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/6
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/6

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}:

40724	0	2	1	2	1	0	2	0	0	1	…	2	0	2	2	2	2	0	2	2	2	0
																						2
40728	0	2	0	2	2	0	2	0	0	2		2	0	2	2	2	2	0	2	2	2	0
																						2
40756	0	2	0	2	2	2	1	1	1	1		1	2	0	1	0	1	2	2	2	1	1
																						2
40798	0	1	1	1	1	1	1	1	1	0		2	1	1	1	0	1	2	0	2	0	0
																						1
40800	0	2	0	2	2	1	2	0	0	1		2	1	1	2	1	0	2	0	2	0	0
																						2
40833	0	1	1	2	2	0	2	0	0	2	…	2	2	0	2	1	2	2	1	2	0	1
																						2
40849	0	2	1	2	1	0	2	0	0	1		2	1	1	1	1	2	1	1	1	1	1
																						2
40876	1	1	1	2	2	2	0	2	2	0		2	1	1	2	1	1	1	1	2	1	0
																						2
40877	0	2	0	2	2	0	2	0	0	1		1	2	0	2	0	1	2	0	2	0	0
																						1
40903	0	2	0	2	2	0	2	0	0	1		2	1	1	2	1	0	2	1	2	0	0
																						2
40910	0	2	1	2	1	0	2	0	0	2	…	2	0	2	2	2	2	0	2	2	1	1
																						2
40935	0	2	1	2	1	0	2	0	0	2		2	0	2	2	2	2	0	2	2	2	0
																						2
40945	0	2	1	2	2	1	2	0	0	1		2	0	2	2	2	2	0	2	2	2	0
																						2
⋮			⋮					⋮			⋱	⋮						⋮				
⋮																						
88710	0	1	1	2	2	2	0	2	2	0		2	2	0	1	0	1	2	0	1	0	1
																						2
88711	1	2	0	2	2	2	0	2	2	0		2	1	1	2	2	1	1	1	1	1	1
																						2
88712	0	2	0	2	2	1	2	0	0	2	…	2	0	2	2	2	2	0	2	2	2	0
																						2
88713	0	1	1	2	2	1	1	1	1	1		2	1	1	2	1	1	1	1	2	1	0
																						2
88714	0	2	0	2	2	1	1	1	1	1		2	0	2	2	1	1	1	1	2	1	0
																						2
88715	0	2	0	2	2	1	2	0	0	2		2	0	1	2	2	1	1	2	2	1	1
																						2
88716	0	1	1	2	2	1	1	1	1	1		2	1	1	1	1	2	1	1	1	1	1
																						2
88717	0	2	0	2	2	2	1	1	0	1	…	2	0	2	2	2	2	0	2	2	2	0
																						2
88718	0	1	1	2	2	1	1	1	1	1		2	1	1	2	1	1	1	1	2	1	0
																						2
88719	0	1	1	2	2	1	1	1	1	1		1	2	0	2	0	0	2	0	1	0	1
																						2
88720	0	2	0	2	2	2	2	0	0	2		2	1	1	2	0	2	2	1	0	0	1
																						2
88721	0	2	0	2	2	1	1	1	1	1		0	2	0	2	2	2	0	2	2	2	0
																						2

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

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

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

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

Out[8]: 9000x150 Array{Float64,2}:
```
 -0.130111   0.271667   0.634444  …   1.09744   -0.501333   0.160333
 -0.130111   0.271667  -0.365556      1.09744   -0.501333   0.160333
 -0.130111   0.271667  -0.365556      0.0974444  0.498667   0.160333
 -0.130111  -0.728333   0.634444     -0.902556  -0.501333  -0.839667
 -0.130111   0.271667  -0.365556     -0.902556  -0.501333   0.160333
 -0.130111  -0.728333   0.634444  …  -0.902556   0.498667   0.160333
 -0.130111   0.271667   0.634444      0.0974444  0.498667   0.160333
  0.869889  -0.728333   0.634444      0.0974444 -0.501333   0.160333
 -0.130111   0.271667  -0.365556     -0.902556  -0.501333  -0.839667
 -0.130111   0.271667  -0.365556     -0.902556  -0.501333   0.160333
 -0.130111   0.271667   0.634444  …   0.0974444  0.498667   0.160333
 -0.130111   0.271667   0.634444      1.09744   -0.501333   0.160333
 -0.130111   0.271667   0.634444      1.09744   -0.501333   0.160333
      ⋮                           ⋱
 -0.130111  -0.728333   0.634444     -0.902556   0.498667   0.160333
  0.869889   0.271667  -0.365556      0.0974444  0.498667   0.160333
 -0.130111   0.271667  -0.365556  …   1.09744   -0.501333   0.160333
 -0.130111  -0.728333   0.634444      0.0974444 -0.501333   0.160333
 -0.130111   0.271667  -0.365556      0.0974444 -0.501333   0.160333
 -0.130111   0.271667  -0.365556      0.0974444  0.498667   0.160333
 -0.130111  -0.728333   0.634444      0.0974444  0.498667   0.160333
 -0.130111   0.271667  -0.365556  …   1.09744   -0.501333   0.160333
 -0.130111  -0.728333   0.634444      0.0974444 -0.501333   0.160333
 -0.130111  -0.728333   0.634444     -0.902556   0.498667   0.160333
 -0.130111   0.271667  -0.365556     -0.902556   0.498667   0.160333
 -0.130111   0.271667  -0.365556      1.09744   -0.501333   0.160333
```

