In [1]:
```julia
include("/home/nicole/Jupyter/SSBRJ/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/5
```

/home/nicole/Jupyter/JG3/Data/0.5a0/M/5

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

```
Correlation.G5.M.C*.txt
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
MarNFCenter.txt
PedAll.txt
Phe.txt
PheAll.txt
Regression.G5.M.C*.txt
Regression.G5.M.JC*.txt
all.ID
alphaEstimatesLeggaraC
alphaEstimatesLeggaraJC
epsiEstimatesLeggaraC
epsiEstimatesLeggaraJC
genotype.ID
noGenotype.ID
sim.bv
sim.phenotype
```

In [5]:
```
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```
;awk '{print $1}' MarNF.txt | sort -b > genotype.ID
```

In [7]:
```
;join -v1 all.ID genotype.ID > noGenotype.ID
```

In [8]:
```
;awk '{print $1,$2}' Phe.txt > sim.phenotype
```

In [9]:
```
;awk '{print $1,$3}' PheAll.txt > sim.bv
```

In [10]:
```
; awk 'NR >=1 && NR <=8000 {print $1}' PedAll.txt | sort -b > G0.ID
```

In [11]:
```
; awk 'NR >=8001 && NR <=16000 {print $1}' PedAll.txt | sort -b > G1.ID
```

```
In [12]:  ; awk 'NR >=16001 && NR <=24000 {print $1}' PedAll.txt | sort -b > G2.ID
```

```
In [13]:  ; awk 'NR >=24001 && NR <=32000 {print $1}' PedAll.txt | sort -b > G3.ID
```

```
In [14]:  ; awk 'NR >=32001 && NR <=40000 {print $1}' PedAll.txt | sort -b > G4.ID
```

```
In [15]:  ; awk 'NR >=40001 && NR <=48000 {print $1}' PedAll.txt | sort -b > G5.ID
```

```
In [16]:  ;join G0.ID genotype.ID > G0.Genotype.ID
```

```
In [17]:  ;join G1.ID genotype.ID > G1.Genotype.ID
```

```
In [18]:  ;join G2.ID genotype.ID > G2.Genotype.ID
```

```
In [19]:  ;join G3.ID genotype.ID > G3.Genotype.ID
```

```
In [20]:  ;join G4.ID genotype.ID > G4.Genotype.ID
```

```
In [21]:  ;join G5.ID genotype.ID > G5.Genotype.ID
```

```
In [22]:  ;join -v1 G0.ID genotype.ID > G0.noGenotype.ID
```

```
In [23]:  ;join -v1 G1.ID genotype.ID > G1.noGenotype.ID
```

```
In [24]:  ;join -v1 G2.ID genotype.ID > G2.noGenotype.ID
```

```
In [25]:  ;join -v1 G3.ID genotype.ID > G3.noGenotype.ID
```

```
In [26]:  ;join -v1 G4.ID genotype.ID > G4.noGenotype.ID
```

```
In [27]:  ;join -v1 G5.ID genotype.ID > G5.noGenotype.ID
```

```
In [28]:  ;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 [29]: ;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 [30]: ped,A_Mats,numSSBayes = calc_Ai("PedAll.txt","genotype.ID",calculateInbreedir
         nothing
         df      = read_genotypes("MarNF.txt",numSSBayes)
         M_Mats = make_MMats(df,A_Mats,ped);                              # witl
         y_Vecs = make_yVecs("sim.phenotype",ped,numSSBayes)
         J_Vecs = make_JVecs(numSSBayes,A_Mats)
         Z_Mats = make_ZMats(ped,y_Vecs,numSSBayes)
         X_Mats, W_Mats = make_XWMats(J_Vecs,Z_Mats,M_Mats,numSSBayes)    # witl
         nothing
```

```
In [31]: vRes    = 0.767
         vG      = 0.767
         nIter  = 50000
         @time aHat1,alphaHat,betaHat,epsiHat =
         ssGibbs(M_Mats,y_Vecs,J_Vecs,Z_Mats,X_Mats,W_Mats,A_Mats, numSSBayes,vRes,vG
         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
         3304.291621 seconds (23.03 G allocations: 723.668 GB, 7.48% gc time)
```

```
In [32]: betaHat
```

```
Out[32]: 2-element Array{Float64,1}:
           3.43408
          -1.35315
```

```
In [33]: mu  = betaHat[1]
         mug = betaHat[2]
```

```
Out[33]: -1.3531549021583122
```

```
In [34]: (mu+mug)/2
```

```
Out[34]: 1.0404650031808669
```

```
In [35]: alphaHat
```

```
Out[35]: 150-element Array{Float64,1}:
         -0.0665019
         -0.184115
         -0.0589919
          0.0583042
          0.152595
          0.122866
          0.136456
          0.121012
         -0.0575866
          0.018198
         -0.0287113
          0.0240554
         -0.00801062
          ⋮
          0.0532176
          0.0617375
          0.000995454
         -0.0180577
         -0.0661523
          0.0561588
         -0.0344211
          0.0660022
          0.0215173
         -0.0479945
         -0.0443088
          0.0265393
```

```
In [36]: writedlm("alphaEstimatesJ",alphaHat)
```

```
In [37]: epsiHat
```

```
Out[37]: 45924-element Array{Float64,1}:
          -0.138394
          -0.502008
          -0.385725
          -1.2941
           0.337091
           0.228556
          -0.0228225
          -0.425516
          -0.525832
           0.104206
          -0.0968787
           0.0110087
          -0.394429
           ⋮
           0.332676
          -0.247543
           0.531938
          -0.40257
           0.382102
          -0.403459
           0.633557
          -0.131121
           0.468601
          -0.543832
          -0.368703
          -0.278162
```

```
In [38]: writedlm("epsiEstimatesJ",epsiHat)
```

```
In [39]: using DataFrames
```

```
In [40]: 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 [41]: 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 =  0.902
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.983
```

```
Out[41]: 0.9023820817104253
```

```
In [42]: TBV = a[posAi]
         mean(TBV)
```

