1	1	1	2	2	1	1	0	0	1
																						2
88719	0	1	1	2	2	1	1	1	1	2		1	1	1	1	1	2	2	2	0	0	2
																						2
88720	1	2	0	2	2	1	1	1	0	0		2	1	1	1	1	1	1	1	1	1	1
																						1
88721	1	2	0	2	2	2	2	2	0	1		2	0	2	2	2	0	2	2	0	2	0
																						0

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

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

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

Out[8]: 9000x150 Array{Float64,2}:
```
        -0.266444   -0.466778    0.322333   …   -0.173333    0.436333    0.221111
        -0.266444   -0.466778    0.322333       -1.17333     1.43633     0.221111
        -0.266444    0.533222   -0.677667       -1.17333     0.436333    1.22111
        -0.266444    0.533222   -0.677667       -1.17333     1.43633     1.22111
        -0.266444   -0.466778    1.32233        -0.173333    0.436333    0.221111
        -0.266444   -0.466778    0.322333   …   -1.17333     1.43633     1.22111
        -0.266444    0.533222   -0.677667        0.826667   -0.563667   -0.778889
        -0.266444   -0.466778    0.322333        0.826667   -0.563667   -0.778889
        -0.266444   -0.466778    0.322333       -0.173333    0.436333    0.221111
        -0.266444    0.533222    0.322333        0.826667   -0.563667   -0.778889
        -0.266444    0.533222   -0.677667   …   -0.173333   -0.563667    0.221111
        -0.266444    0.533222    0.322333        0.826667   -0.563667   -0.778889
        -0.266444    0.533222   -0.677667       -0.173333   -0.563667    0.221111
            ⋮                               ⋱
        -0.266444   -0.466778    0.322333       -1.17333     1.43633     1.22111
         0.733556    0.533222   -0.677667       -0.173333   -0.563667    0.221111
         0.733556    0.533222   -0.677667   …   -1.17333     0.436333    1.22111
        -0.266444    0.533222   -0.677667       -1.17333    -0.563667    1.22111
        -0.266444    0.533222    0.322333       -0.173333    0.436333    0.221111
         0.733556    0.533222   -0.677667       -0.173333    0.436333    0.221111
        -0.266444   -0.466778    0.322333       -1.17333    -0.563667    1.22111
        -0.266444   -0.466778    0.322333   …   -1.17333     0.436333    1.22111
        -0.266444   -0.466778    1.32233        -1.17333     0.436333    1.22111
        -0.266444   -0.466778    0.322333       -1.17333     1.43633     1.22111
         0.733556    0.533222   -0.677667       -0.173333    0.436333    0.221111
         0.733556    0.533222   -0.677667        0.826667   -0.563667   -0.778889
```

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

Out[9]: 1x150 Array{Float64,2}:
```
        -9.4739e-17  -1.92636e-16  -1.76846e-16  …   9.23706e-17  -2.30532e-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   = 0.460
vG     = 0.460
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
3800.019189 seconds (23.04 G allocations: 723.722 GB, 7.49% gc time)
```

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

Out[40]:
```
1-element Array{Float64,1}:
 5.11705
```

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

```
Out[41]: 150-element Array{Float64,1}:
          -0.0601215
          -0.0202526
          -0.0304279
          -0.000411634
          -0.016853
           0.0239313
          -0.0828569
           0.156136
          -0.0625942
           0.0144532
           0.00276264
           0.0541214
           0.0468329
           ⋮
           0.0246016
          -0.032588
          -0.000340231
           0.0281514
          -0.0739896
           0.0494646
           7.14954e-5
          -0.0433988
          -0.0375707
           0.0860813
           0.034631
          -0.0604875
```

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

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

```
Out[43]:  45929-element Array{Float64,1}:
          -0.756671
           0.048752
          -0.535889
          -0.39637
          -0.254018
          -0.461939
          -0.451418
          -0.0932553
           0.0369997
          -0.152044
           0.283874
          -0.70273
          -0.039658
           ⋮
           0.649346
          -0.0328822
          -0.884975
          -0.14448
           0.402631
           0.223321
          -0.0998913
          -0.249181
           0.138136
          -0.258076
          -0.143812
          -1.65089
```

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

```
In [45]:  df = readtable("sim.bv", eltypes =[UTF8String, Float64], separator = ' ',head
          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 =  0.819
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.342
```

```
Out[46]:  0.8191736232023726
```

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

Out[47]: -0.34556212166646516

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 =  0.734
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.316
```

Out[48]: 0.7339805044026398

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

Out[49]: 1.1336388913542174e-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 =  0.821
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.201
```

Out[50]: 0.8209142339796034

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

Out[51]: -0.425307252827316

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 =  0.606
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.712
```

Out[52]: 0.6055791794524144

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

Out[53]: -0.8844153496684213

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 =  0.751
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.038
```

Out[54]: 0.7514175735970838

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

Out[55]: -0.7473352879204078

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 =  0.732
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.052
```

Out[56]: 0.7323410446283849

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

Out[57]: -0.4225463405566688

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 =  0.724
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.070
```

Out[58]: 0.7244840884935376

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

Out[59]: -0.12857029263475103

```
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 =  0.697
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.083
```

Out[60]: 0.6965984396141175

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

Out[61]: 0.09501596558401422

```
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 =  0.712
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.233
```

Out[62]: 0.7119990434446413

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

Out[63]: 0.014478575197444193

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

Out[64]: 0.761813863117852

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

Out[65]: 5-element Array{Float64,1}:
         -0.747335
         -0.422546
         -0.12857
          0.095016
          0.0144786

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

Out[66]: 2-element Array{Float64,1}:
   5.89412
   1.2327

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

Out[67]: 0.10232944565862227

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

Out[68]: 0.30673105008526064

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

Out[69]: 0.1261416744309389

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

Out[70]: 1.2327016297122901

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 = 0.781
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.208

Out[71]: 0.7807264783497618

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

Out[72]: -0.5064033933470002

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 = 0.751
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.163

Out[73]: 0.7510507943524102

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

Out[74]: -0.2062081030437616

```
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 =   0.740
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.263
```

Out[75]: 0.7399362630035752

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

Out[76]: -0.0736865043111088

```
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 =   0.651
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   1.016
```

Out[77]: 0.650562976093362

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

Out[78]: 0.08242333246680708

```
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 =   0.665
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.988
```

Out[79]: 0.6648038503707683

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

Out[80]: 0.12473676171230724

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 =   0.712
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   1.233
```

Out[81]: 0.7119990434446413

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]: 0.014478575197444193

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 =   0.598
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.692
```

Out[85]: 0.59777387413747

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

Out[86]: −0.8941079639330731

```
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 = '
         JCAll = cor14
```

```
         SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.741
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  1.010
```

Out[87]: 0.7409997267213001

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

Out[88]: -0.7612103439428859

```
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 = '
         JCAll = cor15
```

```
         SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.727
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.027
```

Out[89]: 0.7271553956276127

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

Out[90]: -0.4314914645629653

```
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 = '
         JCAll = cor16
```

```
         SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.727
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.051
```

Out[91]: 0.7270222883100277

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

Out[92]: -0.13398038558607303

```
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 =  0.711
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.080
```

Out[93]: 0.711024067614789

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

Out[94]: 0.09425389388841696

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

Out[95]: SSBR.NumSSBayes(54929,45929,9000,40000,39000,1000,150)