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/G/6
```

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

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

```
Correlation.G5.G.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
```

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

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

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

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

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

In [10]:
```julia
; 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",calculateInbreedi
nothing
df      = read_genotypes("GenNF.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   = 0.262
vG     = 0.262
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
2579.051939 seconds (23.05 G allocations: 723.923 GB, 7.44% gc time)
```

In [32]: `betaHat`

Out[32]:
```
2-element Array{Float64,1}:
 3.15829
 1.42424
```

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

Out[33]: `1.4242373941098356`

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

Out[34]: `2.2912629276765086`

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

```
Out[35]:  200-element Array{Float64,1}:
          -0.00423452
          -0.0142036
          -0.00797365
           0.00891164
          -0.0118441
           0.0351081
           0.0401879
           0.0465363
          -0.0030698
           0.00194017
          -0.00572777
           0.023562
          -0.0148758
           ⋮
          -0.0165456
          -0.00429884
           0.00932679
           0.0174854
          -0.00630076
           0.0212287
          -0.0408247
           0.0506944
           0.0315716
          -0.031419
          -0.0103843
           0.0900053
```

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

```
In [37]:  using DataFrames
```

```
In [38]:  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 [39]:  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 =  0.889
          SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.916
```

```
Out[39]:  0.8889679888449568
```

```
In [40]: TBV = a[posAi]
         mean(TBV)
```

Out[40]: 4.017600416666667

```
In [41]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[41]: 0.8636276115460642

```
In [42]: 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 =   0.978
         SSBRJC from Gibbs - genotype.ID : regression of TBV on GEBV =   1.074

Out[42]: 0.9780358936555961

```
In [43]: TBV = a[posAi]
         mean(TBV)
```

Out[43]: 4.7069703333333335

```
In [44]: GEBV = aHat1[posAi]
         mean(GEBV)
```

Out[44]: 1.5879289905333036

```
In [45]: 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 =   0.838
         SSBRJC from Gibbs - noGenotype.ID : regression of TBV on GEBV =   0.885

Out[45]: 0.8384575009142581

```
In [46]: TBV = a[posAi]
         mean(TBV)
```

Out[46]: 3.858515051282051

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

Out[47]: 0.6964811394720857

In [48]:
```
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", r
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.545
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.533
```

Out[48]: 0.5450485537031833

In [49]:
```
TBV = a[posAi]
G0TBV=mean(TBV)
```

Out[49]: 3.2996621250000002

In [50]:
```
GEBV = aHat1[posAi]
G0GEBV=mean(GEBV)
```

Out[50]: 0.06721592608359873

In [51]:
```
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 =  0.765
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.936
```

Out[51]: 0.7647484001254341

In [52]:
```
TBV = a[posAi]
G1TBV=mean(TBV)
```

Out[52]: 3.54218725

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

Out[53]: 0.398647246055671

In [54]:
```
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 =  0.772
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.993
```

Out[54]: 0.7721199803788897

In [55]:
```
TBV = a[posAi]
G2TBV=mean(TBV)
```

Out[55]: 3.877764375

In [56]:
```
GEBV = aHat1[posAi]
G2GEBV=mean(GEBV)
```

Out[56]: 0.7376443414059204

In [57]:
```
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 =  0.774
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.998
```

Out[57]: 0.7740045465947775

In [58]:
```
TBV = a[posAi]
G3TBV=mean(TBV)
```

Out[58]: 4.17377175

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

Out[59]: 1.028368995944298

In [60]:
```
IDs = readtable("G4.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor7 = cor(a[posAi],aHat1[posAi])[1,1]
reg7 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G4.ID : correlation = %6.3f\n", cor7 ) # with e
@printf("SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV = %6.3f\n", r
JCAll = cor7
```

```
SSBRJC from Gibbs - G4.ID : correlation =  0.778
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.981
```

Out[60]: 0.7779269623763142

In [61]:
```
TBV = a[posAi]
G4TBV=mean(TBV)
```

Out[61]: 4.471856625

In [62]:
```
GEBV = aHat1[posAi]
G4GEBV=mean(GEBV)
```

Out[62]: 1.3311901767810839

In [63]:
```
IDs = readtable("G5.ID", eltypes =[UTF8String], separator = ' ',header=false
posAi = getPos(ped,IDs)
cor8 = cor(a[posAi],aHat1[posAi])[1,1]
reg8 = linreg(aHat1[posAi], a[posAi])[2,1]
@printf("SSBRJC from Gibbs - G5.ID : correlation = %6.3f\n", cor8 ) # with e
@printf("SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV = %6.3f\n", r
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =  0.974
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.069
```

Out[63]: 0.9741408359434602

In [64]:
```
TBV = a[posAi]
G5TBV=mean(TBV)
```

Out[64]: 4.740360375

In [65]:
```
GEBV = aHat1[posAi]
G5GEBV=mean(GEBV)
```

Out[65]: 1.6186989830058125

In [66]:
```
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 =  0.980
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  1.112
```

Out[66]: 0.9802365855362842

In [67]:
```
TBV = a[posAi]
mean(TBV)
```

Out[67]: 3.7758950000000002

In [68]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[68]: 0.7497683752311994

