In [1]:
```
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]:
```
; cd Data/0.5a0/G/10
```

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

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

```
Correlation.G5.G.PBLUP.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]:
```
;awk '{print $1}' PedAll.txt | sort -b > all.ID
```

In [6]:
```
;awk '{print $1}' GenNF.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",calculateInbreedi
nothing
df     = read_genotypes("GenNF.txt",numSSBayes)
M_Mats = make_MMats(df,A_Mats,ped);                              # wit
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)    # wit
nothing
```

In [31]:
```
vRes   = 0.460
vG     = 0.460
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
2497.823847 seconds (23.06 G allocations: 724.103 GB, 7.79% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 3.68825
 1.5488
```

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

Out[33]: 1.5488004164793072

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

Out[34]: 2.618524739945871

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

```
Out[35]: 200-element Array{Float64,1}:
           0.0350579
          -0.0323869
          -0.0229403
           0.0279356
          -0.00975021
          -0.0208687
           0.000111059
          -0.0284979
          -0.0714855
           0.073192
           0.118007
          -0.0126511
          -0.0271324
           ⋮
           0.0358784
          -0.0412794
           0.238715
           0.0266207
           0.0119346
          -0.00294719
          -0.024198
           0.0378509
           0.0438402
           0.000536857
           0.00451626
          -0.00117576
```

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

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

```
In [38]: 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 [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 =  0.910
         SSBRJC from Gibbs - all.ID  : regression of TBV on GEBV =  0.947
```

```
Out[39]: 0.9096459749898966
```

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

Out[40]: 4.902233

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

Out[41]: 1.2221440614603314

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 =   0.982
SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =   1.031
```

Out[42]: 0.9822941634876233

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

Out[43]: 5.8692245555555544

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

Out[44]: 2.2354100739826066

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 =   0.867
SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =   0.934
```

Out[45]: 0.8666436190622921

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

Out[46]: 4.679081102564102

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

Out[47]: 0.9883134431859599

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", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G0.ID : correlation =  0.634
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.717
```

Out[48]: 0.634360682589283

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

Out[49]: 3.8552633749999994

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

Out[50]: 0.09574681672029589

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", re
JCAll = cor4
```

```
SSBRJC from Gibbs - G1.ID : correlation =  0.779
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.972
```

Out[51]: 0.7785741544834596

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

Out[52]: 4.25242625

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

Out[53]: 0.5744450081218103

```
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 =   0.764
SSBRJC from Gibbs – G2.ID : regression of TBV on GEBV =  0.988
```

Out[54]: 0.7642436920455075

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

Out[55]: 4.7252624999999995

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

Out[56]: 1.0543172216570065

```
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 =   0.766
SSBRJC from Gibbs – G3.ID : regression of TBV on GEBV =  0.984
```

Out[57]: 0.766150956657029

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

Out[58]: 5.129282125

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

Out[59]: 1.4600810620890894

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 =   0.780
SSBRJC from Gibbs - G4.ID : regression of TBV on GEBV =  0.979
```

Out[60]: 0.7796843799442241

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

Out[61]: 5.53919975

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

Out[62]: 1.8716366272263727

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", re
JCAll = cor8
```

```
SSBRJC from Gibbs - G5.ID : correlation =   0.979
SSBRJC from Gibbs - G5.ID : regression of TBV on GEBV =  1.029
```

Out[63]: 0.979476409165636

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

Out[64]: 5.911964

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

Out[65]: 2.2766376329474123

```
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 =   0.983
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =   1.046
```

Out[66]: 0.9834658386979718

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

Out[67]: 4.654085

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

Out[68]: 1.084938139629865

```
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 =   0.976
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =   1.016
```

Out[69]: 0.9759295120888759

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

Out[70]: 5.209289999999999

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

Out[71]: 1.5861709305630902

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 =  1.016
```

Out[72]: 0.9775662667677435

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

Out[73]: 5.528680000000005

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

Out[74]: 1.8992859078397166

In [75]:
```
IDs = readtable("G3.Genotype.ID", eltypes =[UTF8String], separator = ' ',hea
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 =  0.994
```

Out[75]: 0.9712492047544594

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

Out[76]: 5.93413

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

Out[77]: 2.297509840926639

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 =   0.972
SSBRJC from Gibbs – G4.Genotype.ID : regression of TBV on GEBV =   1.026
```

Out[78]: 0.9721417396789958

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

Out[79]: 6.31036

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

Out[80]: 2.6600431923614885

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 =   0.979
SSBRJC from Gibbs – G5.Genotype.ID : regression of TBV on GEBV =   1.029
```

Out[81]: 0.979476409165636

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]: 5.911964

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

Out[85]: 2.2766376329474123

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", cor1
@printf("SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G0.noGenotype.ID : correlation =  0.610
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.704
```

Out[86]: 0.6102652396064007

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

Out[87]: 3.8347807692307687

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

Out[88]: 0.07038293664569155

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", cor1
@printf("SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV = 
JCAll = cor14
```

