In [1]:
```
include("/home/nicole/Jupyter/SSBRJ/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/0.1/G/4
```

/home/nicole/Jupyter/JG3/Data/0.1/G/4

In [4]:
```
;ls
```
```
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
GenNF.txt
PedAll.txt
Phe.txt
PheAll.txt
all.ID
genotype.ID
meanOfSNPGAll
meanOfSNPGG0
meanOfSNPGG1
```

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 G
          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   = 0.871
vG     = 7.839
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
2590.042824 seconds (23.04 G allocations: 723.607 GB, 7.44% gc time)
```

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

Out[32]:
```
2-element Array{Float64,1}:
 9.17485
 3.05736
```

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

Out[33]: 3.057357344406668

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

Out[34]: 6.1161060308234125

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

Out[35]: 200-element Array{Float64,1}:
          0.220894
          0.437354
          0.166458
          0.0519119
          0.0126312
          0.135817
          0.0725163
          0.112237
         -0.00852127
         -0.0499239
          0.121141
          0.104589
          0.21034
          ⋮
          0.00925363
          0.00775299
         -0.135443
         -0.109457
          0.123448
         -0.111159
         -0.0831058
          0.147872
         -0.0818553
          0.176903
         -0.175547
          0.0856299

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 = 0.526
          SSBRJC from Gibbs - all.ID : regression of TBV on GEBV = 0.250

Out[39]: 0.526345537826908

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

Out[40]: 10.450745875

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

Out[41]: 1.542097075218765

```
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 =  0.874
         SSBRJC from Gibbs - genotype.ID  : regression of TBV on GEBV =  0.827
```

Out[42]: 0.87357857351966

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

Out[43]: 11.171621444444444

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

Out[44]: 3.6101845883469545

```
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 =  0.421
         SSBRJC from Gibbs - noGenotype.ID  : regression of TBV on GEBV =  0.199
```

Out[45]: 0.4208595969621493

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

Out[46]: 10.284389974358973

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

Out[47]: 1.0648461106507214

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 =  0.702
SSBRJC from Gibbs - G0.ID : regression of TBV on GEBV =  0.536
```

Out[48]: 0.7024857401170582

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

Out[49]: 9.452027

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

Out[50]: 0.2001273018168711

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 =  0.316
SSBRJC from Gibbs - G1.ID : regression of TBV on GEBV =  0.124
```

Out[51]: 0.3164645899037169

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

Out[52]: 10.110348125

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

Out[53]: 0.8663550537900654

```
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 =  0.326
SSBRJC from Gibbs - G2.ID : regression of TBV on GEBV =  0.127
```

Out[54]: 0.32642617489683706

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

Out[55]: 10.389132875000001

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

Out[56]: 1.2061684622716284

```
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 =  0.320
SSBRJC from Gibbs - G3.ID : regression of TBV on GEBV =  0.123
```

Out[57]: 0.3203819452045318

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

Out[58]: 10.644380375

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

Out[59]: 1.4795433763986687

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 =  0.341
SSBRJC from Gibbs – G4.ID : regression of TBV on GEBV =  0.135
```

Out[60]: 0.3410263787528397

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

Out[61]: 10.913760875

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

Out[62]: 1.8573646528641612

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 =  0.872
SSBRJC from Gibbs – G5.ID : regression of TBV on GEBV =  0.829
```

Out[63]: 0.8718341700069467

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

Out[64]: 11.194825999999999

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

Out[65]: 3.6430236041711956

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 =  0.837
SSBRJC from Gibbs - G0.Genotype.ID : regression of TBV on GEBV =  0.759
```

Out[66]: 0.8366238883373366

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

Out[67]: 10.763530000000001

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

Out[68]: 2.8996669127928367

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 =  0.874
SSBRJC from Gibbs - G1.Genotype.ID : regression of TBV on GEBV =  0.830
```

Out[69]: 0.874340843786075

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

Out[70]: 10.638454999999997

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

Out[71]: 2.9649351057733044

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 =  0.868
SSBRJC from Gibbs - G2.Genotype.ID : regression of TBV on GEBV =  0.863
```

Out[72]: 0.8676213121533348

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

Out[73]: 10.915555

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

Out[74]: 3.339287442273399

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 =  0.894
SSBRJC from Gibbs - G3.Genotype.ID : regression of TBV on GEBV =  0.884
```

Out[75]: 0.893606868421862

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

Out[76]: 11.159884999999997

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

Out[77]: 3.533511404180818

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 =  0.881
SSBRJC from Gibbs - G4.Genotype.ID : regression of TBV on GEBV =  0.892
```

Out[78]: 0.881286935162782

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

Out[79]: 11.4525

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

Out[80]: 3.9999614437447644

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 =  0.872
SSBRJC from Gibbs - G5.Genotype.ID : regression of TBV on GEBV =  0.829
```

Out[81]: 0.8718341700069467

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]: 11.194825999999999

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

Out[85]: 3.6430236041711956

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 =  0.682
SSBRJC from Gibbs - G0.noGenotype.ID : regression of TBV on GEBV =  0.540
```

Out[86]: 0.6815165882522858

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

Out[87]: 9.418398717948719

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

Out[88]: 0.130908337432872

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 =  0.303
SSBRJC from Gibbs - G1.noGenotype.ID : regression of TBV on GEBV =  0.119
```

Out[89]: 0.3031064773139319

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

Out[90]: 10.096806923076924

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

Out[91]: 0.812545308867418

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", cor1!
@printf("SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor15
```

```
SSBRJC from Gibbs - G2.noGenotype.ID : correlation =  0.314
SSBRJC from Gibbs - G2.noGenotype.ID : regression of TBV on GEBV =  0.122
```