Out[42]: 4.957202791666667

```
In [43]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[43]: 1.5113456303791788

```
In [44]: 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 =   0.887
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   1.002
```

Out[44]: 0.8869707159627377

```
In [45]: TBV = a[posAi]
         mean(TBV)
```

Out[45]: 6.157122333333334

```
In [46]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[46]: 2.675147760612106

```
In [47]: 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 =   0.867
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.962
```

Out[47]: 0.8672183456318918

```
In [48]: TBV = a[posAi]
         mean(TBV)
```

Out[48]: 4.680298282051282

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

Out[49]: 1.242775908017734

In [50]:
```
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 =  0.714
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.891
```

Out[50]: 0.7136032250647363

In [51]:
```
TBV = a[posAi]
G0TBV=mean(TBV)
```

Out[51]: 3.6482481250000003

In [52]:
```
GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

Out[52]: 0.12308402222079273

In [53]:
```
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 =  0.765
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.982
```

Out[53]: 0.7653644003285407

In [54]:
```
TBV = a[posAi]
G1TBV=mean(TBV)
```

Out[54]: 4.197937250000001

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

Out[55]: 0.7843026768748478

```
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 =  0.762
         SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  1.002
```

Out[56]: 0.7618100474690916

```
In [57]: TBV = a[posAi]
         G2TBV=mean(TBV)
```

Out[57]: 4.739230875

```
In [58]: GEBV = aHat1[posAi]
         G2GEBV=mean(GEBV)
```

Out[58]: 1.341519240366726

```
In [59]: 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 =  0.758
         SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  1.010
```

Out[59]: 0.7575607922587584

```
In [60]: TBV = a[posAi]
         G3TBV=mean(TBV)
```

Out[60]: 5.237892250000001

```
In [61]: GEBV = aHat1[posAi]
         G3GEBV=mean(GEBV)
```

Out[61]: 1.824637900396772

```
In [62]: 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 ex
         @printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor7
```

```
         SSBRJC from Gibbs - G4.ID : correlation =   0.747
         SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =   0.980
```

Out[62]: 0.746585821662466

```
In [63]: TBV = a[posAi]
         G4TBV=mean(TBV)
```

Out[63]: 5.710383875

```
In [64]: GEBV = aHat1[posAi]
         G4GEBV=mean(GEBV)
```

Out[64]: 2.276658615822269

```
In [65]: 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 ex
         @printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", re
         JCAll = cor8
```

```
         SSBRJC from Gibbs - G5.ID : correlation =   0.872
         SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =   0.976
```

Out[65]: 0.8717376038199799

```
In [66]: TBV = a[posAi]
         G5TBV=mean(TBV)
```

Out[66]: 6.209524375

```
In [67]: GEBV = aHat1[posAi]
         G5GEBV=mean(GEBV)
```

Out[67]: 2.7178713265936656

```
In [68]: reg8 = linreg(aHat1[posAi], a[posAi])
```

```
Out[68]: 2-element Array{Float64,1}:
          3.55583
          0.976387
```