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

Out[9]: 1x150 Array{Float64,2}:
```
 6.11856e-18  -1.65793e-16  -1.0145e-16  …  2.05268e-17  -2.03689e-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   = 0.262
         vG     = 0.262
         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
        2489.675214 seconds (23.03 G allocations: 723.542 GB, 7.69% gc time)
```

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

```
Out[40]: 1-element Array{Float64,1}:
          4.16143
```

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

```
Out[41]: 150-element Array{Float64,1}:
          0.000112248
          0.127687
          0.0275196
          0.0374555
          0.0665124
          0.0641451
         -0.0456191
          0.0433641
          0.0368868
          0.121547
          0.0851696
         -0.00274885
          0.0584972
          ⋮
          0.00906005
         -0.0378114
         -0.00198723
         -0.00905558
          0.0212053
          0.00947073
          0.0130423
          0.00869591
         -0.0070874
         -0.0249025
          0.00561366
         -0.0176613
```

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

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

```
Out[43]: 45916-element Array{Float64,1}:
          -0.22278
          -0.385849
          -0.372362
           0.0964758
          -0.577713
          -1.00772
          -0.525169
          -0.245436
           0.240457
          -0.120104
           0.25539
          -0.112773
           0.064614
           ⋮
          -0.132089
          -0.558593
          -0.211741
           0.114835
          -0.38545
          -0.252575
           0.0302602
           0.054793
           0.00655223
           0.0959277
           0.00281122
           0.154849
```

```
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 =  0.772
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.208
```

```
Out[46]: 0.7719735574569541
```

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

Out[47]: -0.24050853359021948

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 =  0.591
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.067
```

Out[48]: 0.5908470978540938

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

Out[49]: 2.409570276742872e-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 =  0.780
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.083
```

Out[50]: 0.7800996195257942

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

Out[51]: -0.2960105584857381

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

```
SSBRJC from Gibbs - G0.ID : correlation =  0.521
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.522
```

Out[52]: 0.5209511308604855

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

Out[53]: -0.6227565049937344

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 =   0.731
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.993
```

Out[54]: 0.7305375761549262

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

Out[55]: -0.5217506090380125

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 =   0.737
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.056
```

Out[56]: 0.7367025679134708

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

Out[57]: -0.29532202929218476

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 =   0.720
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.060
```

Out[58]: 0.7199247583517127

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

Out[59]: -0.0879700642809068

```
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 =  0.681
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  1.053
```

Out[60]: 0.680681954724653

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

Out[61]: 0.07519273144159182

```
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 =  0.550
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  0.946
```

Out[62]: 0.5500258810254968

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

Out[63]: 0.009555274621929694

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

Out[64]: 0.5313058836599422

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

Out[65]: 5-element Array{Float64,1}:
         -0.521751
         -0.295322
         -0.0879701
          0.0751927
          0.00955527

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

Out[66]: 2-element Array{Float64,1}:
  4.73132
  0.945695

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

Out[67]: 0.05569774994685925

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

Out[68]: 0.16465454857343112

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

Out[69]: 0.052673092516255814

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

Out[70]: 0.9456951594366158

In [71]:
```
IDs = readtable("G0.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 = 0.770
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV = 1.347

Out[71]: 0.7704390862435836

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

Out[72]: -0.33812058437108355

In [73]:
```
IDs = readtable("G1.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 = 0.718
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV = 1.124

Out[73]: 0.7181341258454653

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

Out[74]: -0.13449147185745544

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 =   0.657
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.112
```

Out[75]: 0.6567046353889067

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

Out[76]: -0.04099503918789602

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 =   0.538
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   0.904
```

Out[77]: 0.5377610776602297

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

Out[78]: 0.06958035910760223

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 =   0.454
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.657
```

Out[79]: 0.45390017006817857

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

Out[80]: 0.06182659449789038

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 =  0.550
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.946
```

Out[81]: 0.5500258810254968

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]: 0.009555274621929694

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 =  0.513
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.507
```

Out[85]: 0.5134424455368086

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

Out[86]: −0.6300548619327767

```
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 =  0.721
         SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.969
```

Out[87]: 0.7210304931925329

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

Out[88]: -0.5316803305041806

```
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 =  0.733
         SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.036
```

Out[89]: 0.7332143541682972

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

Out[90]: -0.3018432341666537

```
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 =  0.724
         SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.042
```

Out[91]: 0.7237914546779289

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

Out[92]: -0.092009818726766

```
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 =  0.699
         SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.062
```

Out[93]: 0.6990711418570619

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

Out[94]: 0.07553545290168671

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

Out[95]: SSBR.NumSSBayes(54916,45916,9000,40000,39000,1000,150)