```
SSBRJC from Gibbs - G1.noGenotype.ID : correlation =  0.760
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.974
```

Out[89]: 0.7599686740396648

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

Out[90]: 4.227891282051282

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

Out[91]: 0.548503317802803

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 =  0.748
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.990
```

Out[92]: 0.7478606412776446

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

Out[93]: 4.704662051282051

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

Out[94]: 1.032651357908732

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 =  0.749
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.985
```

Out[95]: 0.7494919913160467

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

Out[96]: 5.108644999999999

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

Out[97]: 1.4386085292983826

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 = !
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =   0.764
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   0.978
```

Out[98]: 0.7641422140336072

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

Out[99]: 5.519426410256411

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

Out[100]: 1.8514210742741901

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 = !
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]: 5.519426410256411

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

Out[103]: 1.8514210742741901

In [104]: `numSSBayes`

Out[104]: `SSBR.NumSSBayes(54929,45929,9000,40000,39000,1000,200)`

In [105]: `J_Vecs.J1`

Out[105]: 45929x1 Array{Float64,2}:
```
  0.0
 -0.887647
 -0.638433
 -0.501755
 -0.0122736
 -0.751756
 -0.758027
 -0.757471
  1.30155e-19
 -0.848731
 -0.962603
 -0.501464
 -0.943893
  ⋮
 -0.959074
 -0.972085
 -1.1646e-34
 -0.776776
 -0.752047
 -0.529272
 -0.962617
 -0.503581
 -0.924874
 -0.913683
  0.0
 -0.0011216
```

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

Out[106]: 8001x1 Array{Float64,2}:
          -0.985619
          -0.982691
          -0.981522
          -0.98115
          -0.981142
          -0.980868
          -0.980867
          -0.980801
          -0.979438
          -0.979381
          -0.979315
          -0.97927
          -0.97919
           ⋮
           5.55846e-17
           5.57062e-17
           5.57334e-17
           5.57459e-17
           5.57465e-17
           5.58191e-17
           5.58369e-17
           5.67605e-17
           5.73429e-17
           5.83531e-17
           6.61924e-17
           6.85983e-17

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

```
Out[107]: 45929x1 Array{Float64,2}:
           -0.999204
           -0.99309
           -0.989635
           -0.989354
           -0.986951
           -0.985619
           -0.985586
           -0.985568
           -0.98548
           -0.985301
           -0.984423
           -0.98427
           -0.98317
            ⋮
            7.41993e-17
            7.42088e-17
            7.65502e-17
            7.85836e-17
            8.88438e-17
            8.88468e-17
            8.90394e-17
            8.90569e-17
            1.10945e-16
            1.11217e-16
            1.21753e-16
            1.2328e-16
```

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

Out[108]: 43854x1 Array{Float64,2}:
          −0.999204
          −0.99309
          −0.989635
          −0.989354
          −0.986951
          −0.985619
          −0.985586
          −0.985568
          −0.98548
          −0.985301
          −0.984423
          −0.98427
          −0.98317
           ⋮
          −1.12625e−35
          −1.10536e−35
          −7.23354e−36
          −7.22508e−36
          −7.2166e−36
          −7.19638e−36
          −7.19638e−36
          −4.91411e−36
          −7.61803e−65
          −2.53068e−66
          −1.43549e−66
          −8.89359e−67

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

Out[109]: 1344x1 Array{Float64,2}:
 1.59792e-51
 1.60429e-51
 1.60574e-51
 1.60617e-51
 2.45438e-51
 3.20065e-51
 3.20071e-51
 3.21147e-51
 4.00532e-51
 6.46485e-51
 8.01063e-51
 1.09353e-50
 1.13972e-50
 ⋮
 7.41993e-17
 7.42088e-17
 7.65502e-17
 7.85836e-17
 8.88438e-17
 8.88468e-17
 8.90394e-17
 8.90569e-17
 1.10945e-16
 1.11217e-16
 1.21753e-16
 1.2328e-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}:
 0.266444 1.46678 0.677667 1.76589 … 0.563667 1.84611 0.778889

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

Out[112]: 1x200 Array{Float64,2}:
 0.175 1.67 0.53 1.865 1.655 0.325 … 0.985 0.985 0.63 1.8 0.95
 5

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

Out[113]: 1x200 Array{Float64,2}:
 0.16 1.495 0.65 1.78 1.615 0.37 … 0.51 1.03 1.03 0.68 1.87
 0.915

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

Out[114]: 1x200 Array{Float64,2}:
 0.24 1.465 0.715 1.78 1.57 0.34 … 1.09 1.09 0.585 1.815 0.88

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

```
Out[115]: 1x200 Array{Float64,2}:
           0.26  1.515  0.61  1.765  1.605  0.45  …  0.39  1.2  1.2  0.56  1.85  0.
          74
```

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

```
Out[116]: 1x200 Array{Float64,2}:
           0.3  1.39  0.74  1.735  1.585  0.385  …  1.265  1.265  0.515  1.87  0.69
```

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

```
Out[117]: 1x200 Array{Float64,2}:
           0.271375  1.46175  0.68125  1.7635  …  1.18025  0.559875  1.84675  0.771
          75
```

```
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)
```