```
In [69]: VarGEBV=var(aHat1[posAi])
```

Out[69]: 0.39340115854837354

In [70]:
```
VarTBV=var(a[posAi])
```

Out[70]: 0.49352325556280474

In [71]:
```
Cov=cov(aHat1[posAi], a[posAi])
```

Out[71]: 0.3841115874909853

In [72]:
```
b=Cov/VarGEBV
```

Out[72]: 0.9763865183019129

In [73]:
```
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 =  0.864
SSBRJC from Gibbs – G0.Genotype.ID : regression of TBV on GEBV =  0.950
```

Out[73]: 0.8639094287782912

In [74]:
```
TBV = a[posAi]
mean(TBV)
```

Out[74]: 4.735164999999999

In [75]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[75]: 1.498625820761471

In [76]:
```
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 =  0.883
SSBRJC from Gibbs – G1.Genotype.ID : regression of TBV on GEBV =  0.979
```

Out[76]: 0.8834887698993475

In [77]:
```
TBV = a[posAi]
mean(TBV)
```

Out[77]: 5.2959249999999995

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

Out[78]: 1.9785727141798752

In [79]:
```
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 =  0.885
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.958
```

Out[79]: 0.884978418280768

In [80]:
```
TBV = a[posAi]
mean(TBV)
```

Out[80]: 5.739855

In [81]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[81]: 2.333488573661723

In [82]:
```
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 =  0.870
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.917
```

Out[82]: 0.8697790657896675

In [83]:
```
TBV = a[posAi]
mean(TBV)
```

Out[83]: 6.20947

In [84]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[84]: 2.7455708518543003

```
In [85]: 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 =   0.821
         SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =   0.871
```

Out[85]: 0.821312702567632

```
In [86]: TBV = a[posAi]
         mean(TBV)
```

Out[86]: 6.709115

```
In [87]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[87]: 3.1105382033407802

```
In [88]: 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 =   0.872
         SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =   0.976
```

Out[88]: 0.8717376038199799

```
In [89]: writedlm("Correlation.G5.M.J.txt",cor13)
```

```
In [90]: writedlm("Regression.G5.M.J.txt",reg13)
```

```
In [91]: TBVG5Gall = a[posAi]
         TBVG5G=mean(TBVG5Gall)
```

Out[91]: 6.209524375

```
In [92]: GEBVG5Gall = aHat1[posAi]
         GEBVG5G=mean(GEBVG5Gall)
```

Out[92]: 2.7178713265936656

In [93]:
```
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 =  0.698
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.901
```

Out[93]: 0.6976798106595901

In [94]:
```
TBV = a[posAi]
mean(TBV)
```

Out[94]: 3.6203784615384613

In [95]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[95]: 0.08781371969410869

In [96]:
```
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 =  0.750
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.988
```

Out[96]: 0.7497658762692999

In [97]:
```
TBV = a[posAi]
mean(TBV)
```

Out[97]: 4.169783717948718

In [98]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[98]: 0.7536803682260007

In [99]:
```
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 =  0.747
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  1.002
```

Out[99]: 0.7467810812951698

In [100]:
```
TBV = a[posAi]
mean(TBV)
```

Out[100]: 4.713573846153845

In [101]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[101]: 1.316084129256598

In [102]:
```
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 =  0.744
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  1.009
```

Out[102]: 0.7435809165507247

In [103]:
```
TBV = a[posAi]
mean(TBV)
```

Out[103]: 5.212980000000001

In [104]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[104]: 1.8010242349747843

```
In [105]: 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 =   0.731
          SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   0.969

Out[105]: 0.731403882365935

```
In [106]: TBV = a[posAi]
          mean(TBV)
```

Out[106]: 5.684775384615386

```
In [107]: GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[107]: 2.2552770879371784

```
In [108]: numSSBayes
```

Out[108]: SSBR.NumSSBayes(54924,45924,9000,40000,39000,1000,150)

```
In [109]: J_Vecs.J1
```

Out[109]: 45924x1 Array{Float64,2}:
           -0.00234055
           -0.500667
           -0.897156
           -0.522889
           -0.501754
           -0.0122695
           -0.825927
           -0.751907
           -0.768559
            0.0
           -0.75555
           -0.962581
           -0.545309
            ⋮
           -0.943999
           -0.962573
            1.30003e-19
           -0.822729
           -0.75248
           -0.838053
           -0.0501533
           -0.966121
           -0.504111
           -0.887714
           -0.878378
           -0.00235249

