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/2
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/2

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

Correlation.G5.M.JC.txt
G0.Genotype.ID
G0.ID
G0.noGenotype.ID
G1.Genotype.ID
G1.ID
G1.noGenotype.ID
G2.Genotype.ID
G2.ID
G2.noGenotype.ID
G3.Genotype.ID
G3.ID
G3.noGenotype.ID
G4.Genotype.ID
G4.ID
G4.noGenotype.ID
G5.Genotype.ID
G5.ID
G5.noGenotype.ID
MarNF.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.JC.txt
all.ID
alphaEstimatesJC
epsiEstimatesJC
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype

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

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

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

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 40738 | 0 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 2 | … | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 40750 | 0 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | 1 | 1 | 0 | 1 | 2 | 1 | 1 | 1 | 0 | 0 1 |
| 40763 | 0 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 2 | | 2 | 1 | 1 | 0 | 1 | 2 | 1 | 1 | 1 | 0 | 0 1 |
| 40775 | 0 | 1 | 1 | 1 | 1 | 2 | 0 | 0 | 0 | 0 | | 2 | 0 | 1 | 1 | 1 | 2 | 1 | 1 | 1 | 1 | 1 1 |
| 40779 | 1 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | | 2 | 0 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 1 | 1 1 |
| 40804 | 0 | 1 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 2 | … | 1 | 1 | 1 | 1 | 1 | 2 | 0 | 2 | 0 | 0 | 0 2 |
| 40823 | 0 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 2 | | 1 | 1 | 1 | 1 | 2 | 2 | 1 | 1 | 1 | 0 | 0 1 |
| 40831 | 0 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | 1 | 2 | 2 | 1 | 1 | 1 | 2 | 1 | 1 | 1 1 |
| 40839 | 1 | 2 | 2 | 2 | 2 | 2 | 0 | 0 | 2 | 1 | | 1 | 1 | 1 | 0 | 2 | 2 | 1 | 0 | 2 | 0 | 0 2 |
| 40854 | 0 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 1 | | 2 | 1 | 2 | 0 | 1 | 2 | 0 | 1 | 0 | 0 | 0 2 |
| 40881 | 0 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 2 | … | 2 | 0 | 1 | 0 | 1 | 2 | 0 | 0 | 2 | 0 | 0 2 |
| 40888 | 0 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 1 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 40910 | 0 | 2 | 2 | 2 | 0 | 2 | 0 | 0 | 0 | 0 | | 1 | 1 | 1 | 1 | 2 | 2 | 1 | 1 | 1 | 0 | 0 1 |
| ⋮ | | ⋮ | | | | | | ⋮ | ⋱ | ⋮ | | | | | | | ⋮ | | | ⋮ | |
| 88710 | 1 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 2 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88711 | 0 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 2 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88712 | 1 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 1 | … | 1 | 1 | 1 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 1 1 |
| 88713 | 0 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | 1 | 1 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 1 1 |
| 88714 | 0 | 2 | 2 | 2 | 0 | 2 | 0 | 0 | 1 | 1 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88715 | 1 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 0 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88716 | 0 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 2 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88717 | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | … | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88718 | 1 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | | 1 | 1 | 1 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 1 1 |
| 88719 | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88720 | 0 | 1 | 2 | 1 | 2 | 0 | 2 | 2 | 0 | 2 | | 0 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 2 | 2 0 |
| 88721 | 1 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 0 | 1 | | 1 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 1 |

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

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

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

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

Out[8]: 9000x150 Array{Float64,2}:
```
 -0.272778   0.245333   0.0268889   0.110556   …   0.814444    0.819   -0.68
7556
 -0.272778   0.245333   0.0268889   0.110556      -1.18556    -1.181    0.31
2444
 -0.272778  -0.754667   0.0268889   0.110556      -1.18556    -1.181    0.31
2444
 -0.272778  -0.754667  -0.973111   -0.889444      -0.185556   -0.181    0.31
2444
  0.727222   0.245333   0.0268889   0.110556      -0.185556   -0.181    0.31
2444
 -0.272778  -0.754667   0.0268889   0.110556   …  -1.18556    -1.181    1.31
244
 -0.272778  -0.754667   0.0268889   0.110556      -1.18556    -1.181    0.31
2444
 -0.272778   0.245333   0.0268889   0.110556      -0.185556   -0.181    0.31
2444
  0.727222   0.245333   0.0268889   0.110556      -1.18556    -1.181    1.31
244
 -0.272778  -0.754667   0.0268889   0.110556      -1.18556    -1.181    1.31
244
 -0.272778   0.245333   0.0268889   0.110556   …  -1.18556    -1.181    1.31
244
 -0.272778   0.245333   0.0268889   0.110556       0.814444    0.819   -0.68
7556
 -0.272778   0.245333   0.0268889   0.110556      -1.18556    -1.181    0.31
2444
    ⋮                                          ⋱
  0.727222   0.245333   0.0268889   0.110556       0.814444    0.819   -0.68
7556
 -0.272778   0.245333   0.0268889   0.110556       0.814444    0.819   -0.68
7556
  0.727222   0.245333   0.0268889   0.110556   …  -0.185556   -0.181    0.31
2444
 -0.272778   0.245333   0.0268889  -0.889444      -0.185556   -0.181    0.31
2444
 -0.272778   0.245333   0.0268889   0.110556       0.814444    0.819   -0.68
7556
  0.727222   0.245333   0.0268889   0.110556       0.814444    0.819   -0.68
7556
 -0.272778   0.245333   0.0268889   0.110556       0.814444    0.819   -0.68
7556
 -0.272778   0.245333   0.0268889   0.110556   …   0.814444    0.819   -0.68
7556
  0.727222   0.245333   0.0268889   0.110556      -0.185556   -0.181    0.31
2444
 -0.272778   0.245333   0.0268889   0.110556       0.814444    0.819   -0.68
7556
 -0.272778  -0.754667   0.0268889  -0.889444       0.814444    0.819   -0.68
7556
  0.727222   0.245333   0.0268889   0.110556      -0.185556   -0.181    0.31
2444
```