Out[92]: 0.31359332232154474

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

Out[93]: 10.375634871794873

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

Out[94]: 1.1514731038100448

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", cor1(
@printf("SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV = !
JCAll = cor16
```

```
SSBRJC from Gibbs - G3.noGenotype.ID : correlation =  0.307
SSBRJC from Gibbs - G3.noGenotype.ID : regression of TBV on GEBV =  0.117
```

Out[95]: 0.3070375905072054

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

Out[96]: 10.631162307692307

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

Out[97]: 1.4268775295324594

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", cor1
@printf("SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV = 9
JCAll = cor17
```

```
SSBRJC from Gibbs - G4.noGenotype.ID : correlation =   0.328
SSBRJC from Gibbs - G4.noGenotype.ID : regression of TBV on GEBV =   0.129
```

Out[98]: 0.3276284318397311

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

Out[99]: 10.899947051282052

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

Out[100]: 1.8024262736108128

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]: 10.899947051282052

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

Out[103]: 1.8024262736108128

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

```
Out[104]: SSBR.NumSSBayes(54893,45893,9000,40000,39000,1000,200)
```

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

```
Out[105]: 45893x1 Array{Float64,2}:
           5.45266e-17
          -0.631718
          -0.00474188
          -0.918126
          -0.504014
          -0.546338
           1.5167e-18
          -0.76977
          -0.752192
          -0.813909
           1.29781e-19
          -0.751902
          -0.971893
           ⋮
          -0.973802
          -0.00117096
          -0.756733
          -0.756022
          -0.757472
          -0.00234055
          -0.962826
          -0.603242
          -0.918314
          -0.878378
          -0.00359502
          -0.000580881
```

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

Out[106]: 8001x1 Array{Float64,2}:
          -0.986993
          -0.985866
          -0.984183
          -0.982924
          -0.981633
          -0.981292
          -0.981241
          -0.981189
          -0.981167
          -0.980932
          -0.980872
          -0.980424
          -0.979796
           ⋮
           5.55332e-17
           5.55355e-17
           5.55599e-17
           5.55603e-17
           5.55842e-17
           5.55846e-17
           5.57683e-17
           5.58206e-17
           5.59171e-17
           5.62571e-17
           5.73361e-17
           8.13853e-17

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

Out[107]: 45893x1 Array{Float64,2}:
          −0.987798
          −0.986993
          −0.986881
          −0.986735
          −0.985928
          −0.985866
          −0.985598
          −0.985383
          −0.984929
          −0.984203
          −0.984183
          −0.983621
          −0.983618
           ⋮
           5.74992e−17
           5.76943e−17
           6.17928e−17
           6.29071e−17
           6.68468e−17
           6.78908e−17
           8.13853e−17
           8.79606e−17
           8.89031e−17
           9.81802e−17
           1.07219e−16
           1.07751e−16

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

Out[108]: 43922x1 Array{Float64,2}:
          -0.987798
          -0.986993
          -0.986881
          -0.986735
          -0.985928
          -0.985866
          -0.985598
          -0.985383
          -0.984929
          -0.984203
          -0.984183
          -0.983621
          -0.983618
            ⋮
          -7.21449e-36
          -7.21236e-36
          -7.21236e-36
          -7.20395e-36
          -7.1951e-36
          -2.1823e-51
          -3.86994e-66
          -5.46195e-67
          -3.4091e-67
          -1.78216e-67
          -1.77798e-67
          -1.70455e-67

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

```
Out[109]:  1316x1 Array{Float64,2}:
             8.00732e-52
             8.00733e-52
             8.02615e-52
             1.53532e-51
             1.59763e-51
             1.60146e-51
             1.60147e-51
             1.60194e-51
             1.60241e-51
             1.60241e-51
             1.6048e-51
             1.60523e-51
             1.60618e-51
             ⋮
             5.74992e-17
             5.76943e-17
             6.17928e-17
             6.29071e-17
             6.68468e-17
             6.78908e-17
             8.13853e-17
             8.79606e-17
             8.89031e-17
             9.81802e-17
             1.07219e-16
             1.07751e-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}:
            0.202333  1.71433  0.470778  1.898  …  0.728  0.903889  1.71889  1.02322
```

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

```
Out[112]:  1x200 Array{Float64,2}:
            0.22  1.74  0.425  1.915  1.745  0.37  …  0.825  0.82  0.77  1.83  0.965
```

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

```
Out[113]:  1x200 Array{Float64,2}:
            0.16  1.69  0.535  1.87  1.62  0.32  0.71  …  0.8  0.785  0.835  1.755
            1.03
```

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

```
Out[114]:  1x200 Array{Float64,2}:
            0.215  1.73  0.48  1.91  1.725  0.365  …  0.72  0.715  0.95  1.745  1.01
```

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

Out[115]: 1x200 Array{Float64,2}:
0.205   1.69   0.485   1.9   1.74   0.41   …   0.755   0.75   0.835   1.755   1.02

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

Out[116]: 1x200 Array{Float64,2}:
0.22   1.735   0.445   1.905   1.735   …   0.37   0.72   0.71   0.955   1.67   1.03

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

Out[117]: 1x200 Array{Float64,2}:
0.202125   1.714   0.470375   1.89775   …   0.7245   0.90825   1.71487   1.02475

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)`