In [69]:
```
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 =  0.978
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  1.090
```

Out[69]: 0.978176334871302

In [70]:
```
TBV = a[posAi]
mean(TBV)
```

Out[70]: 4.208435

In [71]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[71]: 1.12253363977401

In [72]:
```
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 =  0.978
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  1.100
```

Out[72]: 0.9780962994694055

In [73]:
```
TBV = a[posAi]
mean(TBV)
```

Out[73]: 4.4493849999999995

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

Out[74]: 1.3457291670216243

In [75]:
```
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 =  0.971
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  1.030
```

Out[75]: 0.9710841757591598

In [76]:
```
TBV = a[posAi]
mean(TBV)
```

Out[76]: 4.776925

In [77]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[77]: 1.6390935908577418

In [78]:
```
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 =  0.955
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  1.044
```

Out[78]: 0.9548237641372894

In [79]:
```
TBV = a[posAi]
mean(TBV)
```

Out[79]: 4.9886099999999995

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

Out[80]: 1.851720480881587

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 =  0.974
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  1.069
```

Out[81]: 0.9741408359434602

In [82]:
```
writedlm("Correlation.G5.G.J.txt",cor13)
```

In [83]:
```
writedlm("Regression.G5.G.J.txt",reg13)
```

In [84]:
```
TBVG5Gall = a[posAi]
TBVG5G=mean(TBVG5Gall)
```

Out[84]: 4.740360375

In [85]:
```
GEBVG5Gall = aHat1[posAi]
GEBVG5G=mean(GEBVG5Gall)
```

Out[85]: 1.6186989830058125

In [86]:
```
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 = 9
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.523
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.517
```

Out[86]: 0.5233577827209662

In [87]:
```
TBV = a[posAi]
mean(TBV)
```

Out[87]: 3.287451025641026

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

Out[88]: 0.04971458123366026

In [89]:
```
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 =  0.747
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.935
```

Out[89]: 0.7472665285263284

In [90]:
```
TBV = a[posAi]
mean(TBV)
```

Out[90]: 3.5251039743589745

In [91]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[91]: 0.38008605647314936

In [92]:
```
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 =  0.757
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.995
```

Out[92]: 0.7573346011491399

In [93]:
```
TBV = a[posAi]
mean(TBV)
```

Out[93]: 3.8631074358974358

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

Out[94]: 0.7220524228003894

In [95]:
```
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 =  0.758
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.998
```

Out[95]: 0.7581303435172416

In [96]:
```
TBV = a[posAi]
mean(TBV)
```

Out[96]: 4.158306282051282

In [97]:
```
GEBV = aHat1[posAi]
mean(GEBV)
```

Out[97]: 1.0127093909465177

```
In [98]: 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", cor17
         @printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 9
         JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =  0.765
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =  0.979
```

Out[98]: 0.7649676340055538

```
In [99]: TBV = a[posAi]
         mean(TBV)
```

Out[99]: 4.458606538461539

```
In [100]: GEBV = aHat1[posAi]
          mean(GEBV)
```

Out[100]: 1.317843245906712

```
In [101]: IDs = readtable("G5.noGenotype.ID", eltypes =[UTF8String], separator = ' ',he
          posAi = getPos(ped,IDs)
          cor18 = cor(a[posAi],aHat1[posAi])[1,1]
          reg18 = linreg(aHat1[posAi], a[posAi])[2,1]
          @printf("SSBRJC from Gibbs - G5.noGenotype.ID : correlation = %6.3f\n", cor18
          @printf("SSBRJC from Gibbs - G5.noGenotype.ID : regression of TBV on GEBV = 9
          JCAll = cor17
```

```
LoadError: BoundsError: attempt to access 0-element Array{UInt8,1}
  at index [1]
while loading In[101], in expression starting on line 1

 [inlined code] from /home/nicole/.julia/v0.4/DataFrames/src/dataframe/i
o.jl:167
 in readnrows! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.j
l:222
 in readtable! at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.j
l:774
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:
862
 in readtable at /home/nicole/.julia/v0.4/DataFrames/src/dataframe/io.jl:
956
```

```
In [102]: TBVG5NGall = a[posAi]
          TBVG5NG=mean(TBVG5NGall)
```

Out[102]: 4.458606538461539

```
In [103]: GEBVG5NGall = aHat1[posAi]
          GEBVG5NG=mean(GEBVG5NGall)
```

Out[103]: 1.317843245906712

```
In [104]: numSSBayes
```

Out[104]: SSBR.NumSSBayes(54916,45916,9000,40000,39000,1000,200)

```
In [105]: J_Vecs.J1
```

Out[105]: 45916x1 Array{Float64,2}:
            0.0
           -0.00117028
           -0.0023385
           -0.88846
           -0.516681
           -0.501759
            1.30079e-19
           -0.752161
           -0.797068
           -0.751759
           -0.00117372
           -0.752051
           -0.962559
            ⋮
           -0.962619
            1.59463e-18
           -0.758099
           -0.758366
           -0.751903
           -0.0457756
           -0.974882
           -0.51785
           -0.890304
           -0.894478
           -0.0134387
            1.30311e-19