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

```
Out[9]:  1x150 Array{Float64,2}:
          1.81583e-17  -2.57769e-16  -1.43293e-16  …  -2.479e-16  5.21065e-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 (

          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    = 0.323
         vG      = 0.323
         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
4296.736792 seconds (23.05 G allocations: 724.066 GB, 7.24% gc time)
```

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

```
Out[40]: 1-element Array{Float64,1}:
          3.80665
```

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

```
Out[41]: 150-element Array{Float64,1}:
           0.00632819
           0.0528625
           0.0260905
           0.124587
           0.0670335
           0.0244239
           0.0240367
          -0.0110168
          -0.0615926
           0.0122113
          -0.0178284
          -0.0914743
          -0.0513927
           ⋮
          -0.192146
          -0.156323
          -0.0324866
           0.0394703
           0.0285234
           0.0279937
          -0.00801173
          -0.00635825
          -0.0128877
           0.0286333
          -0.00306281
          -0.0667754
```

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

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

```
Out[43]: 45954-element Array{Float64,1}:
          -0.426595
          -0.354566
          -0.729249
          -0.201541
          -0.585473
          -0.639854
          -0.230025
          -0.285875
          -0.190175
          -0.241631
           0.276334
           0.149416
           0.0905602
           ⋮
           0.743196
          -0.0871133
          -0.221471
          -0.296762
           0.33399
          -0.261378
          -0.556409
           0.144368
          -0.179183
           0.39807
          -0.233318
          -0.980868
```

```
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 =  0.800
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  1.308
```

```
Out[46]: 0.7999122837708921
```

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

Out[47]: -0.2864260022398898

```
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 =  0.693
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  1.322
```

Out[48]: 0.6928162968360454

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

Out[49]: 8.634641339868823e-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 =  0.810
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  1.159
```

Out[50]: 0.8098691799967608

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

Out[51]: -0.3525243303751906

```
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 =  0.550
         SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.579
```

Out[52]: 0.5498688405754308

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

Out[53]: -0.7615457757049453

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 =   0.749
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  1.008
```

Out[54]: 0.7490000500873452

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

Out[55]: -0.624171663068773

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 =   0.753
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.091
```

Out[56]: 0.7531952830509984

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

Out[57]: -0.34553779544540675

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 =   0.729
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.123
```

Out[58]: 0.7294364496287893

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

Out[59]:  -0.09825371209883942

```
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 ef
          @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
          JCAll = cor7
```

```
          SSBRJC from Gibbs - G4.ID : correlation =   0.710
          SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   1.167
```

Out[60]:  0.7100475971522947

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

Out[61]:  0.1000098744667706

```
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 ef
          @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
          JCAll = cor8
```

```
          SSBRJC from Gibbs - G5.ID : correlation =   0.668
          SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   1.228
```

Out[62]:  0.6677492034140949

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

Out[63]:  0.010943058411854752

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

Out[64]:  0.6351147214806278

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

```
Out[65]:  5-element Array{Float64,1}:
           -0.624172
           -0.345538
           -0.0982537
            0.10001
            0.0109431
```

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

Out[66]: 
```
2-element Array{Float64,1}:
 4.5429
 1.22782
```

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

Out[67]: 0.07956885006770546

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

Out[68]: 0.2690228966395174

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

Out[69]: 0.09769662066857515

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

Out[70]: 1.2278249664968728

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 =  0.826
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.312
```

Out[71]: 0.826269548452319

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

Out[72]: -0.3996932194579438

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 =  0.790
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.317
```

Out[73]: 0.7898806697388663

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

```
Out[74]:  -0.16360746742858467
```

```
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 =   0.742
          SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =   1.218
```

```
Out[75]:  0.7424624942939504
```

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

```
Out[76]:  -0.053429386755171206
```

```
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 =   0.703
          SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =   1.162
```

```
Out[77]:  0.7027644359432331
```

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

```
Out[78]:  0.09359120693896314
```

```
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 =   0.591
          SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.905
```

```
Out[79]:  0.5905855224236987
```

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

Out[80]: 0.08542041581714935

```
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 =   0.668
         SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   1.228
```

Out[81]: 0.6677492034140949

```
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]: 0.010943058411854752

```
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 =   0.539
         SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =   0.559
```

Out[85]: 0.5394597031005914

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

Out[86]: -0.7708240463779452

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 =   0.739
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =   0.978
```

Out[87]: 0.7386732033857617

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

Out[88]: -0.6359810014185215

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 =   0.749
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =   1.067
```

Out[89]: 0.7494287487074767

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

Out[90]: -0.3530277546425922

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 =   0.731
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =   1.101
```

Out[91]: 0.731449113373588

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

Out[92]: -0.10317281258698818

```
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 =  0.730
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  1.173
```

Out[93]: 0.7300602549348517

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

Out[94]: 0.10038396315009425

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

Out[95]: SSBR.NumSSBayes(54954,45954,9000,40000,39000,1000,150)