In [110]: `sortrows(J_Vecs.J1[end-8000:end,:])`

Out[110]: 8001x1 Array{Float64,2}:
           −0.984954
           −0.984489
           −0.984394
           −0.982634
           −0.981548
           −0.981238
           −0.981167
           −0.981142
           −0.981142
           −0.980901
           −0.980893
           −0.980805
           −0.98078
            ⋮
            5.55925e−17
            5.56171e−17
            5.58448e−17
            5.60069e−17
            5.64132e−17
            5.70208e−17
            5.83156e−17
            6.07471e−17
            6.08578e−17
            6.62914e−17
            6.66168e−17
            7.44469e−17

```
In [111]:  J1 = sortrows(J_Vecs.J1)
```

Out[111]: 45924x1 Array{Float64,2}:
           -0.989812
           -0.987653
           -0.986861
           -0.986797
           -0.98561
           -0.98559
           -0.985305
           -0.985289
           -0.984954
           -0.98495
           -0.984499
           -0.984489
           -0.984394
            ⋮
            7.41469e-17
            7.44469e-17
            8.57318e-17
            8.88581e-17
            8.89405e-17
            8.91914e-17
            8.93206e-17
            1.07468e-16
            1.10173e-16
            1.11047e-16
            1.1138e-16
            1.11899e-16

```
In [112]: J1[J1 .< 0.0,:]
```

Out[112]: 43918x1 Array{Float64,2}:
          -0.989812
          -0.987653
          -0.986861
          -0.986797
          -0.98561
          -0.98559
          -0.985305
          -0.985289
          -0.984954
          -0.98495
          -0.984499
          -0.984489
          -0.984394
           ⋮
          -1.08312e-35
          -1.08228e-35
          -1.08217e-35
          -8.72663e-36
          -7.2166e-36
          -7.2166e-36
          -7.2166e-36
          -7.2166e-36
          -7.20827e-36
          -5.41087e-36
          -2.54007e-65
          -5.32825e-67

In [113]: `J1[J1 .> 0.0,:]`

Out[113]: 1311x1 Array{Float64,2}:
 1.20145e-51
 1.60056e-51
 1.60241e-51
 1.60241e-51
 2.39963e-51
 3.20106e-51
 4.79926e-51
 4.81291e-51
 1.83882e-50
 6.88311e-50
 1.14395e-49
 2.28789e-49
 2.58203e-49
 ⋮
 7.41469e-17
 7.44469e-17
 8.57318e-17
 8.88581e-17
 8.89405e-17
 8.91914e-17
 8.93206e-17
 1.07468e-16
 1.10173e-16
 1.11047e-16
 1.1138e-16
 1.11899e-16

In [114]: `G = convert(Array,readtable("MarNF.txt", separator = ' ',header=false));`

In [115]: `GAll=mean(G[:,2:end],1)`

Out[115]: 1x150 Array{Float64,2}:
 0.137333 1.08967 1.47956 0.492778 … 0.356444 1.83711 0.583444

In [116]: `GG0=mean(G[1:200,2:end],1)`

Out[116]: 1x150 Array{Float64,2}:
 0.115 1.535 1.6 0.385 0.87 0.765 … 0.29 1.025 0.54 1.785 0.865

In [117]: `GG1=mean(G[201:400,2:end],1)`

Out[117]: 1x150 Array{Float64,2}:
 0.15 1.36 1.555 0.42 1.1 0.995 0.975 … 0.3 1.11 0.495 1.81 0.735

In [118]: `GG2=mean(G[401:600,2:end],1)`

Out[118]: 1x150 Array{Float64,2}:
 0.155 1.24 1.525 0.47 1.16 1.08 … 0.245 1.32 0.375 1.81 0.62

In [119]: ```GG3=mean(G[601:800,2:end],1)```

Out[119]: 1x150 Array{Float64,2}:
 0.145 1.05 1.445 0.535 1.405 … 1.74 0.21 1.33 0.34 1.835 0.62

In [120]: ```GG4=mean(G[801:1000,2:end],1)```

Out[120]: 1x150 Array{Float64,2}:
 0.125 0.935 1.435 0.535 1.47 … 1.77 0.245 1.48 0.3 1.86 0.47

In [121]: ```GG5=mean(G[1001:9000,2:end],1)```

Out[121]: 1x150 Array{Float64,2}:
 0.13725 1.07288 1.4755 0.49575 … 1.35838 0.34975 1.83925 0.57362
 5

In [122]: ```writedlm("meanOfSNPMAll",GAll)```

In [123]: ```writedlm("meanOfSNPMG0",GG0)```

In [124]: ```writedlm("meanOfSNPMG1",GG1)```

In [125]: ```writedlm("meanOfSNPMG2",GG2)```

In [126]: ```writedlm("meanOfSNPMG3",GG3)```

In [127]: ```writedlm("meanOfSNPMG4",GG4)```

In [128]: ```writedlm("meanOfSNPMG5",GG5)```