```
In [106]: sortrows(J_Vecs.J1[end-8000:end,:])
```

Out[106]: 8001x1 Array{Float64,2}:
          -0.986553
          -0.985416
          -0.984239
          -0.981694
          -0.981395
          -0.981335
          -0.981231
          -0.981177
          -0.980851
          -0.98073
          -0.980514
          -0.979571
          -0.97947
           ⋮
           5.56813e-17
           5.57143e-17
           5.57143e-17
           5.61345e-17
           5.65405e-17
           5.72102e-17
           6.06575e-17
           6.31852e-17
           6.66038e-17
           6.95754e-17
           7.11282e-17
           1.11714e-16

In [107]: `J1 = sortrows(J_Vecs.J1)`

Out[107]: 45916x1 Array{Float64,2}:
     −0.988548
     −0.986981
     −0.986553
     −0.985968
     −0.98556
     −0.985416
     −0.985321
     −0.985276
     −0.984341
     −0.984239
     −0.983132
     −0.982628
     −0.981694
      ⋮
      6.66038e−17
      6.95754e−17
      7.11282e−17
      7.11548e−17
      7.17203e−17
      7.29782e−17
      7.43911e−17
      7.92991e−17
      8.60319e−17
      8.91038e−17
      1.11144e−16
      1.11714e−16

```
In [108]: J1[J1 .< 0.0,:]
```

Out[108]:   43939x1 Array{Float64,2}:
            -0.988548
            -0.986981
            -0.986553
            -0.985968
            -0.98556
            -0.985416
            -0.985321
            -0.985276
            -0.984341
            -0.984239
            -0.983132
            -0.982628
            -0.981694
              ⋮
            -7.31545e-36
            -7.24235e-36
            -7.22085e-36
            -7.2166e-36
            -7.21449e-36
            -7.21238e-36
            -7.20815e-36
            -5.41087e-36
            -7.16595e-66
            -2.03618e-66
            -3.51359e-67
            -1.77903e-67

```
In [109]: J1[J1 .> 0.0,:]
```

```
Out[109]: 1304x1 Array{Float64,2}:
           8.01203e-52
           8.12178e-52
           1.20145e-51
           1.58238e-51
           1.60053e-51
           1.60194e-51
           1.60241e-51
           1.60812e-51
           1.62436e-51
           1.6311e-51
           2.41071e-51
           3.16476e-51
           3.20194e-51
           ⋮
           6.66038e-17
           6.95754e-17
           7.11282e-17
           7.11548e-17
           7.17203e-17
           7.29782e-17
           7.43911e-17
           7.92991e-17
           8.60319e-17
           8.91038e-17
           1.11144e-16
           1.11714e-16
```

```
In [110]: G = convert(Array,readtable("GenNF.txt", separator = ' ',header=false));
```

```
In [111]: GAll=mean(G[:,2:end],1)
```

```
Out[111]: 1x200 Array{Float64,2}:
           0.130111  1.72833  0.365556  1.96944  1.84389  …  0.501333  1.83967  1.0
          3167
```

```
In [112]: GG0=mean(G[1:200,2:end],1)
```

```
Out[112]: 1x200 Array{Float64,2}:
           0.155  1.735  0.465  1.93  1.725  …  0.46  0.795  0.8  0.665  1.84  1.09
```

```
In [113]: GG1=mean(G[201:400,2:end],1)
```

```
Out[113]: 1x200 Array{Float64,2}:
           0.115  1.725  0.465  1.92  1.75  0.385  …  0.79  0.795  0.625  1.79  1.0
          8
```

```
In [114]: GG2=mean(G[401:600,2:end],1)
```

```
Out[114]: 1x200 Array{Float64,2}:
           0.14  1.775  0.35  1.96  1.855  0.395  …  0.865  0.87  0.59  1.815  1.07
          5
```

In [115]:
```
GG3=mean(G[601:800,2:end],1)
```

Out[115]: 1x200 Array{Float64,2}:
 0.13 1.795 0.28 1.98 1.895 0.485 … 0.845 0.845 0.555 1.82 1.0
7

In [116]:
```
GG4=mean(G[801:1000,2:end],1)
```

Out[116]: 1x200 Array{Float64,2}:
 0.12 1.705 0.365 1.98 1.845 … 0.245 1.0 0.995 0.4 1.85 0.965

In [117]:
```
GG5=mean(G[1001:9000,2:end],1)
```

Out[117]: 1x200 Array{Float64,2}:
 0.129875 1.726 0.363125 1.97138 … 0.90775 0.493125 1.84175 1.028
63

In [118]:
```
writedlm("meanOfSNPGAll",GAll)
```

In [119]:
```
writedlm("meanOfSNPGG0",GG0)
```

In [120]:
```
writedlm("meanOfSNPGG1",GG1)
```

In [121]:
```
writedlm("meanOfSNPGG2",GG2)
```

In [122]:
```
writedlm("meanOfSNPGG3",GG3)
```

In [123]:
```
writedlm("meanOfSNPGG4",GG4)
```

In [124]:
```
writedlm("meanOfSNPGG5",GG5)
```